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(54) Title: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR ANALYSIS OF GENE EXPRESSION IN HUMAN BONE MARROW

(57) Abstract: A single exon nucleic acid microarray comprising a plurality of single exon nucleic acid probes for measuring gene expression in a sample derived from human bone marrow is described. Also described are single exon nucleic acid probes expressed in the bone marrow and their use in methods for detecting gene expression.

HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL
FOR ANALYSIS OF GENE EXPRESSION IN HUMAN BONE MARROW

CROSS REFERENCE TO RELATED APPLICATIONS

5

The present application is a continuation-in-part of U.S. patent application serial nos. 09/632,366, filed August 3, 2000 and 09/608,408, filed June 30, 2000; claims the benefit under 35 U.S.C. s 119(e) of U.S. provisional patent application serial nos. 60/236,359, filed September 27, 10 2000, 60/234,687, filed September 21, 2000, 60/207,456, filed May 26, 2000, and 60/180,312, filed February 4, 2000; and further claims the benefit under 35 U.S.C. s 119(a) of UK patent application no. 0024263.6, filed October 4, 2000, 15 the disclosures of which are incorporated herein by reference in their entireties.

REFERENCE TO SEQUENCE LISTING AND INCORPORATION BY
REFERENCE THEREOF

20

The present application includes a Sequence Listing in electronic format, filed pursuant to PCT Administrative Instructions 801 - 806 on a single CD-R disc, in triplicate, containing a file named pto_BONE_MARROW.txt, 25 created 24 January 2001, having 26,421,347 bytes. The Sequence Listing contained in said file on said disc is incorporated herein by reference in its entirety.

Field of the Invention

30

The present invention relates to genome-derived single exon microarrays useful for verifying the expression of regions of genomic DNA predicted to encode protein. In particular, the present invention relates to unique genome- 35 derived single exon nucleic acid probes expressed in human

bone marrow and single exon nucleic acid microarrays that include such probes.

Background of the Invention

5 For almost two decades following the invention of general techniques for nucleic acid sequencing, Sanger et al., *Proc. Natl. Acad. Sci. USA* 70(4):1209-13 (1973); Gilbert et al., *Proc. Natl. Acad. Sci. USA* 70(12):3581-4 (1973), these techniques were used principally as tools to
10 further the understanding of proteins - known or suspected - about which a basic foundation of biological knowledge had already been built. In many cases, the cloning effort that preceded sequence identification had been both informed and directed by that antecedent
15 biological understanding.

 For example, the cloning of the T cell receptor for antigen was predicated upon its known or suspected cell type-specific expression, by its suspected membrane association, and by the predicted assembly of its gene via
20 T cell-specific somatic recombination. Subsequent sequencing efforts at once confirmed and extended understanding of this family of proteins. Hedrick et al., *Nature* 308(5955):153-8 (1984).

 More recently, however, the development of high
25 throughput sequencing methods and devices, in concert with large public and private undertakings to sequence the human and other genomes, has altered this investigational paradigm: today, sequence information often precedes understanding of the basic biology of the encoded protein
30 product.

 One of the approaches to large-scale sequencing is predicated upon the proposition that expressed sequences - that is, those accessible through isolation of mRNA - are of greatest initial interest. This "expressed
35 sequence tag" ("EST") approach has already yielded vast

amounts of sequence data (see for example Adams *et al.*,
Science 252:1651 (1991); Williamson, *Drug Discov. Today*
4:115 (1999)). For nucleic acids sequenced by this
approach, often the only biological information that is
5 known *a priori* with any certainty is the likelihood of
biologic expression itself. By virtue of the species and
tissue from which the mRNA had originally been obtained,
most such sequences are also annotated with the identity of
the species and at least one tissue in which expression
10 appears likely.

More recently, the pace of genomic sequencing has
accelerated dramatically. When genomic DNA serves as the
initial substrate for sequencing efforts, expression cannot
be presumed; often the only *a priori* biological information
15 about the sequence includes the species and chromosome (and
perhaps chromosomal map location) of origin.

With the ever-accelerating pace of sequence
accumulation by directed, EST, and genomic sequencing
approaches – and in particular, with the accumulation of
20 sequence information from multiple genera, from multiple
species within genera, and from multiple individuals within
a species – there is an increasing need for methods that
rapidly and effectively permit the functions of nucleic
sequences to be elucidated. And as such functional
25 information accumulates, there is a further need for
methods of storing such functional information in
meaningful and useful relationship to the sequence itself;
that is, there is an increasing need for means and
apparatus for annotating raw sequence data with known or
30 predicted functional information.

Although the increase in the pace of genomic
sequencing is due in large part to technological changes in
sequencing strategies and instrumentation, Service, *Science*
280:995 (1998); Pennisi, *Science* 283: 1822-1823 (1999),
35 there is an important functional motivation as well.

While it was understood that the EST approach would rarely be able to yield sequence information about the noncoding portions of the genome, it now also appears the EST approach is capable of capturing only a fraction of
5 a genome's actual expression complexity.

For example, when the *C. elegans* genome was fully sequenced, gene prediction algorithms identified over 19,000 potential genes, of which only 7,000 had been found by EST sequencing. *C. elegans* Sequencing Consortium,
10 *Science* 282:2012 (1998). Analogously, the recently completed sequence of chromosome 2 of *Arabidopsis* predicts over 4000 genes, Lin et al., *Nature*, 402:761 (1999), of which only about 6% had previously been identified via EST sequencing efforts. Although the human genome has the
15 greatest depth of EST coverage, it is still woefully short of surrendering all of its genes. One recent estimate suggests that the human genome contains more than 146,000 genes, which would at this point leave greater than half of the genes undiscovered. It is now predicted that many
20 genes, perhaps 20 to 50%, will only be found by genomic sequencing.

There is, therefore, a need for methods that permit the functional regions of genomic sequence -- and most importantly, but not exclusively, regions that
25 function to encode genes -- to be identified.

Much of the coding sequence of the human genome is not homologous to known genes, making detection of open reading frames ("ORFs") and predictions of gene function difficult. Computational methods exist for predicting
30 coding regions in eukaryotic genomes. Gene prediction programs such as GRAIL and GRAIL II, Uberbacher et al., *Proc. Natl. Acad. Sci. USA* 88(24):11261-5 (1991); Xu et al., *Genet. Eng.* 16:241-53 (1994); Uberbacher et al., *Methods Enzymol.* 266:259-81 (1996); GENEFINDER, Solovyev et
35 al., *Nucl. Acids. Res.* 22:5156-63 (1994); Solovyev et al.,

Ismb 5:294-302 (1997); and GENESCAN, Burge *et al.*, *J. Mol. Biol.* 268:78-94 (1997), predict many putative genes without known homology or function. Such programs are known, however, to give high false positive rates. Burset *et al.*,
5 *Genomics* 34:353-367 (1996). Using a consensus obtained by a plurality of such programs is known to increase the reliability of calling exons from genomic sequence. Ansari-Lari *et al.*, *Genome Res.* 8(1):29-40 (1998)

Identification of functional genes from genomic
10 data remains, however, an imperfect art. For example, in reporting the full sequence of human chromosome 21, the Chromosome 21 Mapping and Sequencing Consortium reports that prior bioinformatic estimates of human gene number may need to be revised substantially downwards. *Nature*
15 405:311-199 (2000); Reeves, *Nature* 405:283-284 (2000).

Thus, there is a need for methods and apparatus that permit the functions of the regions identified bioinformatically - and specifically, that permit the expression of regions predicted to encode protein - readily
20 to be confirmed experimentally.

Recently, the development of nucleic acid microarrays has made possible the automated and highly parallel measurement of gene expression. Reviewed in Schena (ed.), DNA Microarrays : A Practical Approach
25 (Practical Approach Series), Oxford University Press (1999) (ISBN: 0199637768); *Nature Genet.* 21(1)(suppl):1 - 60 (1999); Schena (ed.), Microarray Biochip: Tools and Technology, Eaton Publishing Company/BioTechniques Books Division (2000) (ISBN: 1881299376).

30 It is common for microarrays to be derived from cDNA/EST libraries, either from those previously described in the literature, such as those from the I.M.A.G.E. consortium, Lennon *et al.*, *Genomics* 33(1):151-2 (1996), or from the construction of "problem specific" libraries
35 targeted at a particular biological question, R.S. Thomas

et al., *Cancer Res.* (in press). Such microarrays by definition can measure expression only of those genes found in EST libraries, and thus have not been useful as probes for genes discovered solely by genomic sequencing.

5 The utility of using whole genome nucleic acid microarrays to answer certain biological questions has been demonstrated for the yeast *Saccharomyces cerevisiae*. De Risi et al., *Science* 278:680 (1997). The vast majority of yeast nuclear genes, approximately 95% however, are single
10 exon genes, i.e., lack introns, Lopez et al., *RNA* 5:1135-1137 (1999); Goffeau et al., *Science* 274:563-67 (1996), permitting coding regions more readily to be identified. Whole genome nucleic acid microarrays have not generally
15 eukaryotic genomes, and in particular from those averaging more than one intron per gene.

 Because bone marrow is the tissue in which blood cells originate, diseases of the bone marrow are a significant cause of human morbidity and mortality.
20 Increasingly, genetic factors are being found that contribute to predisposition, onset, and/or aggressiveness of most, if not all, of these diseases. Although mutations in single genes have in some cases been identified as causal - notably in the thalassemias and sickle cell anemia
25 - disorders of the bone marrow are, for the most part, believed to have polygenic etiologies. There is a need for methods and apparatus that permit prediction, diagnosis and prognosis of diseases of the bone marrow, particularly those diseases with polygenic etiology.

30

Summary of the Invention

 The present invention solves these and other problems in the art by providing methods and apparatus for
35 predicting, confirming, and displaying functional

information derived from genomic sequence. The present invention also provides apparatus for verifying the expression of putative genes identified within genomic sequence.

5 In particular, the invention provides novel genome-derived single exon nucleic acid microarrays useful for verifying the expression of putative genes identified within genomic sequence.

The present invention also provides compositions
10 and kits for the ready production of nucleic acids identical in sequence to, or substantially identical in sequence to, probes on the genome-derived single exon microarrays of the present invention.

Accordingly, in a first aspect of the invention,
15 there is provided a spatially-addressable set of single exon nucleic acid probes for measuring gene expression in a sample derived from human bone marrow, comprising a plurality of single exon nucleic acid probes according to any one of the nucleotide sequences set out in SEQ ID NOs:
20 1 - 13,114 or a complementary sequence, or a portion of such a sequence.

By plurality is meant at least two, suitably at least 20, most suitably at least 100, preferably at least 1000 and, most preferably, upto 5000.

25 In one embodiment of the first aspect, each of said plurality of probes is separately and addressably amplifiable.

In an alternative embodiment, each of said plurality of probes is separately and addressably
30 isolatable from said plurality.

In a preferred embodiment, each of said plurality of probes is amplifiable using at least one common primer. Preferably, each of said plurality of probes is amplifiable using a first and a second common primer.

35 In yet another embodiment, said set of single

exon nucleic acid probes comprises between 50 - 20,000 probes, for example, 50 - 5000.

Suitably, said set of single exon nucleic acid probes comprises at least 50 - 1000 discrete single exon nucleic acid probes having a sequence as set out in any of SEQ ID NOS.: 1 - 26,012 or a complimentary sequence, or a portion of such a sequence.

Preferably, the average length of the single exon nucleic acid probes is between 200 and 500 bp. It is preferred that the average length should be at least 200bp, suitably at least 250bp, most suitably at least 300bp, preferably at least 400bp and, most preferably, 500 bp.

In another embodiment, the single exon nucleic acid probes lack prokaryotic and bacteriophage vector sequence. It is preferred that at least 50%, suitably at least 60%, most suitably at least 70%, preferably at least 75%, more preferably at least 80, 85, 90, 95 or 99% of said single exon nucleic acid probes lack prokaryotic and bacteriophage vector sequence.

In another preferred embodiment, said single exon nucleic acid lack homopolymeric stretches of A or T. It is preferred that at least 50%, suitably at least 60%, most suitably at least 70%, preferably at least 75%, more preferably at least 80, 85, 90, 95 or 99% of said single exon nucleic acid probes lack homopolymeric stretches of A or T.

Preferably, a spatially-addressable set of single exon nucleic acid probes in accordance with the first aspect of the invention is addressably disposed upon a substrate.

Suitable substrates include a filter membrane which may, preferably, be nitrocellulose or nylon. The nylon may preferably, be positively-charged. Other suitable substrates include glass, amorphous silicon, crystalline silicon, and plastic. Further suitable materials include

polymethylacrylic, polyethylene, polypropylene,
polyacrylate, polymethylmethacrylate, polyvinylchloride,
polytetrafluoroethylene, polystyrene, polycarbonate,
polyacetal, polysulfone, celluloseacetate,
5 cellulosenitrate, nitrocellulose, and mixtures thereof.

In a second aspect of the invention, there is provided a microarray comprising a spatially addressable set of single exon nucleic acid probes in accordance with the first aspect of the invention.

10 In one embodiment, a genome-derived single-exon microarray is packaged together with such an ordered set of amplifiable probes corresponding to the probes, or one or more subsets of probes, thereon. In alternative embodiments, the ordered set of amplifiable probes is
15 packaged separately from the genome-derived single exon microarray.

In another aspect, the invention provides genome-derived single exon nucleic acid probes useful for gene expression analysis, and particularly for gene expression
20 analysis by microarray. In particular embodiments of this aspect, the present invention provides human single-exon probes that include specifically-hybridizable fragments of SEQ ID Nos. 13,115 - 26,012, wherein the fragment hybridizes at high stringency to an expressed human gene.
25 In particular embodiments, the invention provides single exon probes comprising SEQ ID Nos. 1 - 13,114.

Accordingly, in a third aspect of the invention, there is provided a single exon nucleic acid probe for measuring human gene expression in a sample derived from
30 human bone marrow which is a nucleic acid molecule comprising a nucleotide sequence as set out in any of SEQ ID NOS.: 1 - 13,114 or a complementary sequence or a fragment thereof wherein said probe hybridizes at high stringency to a nucleic acid expressed in the human bone
35 marrow.

In one embodiment, a single exon nucleic acid probe in accordance with the third aspect comprises a nucleotide sequence as set out in any of SEQ ID NOs.: 13,115 - 26,012 or a complementary sequence or a fragment thereof.

In a fourth aspect of the invention, there is provided a single exon nucleic acid probe for measuring human gene expression in a sample derived from human bone marrow which is a nucleic acid molecule having a sequence encoding a peptide comprising a peptide sequence as set out in any of SEQ ID NOs.: 26,013 - 38,628 or a complementary sequence or a fragment thereof wherein said probe hybridizes at high stringency to a nucleic acid expressed in the human bone marrow.

Preferably, a single exon nucleic acid probe in accordance with the third or fourth aspects of the invention comprises between at least 15 and 50 contiguous nucleotides of said SEQ ID NO:. It is preferred that the single exon nucleic acid probe comprises at least 15, suitably at least 20, more suitably at least 25 or preferably at least 50 contiguous nucleotides of said SEQ ID NO:.

In another preferred embodiment, a single exon nucleic acid probe in accordance with the third or fourth aspects of the invention is between 3kb and 25kb in length. It is preferred that said probe is no more than 3kb, suitably no more than 5kb, more suitably no more than 10kb, preferably 15kb, more preferably 20kb or, most preferably, no more than 20kb in length.

Preferably, a single exon nucleic acid probe in accordance with either the fifth or sixth aspect of the invention is DNA, preferably single-stranded DNA, RNA or PNA.

In another embodiment of either the third or fourth aspect of the invention, a single exon nucleic acid

probe is detectably labeled. Suitable detectable labels include a radionuclide, a fluorescent label or a first member of a specific binding pair. Suitable fluorescent labels include dyes such as cyanine dyes, preferably Cy3 and Cy5 although other suitable dyes will be known to those skilled in the art.

In a particularly preferred embodiment, a single exon nucleic acid probe in accordance with either the third or fourth aspect of the invention lacks prokaryotic and bacteriophage vector sequence. In yet another embodiment, a single exon nucleic acid probe in accordance with either the third or fourth aspect of the invention lacks homopolymeric stretches of A or T.

In a fifth aspect of the invention, there is provided an amplifiable nucleic acid composition, comprising:

the single exon nucleic acid probe in accordance with either of the third or fourth aspects of the invention; and at least one nucleic acid primer;

wherein said at least one primer is sufficient to prime enzymatic amplification of said probe.

In an sixth aspect of the invention, there is provided a method of measuring gene expression in a sample derived from human bone marrow, comprising:

contacting the single exon microarray in accordance with the second aspect of the invention, with a first collection of detectably labeled nucleic acids, said first collection of nucleic acids derived from mRNA of human bone marrow; and then

measuring the label detectably bound to each probe of said microarray.

In a seventh aspect of the invention, there is provided a method of identifying exons in a eukaryotic genome, comprising:

algorithmically predicting at least one exon from

genomic sequence of said eukaryote; and then
detecting specific hybridization of detectably
labeled nucleic acids to a single exon probe,
wherein said detectably labeled nucleic acids are
5 derived from mRNA from the bone marrow of said eukaryote,
said probe is a single exon probe having a fragment
identical in sequence to, or complementary in sequence to,
said predicted exon, said probe is included within a single
exon microarray in accordance with the first aspect of the
10 invention, and said fragment is selectively hybridizable at
high stringency.

In a eighth aspect of the invention, there is
provided a method of assigning exons to a single gene,
comprising:
15 identifying a plurality of exons from genomic
sequence in accordance with the seventh aspect of the
invention; and then
measuring the expression of each of said exons in
a plurality of tissues and/or cell types using
20 hybridization to single exon microarrays having a probe
with said exon,
wherein a common pattern of expression of said
exons in said plurality of tissues and/or cell types
indicates that the exons should be assigned to a single
25 gene.

In an ninth aspect of the invention, there is
provided a nucleic acid sequence as set out in any of SEQ
ID NOs: 1 - 26,012 wherein said sequence encodes a peptide.

In a tenth aspect of the invention, there is
30 provided a peptide encoded by a sequence comprising a
sequence as set out in any of SEQ ID NOs: 13,115 - 26,012,
or a complementary sequence or coding portion thereof.

In a preferred embodiment, a peptide may be
encoded by a sequence comprising a sequence set out in any
35 of SEQ ID NOS.: 1 - 13,114.

In a further aspect, the invention provides peptides comprising an amino acid sequence translated from the DNA fragments, said amino acid sequences comprising SEQ ID NOS.: 26,013 - 38,628.

5 Accordingly in a eleventh aspect of the invention there is provided a peptide comprising a sequence as set out in any of SEQ ID NOS: 26,013 - 38,628, or fragment thereof.

 In another aspect, the invention provides means
10 for displaying annotated sequence, and in particular, for displaying sequence annotated according to the methods and apparatus of the present invention. Further, such display can be used as a preferred graphical user interface for electronic search, query, and analysis of such annotated
15 sequence.

Detailed Description of the Invention

20 Definitions

 As used herein, the term "microarray" and phrase "nucleic acid microarray" refer to a substrate-bound collection of plural nucleic acids, hybridization to each of the plurality of bound nucleic acids being separately
25 detectable. The substrate can be solid or porous, planar or non-planar, unitary or distributed.

 As so defined, the term "microarray" and phrase "nucleic acid microarray" include all the devices so called in Schena (ed.), DNA Microarrays: A Practical Approach
30 (Practical Approach Series), Oxford University Press (1999) (ISBN: 0199637768); Nature Genet. 21(1)(suppl):1 - 60 (1999); and Schena (ed.), Microarray Biochip: Tools and Technology, Eaton Publishing Company/BioTechniques Books Division (2000) (ISBN: 1881299376). As so defined, the
35 term "microarray" and phrase "nucleic acid microarray"

further include substrate-bound collections of plural nucleic acids in which the nucleic acids are distributably disposed on a plurality of beads, rather than on a unitary planar substrate, as is described, *inter alia*, in Brenner
5 *et al.*, *Proc. Natl. Acad. Sci. USA* 97(4):166501670 (2000); in such case, the term "microarray" and phrase "nucleic acid microarray" refer to the plurality of beads in aggregate.

As used herein with respect to a nucleic acid
10 microarray, the term "probe" refers to the nucleic acid that is, or is intended to be, bound to the substrate; in such context, the term "target" thus refers to nucleic acid intended to be bound thereto by Watson-Crick complementarity. As used herein with respect to solution
15 phase hybridization, the term "probe" refers to the nucleic acid of known sequence that is detectably labeled.

As used herein, the expression "probe comprising SEQ ID NO.", and variants thereof, intends a nucleic acid probe, at least a portion of which probe has either (i) the
20 sequence directly as given in the referenced SEQ ID NO., or (ii) a sequence complementary to the sequence as given in the referenced SEQ ID NO., the choice as between sequence directly as given and complement thereof dictated by the requirement that the probe hybridize to mRNA.

25 As used herein, the term "open reading frame" and the equivalent acronym "ORF" refer to that portion of an exon that can be translated in its entirety into a sequence of contiguous amino acids i.e. a nucleic acid sequence that, in at least one reading frame, does not possess stop
30 codons; the term does not require that the ORF encode the entirety of a natural protein.

As used herein, the term "amplicon" refers to a PCR product amplified from human genomic DNA, containing the predicted exon.

35 As used herein the term "exon" refers to the

consensus prediction of the various exon and gene predicting algorithms i.e. a nucleic acid sequence bioinformatically predicted to encode a portion of a natural protein.

5 As used herein, the term "peptide" refers to a sequence of amino acids. The sequences referred to as PEPTIDE SEQ ID NOS.: are the predicted peptide sequences that would be translated from one of the exons, or a portion thereof set out in exon SEQ ID NOS.:. The codons
10 encoding the peptide are wholly contained within the exon.

 As used herein, a "portions" of a defined nucleotide sequence or sequences can be and, preferably, are fragments unique to that sequence or to one or a combination of those sequences. A fragment unique to a
15 nucleic acid molecule is one that is a signature for the larger nucleic acid molecule.

 As used herein, the phrase "expression of a probe" and its linguistic variants means that the ORF present within the probe, or its complement, is present
20 within a target mRNA.

 As used herein, "stringent conditions" refers to parameters well known to those skilled in the art. When a nucleic acid molecule is said to be hybridisable to another of a given sequence under "stringent conditions" it is
25 meant that it is homologous to the given sequence.

 As used herein, the phrase "specific binding pair" intends a pair of molecules that bind to one another with high specificity. Binding pairs are said to exhibit specific binding when they exhibit avidity of at least 10^7 ,
30 preferably at least 10^8 , more preferably at least 10^9 liters/mole. Nonlimiting examples of specific binding pairs are: antibody and antigen; biotin and avidin; and biotin and streptavidin.

 As used herein with respect to the visual display
35 of annotated genomic sequence, the term "rectangle" means

any geometric shape that has at least a first and a second border, wherein the first and second borders each are capable of mapping uniquely to a point of another visual object of the display.

5 As used herein, a "Mondrian" means a visual display in which a single genomic sequence is annotated with predicted and experimentally confirmed functional information.

10

Brief Description of the Drawings

The present invention is further illustrated with reference to the following non-limiting figures and
15 examples in which:

FIG. 1 illustrates a process for predicting functional regions from genomic sequence, confirming the functional activity of such regions experimentally, and associating and displaying the data so obtained in
20 meaningful and useful relationship to the original sequence data;

FIG. 2 further elaborates that portion of the process schematized in FIG. 1 for predicting functional regions from genomic sequence;

25 FIG. 3 illustrates a Mondrian visual display;

FIG. 4 presents a Mondrian showing a hypothetical annotated genomic sequence;

FIG. 5 is a histogram showing the distribution of ORF length and PCR products as obtained, with ORF length
30 shown in black and PCR product length shown in dotted lines;

FIG. 6 is a histogram showing the distribution, among exons predicted according to the methods described, of expression as measured using simultaneous two color
35 hybridization to a genome-derived single exon microarray.

The graph shows the number of sequence-verified products that were either not expressed ("0"), expressed in one or more but not all tested tissues ("1" - "9"), or expressed in all tissues tested ("10");

5 FIG. 7 is a pictorial representation of the expression of verified sequences that showed expression with signal intensity greater than 3 in at least one tissue, with: FIG. 7A showing the expression as measured by microarray hybridization in each of the 10 measured
10 tissues, and the expression as measured "bioinformatically" by query of EST, NR and SwissProt databases; with FIG. 7B showing the legend for display of physical expression (ratio) in FIG. 7A; and with FIG. 7C showing the legend for scoring EST hits as depicted in FIG. 7A;

15 FIG. 8 shows a comparison of normalized CY3 signal intensity for arrayed sequences that were identical to sequences in existing EST, NR and SwissProt databases or that were dissimilar (unknown), where black denotes the signal intensity for all sequence-verified products with a
20 BLAST Expect ("E") value of greater than $1e-30$ (1×10^{-30}) ("unknown") and a dotted line denotes sequence-verified spots with a BLAST expect ("E") value of less than $1e-30$ (1×10^{-30}) ("known");

FIG. 9 presents a Mondrian of BAC AC008172 (bases
25 25,000 to 130,000), containing the carbamyl phosphate synthetase gene (AF154830.1); and

FIG. 10 is a Mondrian of BAC A049839.

30 Methods and Apparatus for Predicting, Confirming,
Annotating, and Displaying Functional Regions From Genomic
Sequence Data

FIG. 1 is a flow chart illustrating in broad
35 outline a process for predicting functional regions from

genomic sequence, confirming and characterizing the functional activity of such regions experimentally, and then associating and displaying the information so obtained in meaningful and useful relationship to the original
5 sequence data.

The initial input into process 10 of the present invention is drawn from one or more databases 100 containing genomic sequence data. Because genomic sequence is usually obtained from subgenomic fragments, the sequence
10 data typically will be stored in a series of records corresponding to these subgenomic sequenced fragments. Some fragments will have been catenated to form larger contiguous sequences ("contigs"); others will not. A finite percentage of sequence data in the database will
15 typically be erroneous, consisting *inter alia* of vector sequence, sequence created from aberrant cloning events, sequence of artificial polylinkers, and sequence that was erroneously read.

Each sequence record in database 100 will
20 minimally contain as annotation a unique sequence identifier (accession number), and will typically be annotated further to identify the date of accession, species of origin, and depositor. Because database 100 can contain nongenomic sequence, each sequence will typically
25 be annotated further to permit query for genomic sequence. Chromosomal origin, optionally with map location, can also be present. Data can be, and over time increasingly will be, further annotated with additional information, in part through use of the present invention, as described below.
30 Annotation can be present within the data records, in information external to database 100 and linked to the records thereto, or through a combination of the two.

Databases useful as genomic sequence database 100 in the present invention include GenBank, and particularly
35 include several divisions thereof, including the

htgs(draft), NT (nucleotide, command line), and NR (nonredundant) divisions. GenBank is produced by the National Institutes of Health and is maintained by the National Center for Biotechnology Information (NCBI).

5 Databases of genomic sequence from species other than human, such as mouse, rat, Arabidopsis, *C. elegans*, *C. brigssii*, *Drosophila*, zebra fish, and other higher eukaryotic organisms will also prove useful as genomic sequence database 100.

10 Genomic sequence obtained by query of genomic sequence database 100 is then input into one or more processes 200 for identification of regions therein that are predicted to have a biological function as specified by the user. Such functions include, but are not limited to,
15 encoding protein, regulating transcription, regulating message transport after transcription into mRNA, regulating message splicing after transcription into mRNA, of regulating message degradation after transcription into mRNA, and the like. Other functions include directing
20 somatic recombination events, contributing to chromosomal stability or movement, contributing to allelic exclusion or X chromosome inactivation, and the like.

The particular genomic sequence to be input into process 200 will depend upon the function for which
25 relevant sequence is to be identified as well as upon the approach chosen for such identification. Process step 200 can be iterated to identify different functions within a given genomic region. In such case, the input often will be different for the several iterations.

30 Sequences predicted to have the requisite function by process 200 are then input into process 300, where a subset of the input sequences suitable for experimental confirmation is identified. Experimental confirmation can involve physical and/or bioinformatic
35 assay. Where the subsequent experimental assay is

bioinformatic, rather than physical, there are fewer constraints on the sequences that can be tested, and in this latter case therefore process 300 can output the entirety of the input sequence.

5 The subset of sequences output from process 300 is then used in process 400 for experimental verification and characterization of the function predicted in process 200, which experimental verification can, and often will, include both physical and bioinformatic assay.

10 Process 500 annotates the sequence data with the functional information obtained in the physical and/or bioinformatic assays of process 400. Such annotation can be done using any technique that usefully relates the functional information to the sequence, as, for example, by
15 incorporating the functional data into the sequence data record itself, by linking records in a hierarchical or relational database, by linking to external databases, by a combination thereof, or by other means well known within the database arts. The data can even be submitted for
20 incorporation into databases maintained by others, such as GenBank, which is maintained by NCBI.

As further noted in FIG. 1, additional annotation can be input into process 500 from external sources 600.

The annotated data is then displayed in process
25 800, either before, concomitantly with, or after optional storage 700 on nontransient media, such as magnetic disk, optical disc, magnetooptical disk, flash memory, or the like.

FIG. 1 shows that the experimental data output
30 from process 400 can be used in each preceding step of process 10: e.g., facilitating identification of functional sequences in process 200, facilitating identification of an experimentally suitable subset thereof in process 300, and facilitating creation of physical and/or informational
35 substrates for, and performance of subsequent assay, of

functional sequences in process 400.

Information from each step can be passed directly to the succeeding process, or stored in permanent or interim form prior to passage to the succeeding process.

5 Often, data will be stored after each, or at least a plurality, of such process steps. Any or all process steps can be automated.

FIG. 2 further elaborates the prediction of functional sequence within genomic sequence according to
10 process 200.

Genomic sequence database 100 is first queried 20 for genomic sequence.

The sequence required to be returned by query 20 will depend, in the first instance, upon the function to be
15 identified.

For example, genomic sequences that function to encode protein can be identified *inter alia* using gene prediction approaches, comparative sequence analysis approaches, or combinations of the two. In gene prediction
20 analysis, sequence from one genome is input into process 200 where at least one, preferably a plurality, of algorithmic methods are applied to identify putative coding regions. In comparative sequence analysis, by contrast, corresponding, e.g., syntenic, sequence from a plurality of
25 sources, typically a plurality of species, is input into process 200, where at least one, possibly a plurality, of algorithmic methods are applied to compare the sequences and identify regions of least variability.

The exact content of query 20 will also depend
30 upon the database queried. For example, if the database contains both genomic and nongenomic sequence, perhaps derived from multiple species, and the function to be determined is protein coding regions in human genomic sequence, the query will accordingly require that the
35 sequence returned be genomic and derived from humans.

Query 20 can also incorporate criteria that compel return of sequence that meets operative requirements of the subsequent analytical method. Alternatively, or in addition, such operative criteria can be enforced in subsequent preprocess step 24.

For example, if the function sought to be identified is protein coding, query 20 can incorporate criteria that return from genomic sequence database 100 only those sequences present within contigs sufficiently long as to have obviated substantial fragmentation of any given exon among a plurality of separate sequence fragments.

Such criteria can, for example, consist of a required minimal individual genomic sequence fragment length, such as 10 kb, more typically 20 kb, 30 kb, 40kb, and preferably 50 kb or more, as well as an optional further or alternative requirement that sequence from any given clone, such as a bacterial artificial chromosome ("BAC"), be presented in no more than a finite maximal number of fragments, such as no more than 20 separate pieces, more typically no more than 15 fragments, even more typically no more than about 10 - 12 fragments.

Results using the present invention have shown that genomic sequence from bacterial artificial chromosomes (BACs) is sufficient for gene prediction analysis according to the present invention if the sequence is at least 50 kb in length, and if additionally the sequence from any given BAC is presented in fewer than 15, and preferably fewer than 10, fragments. Accordingly, query 20 can incorporate a requirement that data accessioned from BAC sequencing be in fewer than 15, preferably fewer than 10, fragments.

An additional criterion that can be incorporated into the query can be the date, or range of dates, of sequence accession. Although the process has been described above as if genomic sequence database 100 were

static, it is of course understood that the genomic sequence databases need not be static, and indeed are typically updated on a frequent, even hourly, basis. Thus, as further described in Examples 1 and 2, *infra*, it is possible to query the database for newly added sequence, either newly added after an absolute date, or newly added relative to a prior analysis performed using the methods and apparatus of the present invention. In this way, the process herein described can incorporate a dynamic, temporal component.

One utility of such temporal limitation is to identify, from newly accessioned genomic sequence, the presence of novel genes, particularly those not previously identified by EST sequencing (or other sequencing efforts that are similarly based upon gene expression). As further described in Example 1, such an approach has shown that newly accessioned human genomic sequence, when analyzed for sequences that function to encode protein, readily identifies genes that are novel over those in existing EST and other expression databases. This makes the methods of the present invention extremely powerful gene discovery tools. And as would be appreciated, such gene discovery can be performed using genomic sequence from species other than human.

If query 20 incorporates multiple criteria, such as above-described, the multiple criteria can be performed as a series of separate queries or as a single query, depending in part upon the query language, the complexity of the query, and other considerations well known in the database arts.

If query 20 returns no genomic sequence meeting the query criteria, the negative result can be reported by process 22, and process 200 (and indeed, entire process 10) ended 23, as shown. Alternatively, or in addition to report and termination of the initial inquiry, a new query

20 can be generated that takes into account the initial negative result.

When query 20 returns sequence meeting the query criteria, the returned sequence is then passed to optional preprocessing 24, suitable and specific for the desired analytical approach and the particular analytical methods thereof to be used in process 25.

Preprocessing 24 can include processes suitable for many approaches and methods thereof, as well as processes specifically suited for the intended subsequent analysis.

Preprocessing 24 suitable for most approaches and methods will include elimination of sequence irrelevant to, or that would interfere with, the subsequent analysis. Such sequence includes repetitive sequence, such as Alu repeats and LINE elements, vector sequence, artificial sequence, such as artificial polylinkers, and the like. Such removal can readily be performed by identification and subsequent masking of the undesired sequence.

Identification can be effected by comparing the genomic sequence returned by query 20 with public or private databases containing known repetitive sequence, vector sequence, artificial sequence, and other artifactual sequence. Such comparison can readily be done using programs well known in the art, such as CROSS_MATCH, or by proprietary sequence comparison programs the engineering of which is well within the skill in the art.

Alternatively, or in addition, undesirable, including artifactual, sequence can be identified algorithmically without comparison to external databases and thereafter removed. For example, synthetic polylinker sequence can be identified by an algorithm that identifies a significantly higher than average density of known restriction sites. As another example, vector sequence can be identified by algorithms that identify nucleotide or

codon usage at variance with that of the bulk of the genomic sequence.

Once identified, undesired sequence can be removed. Removal can usefully be done by masking the
5 undesired sequence as, for example, by converting the specific nucleotide references to one that is unrecognized by the subsequent bioinformatic algorithms, such as "X". Alternatively, but at present less preferred, the undesired sequence can be excised from the returned genomic sequence,
10 leaving gaps.

Preprocessing 24 can further include selection from among duplicative sequences of that one sequence of highest quality. Higher quality can be measured as a lower percentage of, fewest number of, or least densely clustered
15 occurrence of ambiguous nucleotides, defined as those nucleotides that are identified in the genomic sequence using symbols indicating ambiguity. Higher quality can also or alternatively be valued by presence in the longest contig.

20 Preprocessing 24 can, and often will, also include formatting of the data as specifically appropriate for passage to the analytical algorithms of process 25. Such formatting can and typically will include, *inter alia*, addition of a unique sequence identifier, either derived
25 from the original accession number in genomic sequence database 100, or newly applied, and can further include additional annotation. Formatting can include conversion from one to another sequence listing standard, such as conversion to or from FASTA or the like, depending upon the
30 input expected by the subsequent process.

Preprocessing, which can be optional depending upon the function desired to be identified and the informational requirements of the methods for effecting such identification, is followed by sequence processing 25,
35 where sequences with the desired function are identified

within the genomic sequence.

As mentioned above, such functions can include, but are not limited to, encoding protein, regulating transcription, regulating message transport after
5 transcription into mRNA, regulating message splicing after transcription, of regulating message degradation, and the like. Other functions include directing somatic recombination events, contributing to chromosomal stability or movement, contributing to allelic exclusion or X
10 chromosome inactivation, or the like.

The methods of the present invention are particularly useful for gene discovery, that is, for identifying, from genomic sequence, regions that function to encode genes, and in a particularly useful embodiment,
15 for identifying regions that function to encode genes not hitherto identified by expression-based or directed cloning and sequencing. In conjunction with verification using the novel single exon microarrays of the present invention, as further described below, the methods herein described
20 become powerful gene discovery tools.

Accordingly, in a preferred embodiment of the present invention, process 25 is used to identify putative coding regions. Two preferred approaches in process 25 for identifying sequence that encodes putative genes are gene
25 prediction and comparative sequence analysis.

Gene prediction can be performed using any of a number of algorithmic methods, embodied in one or more software programs, that identify open reading frames (ORFs) using a variety of heuristics, such as GRAIL, DICTION, and
30 GENEFINDER. Comparative sequence analysis similarly can be performed using any of a variety of known programs that identify regions with lower sequence variability.

As further described in Example 1, below, gene finding software programs yield a range of results. For
35 the newly accessioned human genomic sequence input in

Example 1, for example, GRAIL identified the greatest percentage of genomic sequence as putative coding region, 2% of the data analyzed; GENEFINDER was second, calling 1%; and DICTION yielded the least putative coding region, with
5 0.8% of genomic sequence called as coding region.

Increased reliability can be obtained when consensus is required among several such methods. Although discussed herein particularly with respect to exon calling, consensus among methods will in general increase
10 reliability of predicting other functions as well.

Thus, as indicated by query 26, sequence processing 25, optionally with preprocessing 24, can be repeated with a different method, with consensus among such iterations determined and reported in process 27.

15 Process 27 compares the several outputs for a given input genomic sequence and identifies consensus among the separately reported results. The consensus itself, as well as the sequence meeting that consensus, is then stored in process 29a, displayed in process 29b, and/or output to
20 process 300 for subsequent identification of a subset thereof suitable for assay.

Multiple levels of consensus can be calculated and reported by process 27. For example, as further described in Example 1, *infra*, process 27 can report
25 consensus as between all specific pairs of methods of gene prediction, as consensus among any one or more of the pairs of methods of gene prediction, or as among all of the gene prediction algorithms used. Thus, in Example 1, process 27 reported that GRAIL and GENEFINDER programs agreed on 0.7%
30 of genomic sequence, that GRAIL and DICTION agreed on 0.5% of genomic sequence, and that the three programs together agreed on 0.25% of the data analyzed. Put another way, 0.25% of the genomic sequence was identified by all three of the programs as containing putative coding region.

35 Furthermore, consensus can be required among

different approaches to identifying a chosen function.

For example, if the function desired to be identified is coding of protein sequence, and a first used approach to exon calling is gene prediction, the process
5 can be repeated on the same input sequence, or subset thereof, with another approach, such as comparative sequence analysis. In such a case, where comparative sequence analysis follows gene prediction, the comparison can be performed not only on genomic nucleic acid sequence,
10 but additionally or alternatively can be performed on the predicted amino acid sequence translated from the ORFs prior identified by the gene prediction approach.

Although shown as an iterative process, the multiple analyses required to achieve consensus can be done
15 in series, in parallel, or some combination thereof.

Predicted functional sequence, optionally representing a consensus among a plurality of methods and approaches for determination thereof, is passed to process
300 for identification of a subset thereof for functional
20 assay.

In the preferred embodiment of the methods of the present invention, wherein the function sought to be identified is protein coding, process 300 is used to identify a subset thereof suitable for experimental
25 verification by physical and/or bioinformatic approaches.

For example, putative ORFs identified in process 200 can be classified, or binned, bioinformatically into putative genes. This binning can be based *inter alia* upon consideration of the average number of exons/gene in the
30 species chosen for analysis, upon density of exons that have been called on the genomic sequence, and other empirical rules. Thereafter, one or more among the gene-specific ORFs can be chosen for subsequent use in gene expression assay.

35 Where such subsequent gene expression assay uses

amplified nucleic acid, considerations such as desired amplicon length, primer synthesis requirements, putative exon length, sequence GC content, existence of possible secondary structure, and the like can be used to identify
5 and select those ORFs that appear most likely successfully to amplify. Where subsequent gene expression assay relies upon nucleic acid hybridization, whether or not using amplified product, further considerations involving hybridization stringency can be applied to identify that
10 subset of sequences that will most readily permit sequence-specific discrimination at a chosen hybridization and wash stringency. One particular such consideration is avoidance of putative exons that span repetitive sequence; such sequence can hybridize spuriously to nonspecific message,
15 reducing specific signal in the hybridization.

For bioinformatic assay, there are fewer constraints on the sequences that can be tested experimentally, and in this latter case therefore process 300 can output the entirety of the input sequence.

20 The subset of sequences identified by process 300 as suitable for use in assay is then used in process 400 to create the physical and/or informational substrate for experimental verification of the predictions made in process 200, and thereafter to assay those substrates.

25 As mentioned, the methods of the present invention are particularly useful for identifying potential coding regions within genomic sequence. In a preferred embodiment of process 400, therefore, the expression of the sequences predicted to encode protein is verified. The
30 combination of the predictive and experimental methods provides a powerful gene discovery engine.

Thus, in another aspect, the present invention provides methods and apparatus for verifying the expression of putative genes identified within genomic sequence. In
35 particular, the invention provides a novel method of

verifying gene expression in which expression of predicted ORFs is measured and confirmed using a novel type of nucleic acid microarray, the genome-derived single exon nucleic acid microarrays of the present invention.

5 Putative ORFs as predicted by a consensus of gene calling, particularly gene prediction, algorithms in process 200, and as further identified as suitable by process 300, are amplified from genomic DNA using the polymerase chain reaction (PCR). Although PCR is
10 conveniently used, other amplification approaches can also be used.

Amplification schemes can be designed to capture the entirety of each predicted ORF in an amplicon with minimal additional (that is, intronic or intergenic)
15 sequence. Because ORFs predicted from human genomic sequence using the methods of the present invention differ in length, such an approach results in amplicons of varying length.

However, most predicted ORFs are shorter than 500
20 bp in length, and although amplicons of at least about 100 or 200 base pairs can be immobilized as probes on nucleic acid microarrays, early experimental results using the methods of the present invention have suggested that longer amplicons, at least about 400 or 500 base pairs, are more
25 effective. Furthermore, certain advantages derive from application to the microarray of amplicons of defined size.

Therefore, amplification schemes can alternatively, and preferably, be designed to amplify regions of defined size, preferably at least about 300, 400
30 or 500 bp, centered about each predicted ORF. Such an approach results in a population of amplicons of limited size diversity, but that typically contain intronic and/or intergenic nucleic acid in addition to putative ORF.

Conversely, somewhat fewer than 10% of ORFs
35 predicted from human genomic sequence according to the

methods of the present invention exceed 500 bp in length. Portions of such extended ORFs, preferably at least about 300, 400 or 500 bp in length, can be amplified. However, it has been discovered that the percentage success at
5 amplifying pieces of such ORFs is low, and that such putative exons are more effectively amplified when larger fragments, at least about 1000 or 1500 bp, and even as large as 2000 bp are amplified.

The putative ORFs selected in process 300 are
10 thus input into one or more primer design programs, such as PRIMER3 (available online for use at <http://www-genome.wi.mit.edu/cgi-bin/primer/>), with a goal of amplifying at least about 500 base pairs of genomic sequence centered within or about ORFs predicted to be no
15 more than about 500 bp, or at least about 1000 - 1500 bp of genomic sequence for ORFs predicted to exceed 500 bp in length, and the primers synthesized by standard techniques. Primers with the requisite sequences can be purchased commercially or synthesized by standard techniques.

20 Conveniently, a first predetermined sequence can be added commonly to the ORF-specific 5' primer and a second, typically different, predetermined sequence commonly added to each 3' ORF-unique primer. This serves to immortalize the amplicon, that is, serves to permit
25 further amplification of any amplicon using a single set of primers complementary respectively to the common 5' and common 3' sequence elements. The presence of these "universal" priming sequences further facilitates later sequence verification, providing a sequence common to all
30 amplicons at which to prime sequencing reactions. The common 5' and 3' sequences further serve to add a cloning site should any of the ORFs warrant further study.

Such predetermined sequence is usefully at least about 10, 12 or 15 nt in length, and usually does not
35 exceed about 25 nt in length. The "universal" priming

sequences used in the examples presented *infra* were each 16 nt long.

The genomic DNA to be used as substrate for amplification will come from the eukaryotic species from which the genomic sequence data had originally been obtained, or a closely related species, and can conveniently be prepared by well known techniques from somatic or germline tissue or cultured cells of the organism. See, e.g., Short Protocols in Molecular Biology : A Compendium of Methods from Current Protocols in Molecular Biology, Ausubel et al. (eds.), 4th edition (April 1999), John Wiley & Sons (ISBN: 047132938X) and Maniatis et al., Molecular Cloning : A Laboratory Manual, 2nd edition (December 1989), Cold Spring Harbor Laboratory Press (ISBN: 0879693096). Many such prepared genomic DNAs are available commercially, with the human genomic DNAs additionally having certification of donor informed consent.

Although the intronic and intergenic material flanking putative coding regions in the amplicons could potentially interfere with hybridizations during microarray experiments, we have found, surprisingly, that differential expression ratios are not significantly affected. Rather, the predominant effect of exon size is to alter the absolute signal intensity, rather than its ratio. Equally surprising, the art had suggested that single exon probes would not provide sufficient signal intensity for high stringency hybridization analyses; we find that such probes not only provide adequate signal, but have substantial advantages, as herein described.

After partial purification, as by size exclusion spin column, with or without confirmation as to amplicon quality as by gel electrophoresis, each amplicon (single exon probe) is disposed in an array upon a support substrate.

Methods for creating microarrays by deposition and fixation of nucleic acids onto support substrates are well known in the art (Reviewed by Schena et al., see above).

5 Typically, the support substrate will be glass, although other materials, such as amorphous or crystalline silicon or plastics. Such plastics include polymethylacrylic, polyethylene, polypropylene, polyacrylate, polymethylmethacrylate, polyvinylchloride, 10 polytetrafluoroethylene, polystyrene, polycarbonate, polyacetal, polysulfone, celluloseacetate, cellulosenitrate, nitrocellulose, or mixtures thereof, can also be used. Typically, the support will be rectangular, although other shapes, particularly circular disks and even 15 spheres, present certain advantages. Particularly advantageous alternatives to glass slides as support substrates for array of nucleic acids are optical discs, as described in WO 98/12559.

 The amplified nucleic acids can be attached 20 covalently to a surface of the support substrate or, more typically, applied to a derivatized surface in a chaotropic agent that facilitates denaturation and adherence by presumed noncovalent interactions, or some combination thereof.

25 Robotic spotting devices useful for arraying nucleic acids on support substrates can be constructed using public domain specifications (The MGuide, version 2.0, <http://cmgm.stanford.edu/pbrown/mguide/index.html>), or can conveniently be purchased from commercial sources 30 (MicroArray GenII Spotter and MicroArray GenIII Spotter, Molecular Dynamics, Inc., Sunnyvale, CA). Spotting can also be effected by printing methods, including those using ink jet technology.

 As is well known in the art, microarrays 35 typically also contain immobilized control nucleic acids.

For controls useful in providing measurements of background signal for the genome-derived single exon microarrays of the present invention, a plurality of *E. coli* genes can readily be used. As further described in Example 1, 16 or
5 32 *E. coli* genes suffice to provide a robust measure of background noise in such microarrays.

As is well known in the art, the amplified product disposed in arrays on a support substrate to create a nucleic acid microarray can consist entirely of natural
10 nucleotides linked by phosphodiester bonds, or alternatively can include either nonnative nucleotides, alternative internucleotide linkages, or both, so long as complementary binding can be obtained in the hybridization. If enzymatic amplification is used to produce the
15 immobilized probes, the amplifying enzyme will impose certain further constraints upon the types of nucleic acid analogs that can be generated.

Although particularly described herein as using high density microarrays constructed on planar substrates,
20 the methods of the present invention for confirming the expression of ORFs predicted from genomic sequence can use any of the known types of microarrays, as herein defined, including lower density planar arrays, and microarrays on nonplanar, nonunitary, distributed substrates.

25 For example, gene expression can be confirmed using hybridization to lower density arrays, such as those constructed on membranes, such as nitrocellulose, nylon, and positively-charged derivatized nylon membranes. Further, gene expression can also be confirmed using
30 nonplanar, bead-based microarrays such as are described in Brenner *et al.*, *Proc. Natl. Acad. Sci. USA* 97(4):166501670 (2000); U.S. Patent No. 6,057,107; and U.S. Patent No. 5,736,330. In theory, a packed collection of such beads provides in aggregate a higher density of nucleic acid
35 probe than can be achieved with spotting or lithography

techniques on a single planar substrate.

Planar microarrays on solid substrates, however, provide certain useful advantages, including high throughput and compatibility with existing readers. For example, each standard microscope slide can include at least 1000, typically at least 2000, preferably 5000 and upto 10,000 - 50,000 or more nucleic acid probes of discrete sequence. The number of sequences deposited will depend on their required application.

Each putative gene can be represented in the array by a single predicted ORF. Alternatively, genes can be represented by more than one predicted ORF. For purposes of measuring differential splicing, more than one predicted ORF will be provided for a putative gene. And as is well known in the art, each probe of defined sequence, representing a single predicted ORF, can be deposited in a plurality of locations on a single microarray to provide redundancy of signal.

The genome-derived single exon microarrays described above differ in several fundamental and advantageous ways from microarrays presently used in the gene expression art, including (1) those created by deposition of mRNA-derived nucleic acids, (2) those created by *in situ* synthesis of oligonucleotide probes, and (3) those constructed from yeast genomic DNA.

Most nucleic acid microarrays that are in use for study of eukaryotic gene expression have as immobilized probes nucleic acids that are derived - either directly or indirectly - from expressed message. As discussed above, it is common, for example, for such microarrays to be derived from cDNA/EST libraries, either from those previously described in the literature, see Lennon *et al.*, or from the *de novo* construction of "problem specific" libraries targeted at a particular biological question, R.S. Thomas *et al.*, *Cancer Res.* (in press). Such

microarrays are herein collectively denominated "EST microarrays".

Such EST microarrays by definition can measure expression only of those genes found in EST libraries, shown herein to represent only a fraction of expressed genes. Furthermore, such libraries - and thus microarrays based thereupon - are biased by the tissue or cell type of message origin, by the expression levels of the respective genes within the tissues, and by the ability of the message successfully to have been reverse-transcribed and cloned.

Thus, as further discussed in Example 1, the methods of the present invention enable sequences that do not appear in EST or other expression databases to be determined - subsequently arrayed for expression measurements could not, therefore, have been represented as probes on an EST microarray. And as further demonstrated in the examples, *infra*, the remaining population of genes identified from genomic sequence by the methods of the present invention - that is, the one third of sequences that had previously been accessioned in EST or other expression databases - are biased toward genes with higher expression levels.

Representation of a message in an EST and/or cDNA library depends upon the successful reverse transcription, optionally but typically with subsequent successful cloning, of the message. This introduces substantial bias into the population of probes available for arraying in EST microarrays.

In contrast, neither reverse transcription nor cloning is required to produce the probes arrayed on the genome-derived single exon microarrays of the present invention. And although the ultimate deposition of a probe on the genome-derived single exon microarray of the present invention depends upon a successful amplification from genomic material, *a priori* knowledge of the sequence of the

desired amplicon affords greater opportunity to recover any given probe sequence recalcitrant to amplification than is afforded by the requirement for successful reverse transcription and cloning of unknown message in EST approaches.

Thus, the genome-derived single exon microarrays of the present invention present a far greater diversity of probes for measuring gene expression, with far less bias, than do EST microarrays presently used in the art.

As a further consequence of their ultimate origin from expressed message, the probes in EST microarrays often contain poly-A (or complementary poly-T) stretches derived from the poly-A tail of mature mRNA. These homopolymeric stretches contribute to cross-hybridization, that is, to a spurious signal occasioned by hybridization to the homopolymeric tail of a labeled cDNA that lacks sequence homology to the gene-specific portion of the probe.

In contrast, the probes arrayed in the genome-derived single exon microarrays of the present invention lack homopolymeric stretches derived from message polyadenylation, and thus can provide more specific signal. Typically, at least about 50, 60 or 75% of the probes on the genome-derived single exon microarrays of the present invention lack homopolymeric regions consisting of A or T, where a homopolymeric region is defined for purposes herein as stretches of 25, or more, typically 30 or more, identical nucleotides.

A further distinction, which also affects the specificity of hybridization, is occasioned by the typical derivation of EST microarray probes from cloned material. Because much of the probe material disposed as probes on EST microarrays is excised or amplified from plasmid, phage, or phagemid vectors, EST microarrays typically include a fair amount of vector sequence, more so when the probes are amplified, rather than excised, from the vector.

In contrast, the vast majority of probes in the genome-derived single exon microarrays of the present invention contain no prokaryotic or bacteriophage vector sequence, having been amplified directly or indirectly from genomic DNA. Typically, therefore, at least about 50, 60, 70 or 80% or more of individual exon-including probes disposed on a genome-derived single exon microarray of the present invention lack vector sequence, and particularly lack sequences drawn from plasmids and bacteriophage. Preferably, at least about 85, 90 or more than 90% of exon-including probes in the genome-derived single exon microarray of the present invention lack vector sequence. With attention to removal of vector sequences through preprocessing 24, percentages of vector-free exon-including probes can be as high as 95 - 99%. The substantial absence of vector sequence from the genome-derived single exon microarrays of the present invention results in greater specificity during hybridization, since spurious cross-hybridization to a probe vector sequence is reduced.

As a further consequence of excision or amplification of probes from vectors in construction of EST microarrays, the probes arrayed thereon often contain artificial sequence, derived from vector polylinker multiple cloning sites, at both 5' and 3' ends. The probes disposed upon the genome-derived single exon microarrays need have no such artificial sequence appended thereto.

As mentioned above, however, the ORF-specific primers used to amplify putative ORFs can include artificial sequences, typically 5' to the ORF-specific primer sequence, useful for "universal" (that is, independent of ORF sequence) priming of subsequent amplification or sequencing reactions. When such "universal" 5' and/or 3' priming sequences are appended to the amplification primers, the probes disposed upon the genome-derived single exon microarray will include

artificial sequence similar to that found in EST
microarrays. However, the genome-derived single exon
microarray of the present invention can be made without
such sequences, and if so constructed, presents an even
5 smaller amount of nonspecific sequence that would
contribute to nonspecific hybridization.

Yet another consequence of typical use of cloned
material as probes in EST microarrays is that such
microarrays contain probes that result from cloning
10 artifacts, such as chimeric molecules containing coding
region of two separate genes. Derived from genomic
material, typically not thereafter cloned, the probes of
the genome-derived single exon microarrays of the present
invention lack such cloning artifacts, and thus provide
15 greater specificity of signal in gene expression
measurements.

A further consequence of the cloned origin of
probes on many EST microarrays is that the individual
probes often have disparate sizes, which can cause the
20 optimal hybridization stringency to vary among probes on a
single microarray. In contrast, as discussed above, the
probes arrayed on the genome-derived single exon
microarrays of the present invention can readily be
designed to have a narrow distribution in sizes, with the
25 range of probe sizes no greater than about 10% of the
average size, typically no greater than about 5% of the
average probe size.

Because of their origin from fully- or partially-
spliced message, probes disposed upon EST arrays will often
30 include multiple exons. The percentage of such exon-
spanning probes in an EST microarray can be calculated, on
average, based upon the predicted number of exons/gene for
the given species and the average length of the immobilized
probes. For human genes, the near-complete sequence of
35 human chromosome 22, Dunham *et al.*, *Nature* 402(6761):489-95

(1999), predicts that human genes average 5.5 exons/gene. Even with probes of 200 - 500 bp, the vast majority of human EST microarray probes include more than one exon.

In contrast, by virtue of their origin from
5 algorithmically identified ORFs in genomic sequence, the probes in the genome-derived single exon microarrays of the present invention can consist of individual exons. Thus, in contrast to EST microarrays, at least about 50, 60, 70, 75, 80, 85, 95 or 99% of probes deposited in the genome-
10 derived microarray of the present invention consist of, or include, no more than one predicted ORF.

This provides the ability, not readily achieved using EST microarrays, to use the genome-derived single exon microarrays of the present invention to measure
15 tissue-specific expression of individual exons, which in turn allows differential splicing events to be detected and characterized, and in particular, allows the correlation of differential splicing to tissue-specific expression patterns.

20 Furthermore, the exons that are represented in EST microarrays are often biased toward the 3' or 5' end of their respective genes, since sequencing strategies used for EST identification are so biased. In contrast, no such 3' or 5' bias necessarily inheres in the selection of exons
25 for disposition on the genome-derived single exon microarrays of the present invention.

Conversely, the probes provided on the genome-derived single exon microarrays of the present invention typically, but need not necessarily, include intronic
30 and/or intergenic sequence that is absent from EST microarrays, which are derived from mature mRNA. Typically, at least about 50, 60, 70, 80 or 90% of the exon-including probes on the genome-derived single exon microarrays of the present invention include sequence drawn
35 from noncoding regions. As discussed above, the additional

presence of noncoding region does not significantly interfere with measurement of gene expression, and provides the additional opportunity to assay prespliced RNA, and thus measure such phenomena such as nuclear export control.

5 The genome-derived single exon microarrays of the present invention are also quite different from *in situ* synthesis microarrays, where probe size is severely constrained by inadequacies in the photolithographic synthesis process.

10 Typically, probes arrayed on *in situ* synthesis microarrays are limited to a maximum of about 25 bp. As a well known consequence, hybridization to such chips must be performed at low stringency. In order, therefore, to achieve unambiguous sequence-specific hybridization
15 results, the *in situ* synthesis microarray requires substantial redundancy, with concomitant programmed arraying for each probe of probe analogues with altered (*i.e.*, mismatched) sequence.

 In contrast, the longer probe length of the
20 genome-derived single exon microarrays of the present invention allows much higher stringency hybridization and wash. Typically, therefore, exon-including probes on the genome-derived single exon microarrays of the present invention average at least about 100, 200, 300, 400 or
25 500 bp in length. By obviating the need for substantial probe redundancy, this approach permits a higher density of probes for discrete exons or genes to be arrayed on the microarrays of the present invention than can be achieved for *in situ* synthesis microarrays.

30 A further distinction is that the probes in *in situ* synthesis microarrays typically are covalently linked to the substrate surface. In contrast, the probes disposed on the genome-derived microarray of the present invention typically are, but need not necessarily be, bound
35 noncovalently to the substrate.

Furthermore, the short probe size on *in situ* microarrays causes large percentage differences in the melting temperature of probes hybridized to their complementary target sequence, and thus causes large percentage differences in the theoretically optimum stringency across the array as a whole.

In contrast, the larger probe size in the microarrays of the present invention create lower percentage differences in melting temperature across the range of arrayed probes.

A further significant advantage of the microarrays of the present invention over *in situ* synthesized arrays is that the quality of each individual probe can be confirmed before deposition. In contrast, the quality of probes cannot be assessed on a probe-by-probe basis for the *in situ* synthesized microarrays presently being used.

The genome-derived single exon microarrays of the present invention are also distinguished over, and present substantial benefits over, the genome-derived microarrays from lower eukaryotes such as yeast. Lashkari *et al.*, *Proc. Natl. Acad. Sci. USA* 94:13057-13062 (1997).

Only about 220 - 250 of the 6100 or so nuclear genes in *Saccharomyces cerevisiae* - that is, only about 4 - 5% - have standard, spliceosomal, introns, Lopez *et al.*, *Nucl. Acids Res.* 28:85-86 (2000); Spingola *et al.*, *RNA* 5(2):221-34 (1999). Furthermore, the entire yeast genome has already been sequenced. These two facts permit the ready amplification and disposition of single-ORF amplicons on such microarray without the requirement for antecedent use of gene prediction and/or comparative sequence analyses.

Thus, a significant aspect of the present invention is the ability to identify and to confirm expression of predicted coding regions in genomic sequence

drawn from eukaryotic organisms that have a higher percentage of genes having introns than do yeast such as *Saccharomyces cerevisiae*, particularly in genomic sequence drawn from eukaryotes in which at least about 10, 20 or 50% of protein-encoding genes have introns. In preferred embodiments, the methods and apparatus of the present invention are used to identify and confirm expression of novel genes from genomic sequence of eukaryotes in which the average number of introns per gene is at least about one, two or three or more.

After the physical substrate is prepared, experimental verification of predicted function is performed.

In a preferred embodiment of the present invention, where the function sought to be identified in genomic sequence is protein coding, experimental verification is performed by measuring expression of the putative ORFs, typically through nucleic acid hybridization experiments, and in particularly preferred embodiments, through hybridization to genome-derived single exon microarrays prepared as above- described.

Expression is conveniently measured and expressed for each probe in the microarray as a ratio of the expression measured concurrently in a plurality of mRNA sources, according to techniques well known in the microarray art, Reviewed in Schena et al., and as further described in Example 2, below. The mRNA source for the reference against which specific expression is measured can be drawn from a homogeneous mRNA source, such as a single cultured cell-type, or alternatively can be heterogeneous, as from a pool of mRNA derived from multiple tissues and/or cell types, as further described in Example 2, *infra*.

mRNA can be prepared by standard techniques, see Ausubel et al. and Maniatis et al., or purchased commercially. The mRNA is then typically reverse-

transcribed in the presence of labeled nucleotides: the index source (that in which expression is desired to be measured) is reverse transcribed in the presence of nucleotides labeled with a first label, typically a fluorophore (fluorochrome; fluor; fluorescent dye); the reference source is reverse transcribed in the presence of a second label, typically a fluorophore, typically fluorometrically-distinguishable from the first label. As further described in Example 2, *infra*, Cy3 and Cy5 dyes prove particularly useful in these methods. After partial purification of the index and reference targets, hybridization to the probe array is conducted according to standard techniques, typically under a coverslip.

After wash, microarrays are conveniently scanned using a commercial microarray scanning device, such as a Gen3 Scanner (Molecular Dynamics, Sunnyvale, CA). Data on expression is then passed, with or without interim storage, to process 500, where the results for each probe are related to the original sequence.

Often, hybridization of target material to the genome-derived single exon microarray will identify certain of the probes thereon as of particular interest. Thus, it is often desirable that the user be able readily to obtain sufficient quantities of an individual probe, either for subsequent arrayed deposition upon an additional support substrate, often as part of a microarray having a plurality of probes so identified, or alternatively or additionally as a solitary solid-phase or solution-phase probe, for further use.

Thus, in another aspect, the present invention provides compositions and kits for the ready production of nucleic acids identical in sequence to, or substantially identical in sequence to, probes on the genome-derived single exon microarrays of the present invention.

In this aspect, a small quantity of each probe is

disposed, typically without attachment to substrate, in a spatially-addressable ordered set, typically one per well of a microtiter dish. Although a 96 well microtiter plate can be used, greater efficiency is obtained using higher
5 density arrays, such as are provided by microtiter plates having 384, 864, 1536, 3456, 6144, or 9600 wells, and although microtiter plates having physical depressions (wells) are conveniently used, any device that permits addressable withdrawal of reagent from fluidly-
10 noncommunicating areas can be used.

In this aspect of the invention, therefore, a fluidly noncommunicating addressable ordered set of individual probes, corresponding to those on a genome-derived single exon microarray, is provided, with each
15 probe in sufficient quantity to permit amplification, such as by PCR. As earlier mentioned, the ORF-specific 5' primers used for genomic amplification can have a first common sequence added thereto, and the ORF-specific 3' primers used for genomic amplification can have a second,
20 different, common sequence added thereto, thus permitting, in this preferred embodiment, the use of a single set of 5' and 3' primers to amplify any one of the probes from the amplifiable ordered set.

Each discrete amplifiable probe can also be
25 packaged with amplification primers, solutes, buffers, etc., and can be provided in dry (e.g., lyophilized) form or wet, in the latter case typically with addition of agents that retard evaporation.

In another aspect of the present invention, a
30 genome-derived single-exon microarray is packaged together with such an ordered set of amplifiable probes corresponding to the probes, or one or more subsets of probes, thereon. In alternative embodiments, the ordered set of amplifiable probes is packaged separately from the
35 genome-derived single exon microarray.

In some embodiments, the microarray and/or ordered probe set are further packaged with recordable media that provide probe identification and addressing information, and that can additionally contain annotation
5 information, such as gene expression data. Such recordable media can be packaged with the microarray, with the ordered probe set, or with both.

If the microarray is constructed on a substrate that incorporates recordable media, such as is described in
10 international patent application no. WO 98/12559, then separate packaging of the genome-derived single exon microarray and the bioinformatic information is not required.

The amount of amplifiable probe material should
15 be sufficient to permit at least one amplification sufficient for subsequent hybridization assay.

Although the use of high density genome-derived microarrays on solid planar substrates is presently a preferred approach for the physical confirmation and
20 characterization of the expression of sequences predicted to encode protein, other types of microarrays (as herein defined) can also be used.

Furthermore, as earlier mentioned, experimental verification of the function predicted from genomic
25 sequence in process 200 can be bioinformatic, rather than, or additional to, physical verification.

For example, where the function desired to be identified is protein coding, the predicted ORFs can be compared bioinformatically to sequences known or suspected
30 of being expressed.

Thus, the sequences output from process 300 (or process 200), can be used to query expression databases, such as EST databases, SNP ("single nucleotide polymorphism") databases, known cDNA and mRNA sequences,
35 SAGE ("serial analysis of gene expression") databases, and

more generalized sequence databases that allow query for expressed sequences. Such query can be done by any sequence query algorithm, such as BLAST ("basic local alignment search tool"). The results of such query -
5 including information on identical sequences and information on nonidentical sequences that have diffuse or focal regions of sequence homology to the query sequence - can then be passed directly to process 500, or used to inform analyses subsequently undertaken in process 200,
10 process 300, or process 400.

Experimental data, whether obtained by physical or bioinformatic assay in process 400, is passed to process 500 where it is usefully related to the sequence data itself, a process colloquially termed "annotation". Such
15 annotation can be done using any technique that usefully relates the functional information to the sequence, as, for example, by incorporating the functional data into the record itself, by linking records in a hierarchical or relational database, by linking to external databases, or
20 by a combination thereof. Such database techniques are well within the skill in the art.

The annotated sequence data can be stored locally, uploaded to genomic sequence database 100, and/or displayed 800.

25 The methods and apparatus of the present invention rapidly produce functional information from genomic sequence. Coupled with the escalating pace at which sequence now accumulates, the rapid pace of sequence annotation produces a need for methods of displaying the
30 information in meaningful ways.

FIG. 3 shows visual display 80 presenting a single genomic sequence annotated according to the present invention. Because of its nominal resemblance to artistic works of Piet Mondrian, visual display 80 is alternatively
35 described herein as a "Mondrian".

Each of the visual elements of display 80 is aligned with respect to the genomic sequence being annotated (hereinafter, the "annotated sequence"). Given the number of nucleotides typically represented in an annotated sequence, representation of individual nucleotides would rarely be readable in hard copy output of display 80. Typically, therefore, the annotated sequence is schematized as rectangle 89, extending from the left border of display 80 to its right border. By convention herein, the left border of rectangle 89 represents the first nucleotide of the sequence and the right border of rectangle 89 represents the last nucleotide of the sequence.

As further discussed below, however, the Mondrian visual display of annotated sequence can serve as a convenient graphical user interface for computerized representation, analysis, and query of information stored electronically. For such use, the individual nucleotides can conveniently be linked to the X axis coordinate of rectangle 89. This permits the annotated sequence at any point within rectangle 89 readily to be viewed, either automatically - for example, by time-delayed appearance of a small overlaid window upon movement of a cursor or other pointer over rectangle 89 - or through user intervention, as by clicking a mouse or other pointing device at a point in rectangle 89.

Visual display 80 is generated after user specification of the genomic sequence to be displayed. Such specification can consist of or include an accession number for a single clone (e.g., a single BAC accessioned into GenBank), wherein the starting and stopping nucleotides are thus absolutely identified, or alternatively can consist of or include an anchor or fulcrum point about which a chosen range of sequence is anchored, thus providing relative endpoints for the

sequence to be displayed. For example, the user can anchor such a range about a given chromosomal map location, gene name, or even a sequence returned by query for similarity or identity to an input query sequence. When visual display 80 is used as a graphical user interface to computerized data, additional control over the first and last displayed nucleotide will typically be dynamically selectable, as by use of standard zooming and/or selection tools.

Field 81 of visual display 80 is used to present the output from process 200, that is, to present the bioinformatic prediction of those sequences having the desired function within the genomic sequence. Functional sequences are typically indicated by at least one rectangle 83 (83a, 83b, 83c), the left and right borders of which respectively indicate, by their X-axis coordinates, the starting and ending nucleotides of the region predicted to have function.

Where a single bioinformatic method or approach identifies a plurality of regions having the desired function, a plurality of rectangles 83 is disposed horizontally in field 81. Where multiple methods and/or approaches are used to identify function, each such method and/or approach can be represented by its own series of horizontally disposed rectangles 83, each such horizontally disposed series of rectangles offset vertically from those representing the results of the other methods and approaches.

Thus, rectangles 83a in FIG. 3 represent the functional predictions of a first method of a first approach for predicting function, rectangles 83b represent the functional predictions of a second method and/or second approach for predicting that function, and rectangles 83c represent the predictions of a third method and/or approach.

Where the function desired to be identified is protein coding, field 81 is used to present the bioinformatic prediction of sequences encoding protein. For example, rectangles 83a can represent the results from
5 GRAIL or GRAIL II, rectangles 83b can represent the results from GENEFINDER, and rectangles 83c can represent the results from DICTION.

Optionally, and preferably, rectangles 83 collectively representing predictions of a single method
10 and/or approach are identically colored and/or textured, and are distinguishable from the color and/or texture used for a different method and/or approach.

Alternatively, or in addition, the color, hue, density, or texture of rectangles 83 can be used further to
15 report a measure of the bioinformatic reliability of the prediction. For example, many gene prediction programs will report a measure of the reliability of prediction. Thus, increasing degrees of such reliability can be indicated, e.g., by increasing density of shading. Where
20 display 80 is used as a graphical user interface, such measures of reliability, and indeed all other results output by the program, can additionally or alternatively be made accessible through linkage from individual rectangles 83, as by time-delayed window ("tool tip" window), or by
25 pointer (e.g., mouse)-activated link.

As earlier described, increased predictive reliability can be achieved by requiring consensus among methods and/or approaches to determining function. Thus, field 81 can include a horizontal series of rectangles 83
30 that indicate one or more degrees of consensus in predictions of function.

Although FIG. 3 shows three series of horizontally disposed rectangles in field 81, display 80 can include as few as one such series of rectangles and as
35 many as can discriminably be displayed, depending upon the

number of methods and/or approaches used to predict a given function.

Furthermore, field 81 can be used to show predictions of a plurality of different functions.

5 However, the increased visual complexity occasioned by such display makes more useful the ability of the user to select a single function for display. When display 80 is used as a graphical user interface for computer query and analysis, such function can usefully be indicated and user-
10 selectable, as by a series of graphical buttons or tabs (not shown in FIG. 3).

Rectangle 89 is shown in FIG. 3 as including interposed rectangle 84. Rectangle 84 represents the portion of annotated sequence for which predicted
15 functional information has been assayed physically, with the starting and ending nucleotides of the assayed material indicated by the X axis coordinates of the left and right borders of rectangle 84. Rectangle 85, with optional inclusive circles 86 (86a, 86b, and 86c) displays the
20 results of such physical assay.

Although a single rectangle 84 is shown in FIG. 3, physical assay is not limited to just one region of annotated genomic sequence. It is expected that an increasing percentage of regions predicted to have function
25 by process 200 will be assayed physically, and that display 80 will accordingly, for any given genomic sequence, have an increasing number of rectangles 84 and 85, representing an increased density of sequence annotation.

Where the function desired to be identified is
30 protein coding, rectangle 84 identifies the sequence of the probe used to measure expression. In embodiments of the present invention where expression is measured using genome-derived single exon microarrays, rectangle 84 identifies the sequence included within the probe
35 immobilized on the support surface of the microarray. As

noted *supra*, such probe will often include a small amount of additional, synthetic, material incorporated during amplification and designed to permit reamplification of the probe, which sequence is typically not shown in display 80.

5 Rectangle 87 is used to present the results of bioinformatic assay of the genomic sequence. For example, where the function desired to be identified is protein coding, process 400 can include bioinformatic query of expression databases with the sequences predicted in
10 process 200 to encode exons. And as earlier discussed, because bioinformatic assay presents fewer constraints than does physical assay, often the entire output of process 200 can be used for such assay, without further subsetting thereof by process 300. Therefore, rectangle 87 typically
15 need not have separate indicators therein of regions submitted for bioinformatic assay; that is, rectangle 87 typically need not have regions therein analogous to rectangles 84 within rectangle 89.

 Rectangle 87 as shown in FIG. 3 includes smaller
20 rectangles 880 and 88. Rectangles 880 indicate regions that returned a positive result in the bioinformatic assay, with rectangles 88 representing regions that did not return such positive results. Where the function desired to be predicted and displayed is protein coding, rectangles 880
25 indicate regions of the predicted exons that identify sequence with significant similarity in expression databases, such as EST, SNP, SAGE databases, with rectangles 88 indicating genes novel over those identified in existing expression data bases.

30 Rectangles 880 can further indicate, through color, shading, texture, or the like, additional information obtained from bioinformatic assay.

 For example, where the function assayed and displayed is protein coding, the degree of shading of
35 rectangles 880 can be used to represent the degree of

sequence similarity found upon query of expression databases. The number of levels of discrimination can be as few as two (identity, and similarity, where similarity has a user-selectable lower threshold). Alternatively, as
5 many different levels of discrimination can be indicated as can visually be discriminated.

Where display 80 is used as a graphical user interface, rectangles 880 can additionally provide links directly to the sequences identified by the query of
10 expression databases, and/or statistical summaries thereof. As with each of the precedingly-discussed uses of display 80 as a graphical user interface, it should be understood that the information accessed via display 80 need not be resident on the computer presenting such display, which
15 often will be serving as a client, with the linked information resident on one or more remotely located servers.

Rectangle 85 displays the results of physical assay of the sequence delimited by its left and right
20 borders.

Rectangle 85 can consist of a single rectangle, thus indicating a single assay, or alternatively, and increasingly typically, will consist of a series of rectangles (85a, 85b, 85c) indicating separate physical
25 assays of the same sequence.

Where the function assayed is gene expression, and where gene expression is assayed as herein described using simultaneous two-color fluorescent detection of hybridization to genome-derived single exon microarrays,
30 individual rectangles 85 can be colored to indicate the degree of expression relative to control. Conveniently, shades of green can be used to depict expression in the sample over control values, and shades of red used to depict expression less than control, corresponding to the
35 spectra of the Cy3 and Cy5 dyes conventionally used for

respective labeling thereof. Additional functional information can be provided in the form of circles 86 (86a, 86b, 86c), where the diameter of the circle can be used to indicate expression intensity. As discussed *infra*, such relative expression (expression ratios) and absolute expression (signal intensity) can be expressed using normalized values.

Where display 80 is used as a graphical user interface, rectangle 85 can be used as a link to further information about the assay. For example, where the assay is one for gene expression, each rectangle 85 can be used to link to information about the source of the hybridized mRNA, the identity of the control, raw or processed data from the microarray scan, or the like.

FIG. 4 is rendition of display 80 representing gene prediction and gene expression for a hypothetical BAC, showing conventions used in the Examples presented *infra*. BAC sequence ("Chip seq.") 89 is presented, with the physically assayed region thereof (corresponding to rectangle 84 in FIG. 3) shown in white. Algorithmic gene predictions are shown in field 81, with predictions by GRAIL shown, predictions by GENEFINDER, and predictions by DICTION shown. Within rectangle 87, regions of sequence that, when used to query expression databases, return identical or similar sequences ("EST hit") are shown as white rectangles (corresponding to rectangles 880 in FIG. 3), gray indicates low homology, and black indicates unknowns (where black and gray would correspond to rectangles 88 in FIG. 3).

Although FIGS. 3 and 4 show a single stretch of sequence, uninterrupted from left to right, longer sequences are usefully represented by vertical stacking of such individual Mondrians, as shown in FIGS. 9 and 10.

Single Exon Probes Useful For Measuring Gene Expression

The methods and apparatus of the present invention rapidly produce functional information from genomic sequence. Where the function to be identified is protein coding, the methods and apparatus of the present invention rapidly identify and confirm the expression of portions of genomic sequence that function to encode protein. As a direct result, the methods and apparatus of the present invention rapidly yield large numbers of single-exon nucleic acid probes, the majority from previously unknown genes, each of which is useful for measuring and/or surveying expression of a specific gene in one or more tissues or cell types.

It is, therefore, another aspect of the present invention to provide genome-derived single exon nucleic acid probes useful for gene expression analysis, and particularly for gene expression analysis by microarray.

Using the methods and genome-derived single-exon microarrays of the present invention, we have for example readily identified a large number of unique ORFs from human genomic sequence. Using single exon probes that encompass these ORFs, we have demonstrated, through microarray hybridization analysis, the expression of 13,114 of these ORFs in bone marrow.

As would immediately be appreciated by one of skill in the art, each single exon probe having demonstrable expression in bone marrow is currently available for use in measuring the level of its ORF's expression in bone marrow.

Because bone marrow is the tissue in which blood cells originate, diseases of the bone marrow are a significant cause of human morbidity and mortality. Increasingly, genetic factors are being found that contribute to predisposition, onset, and/or aggressiveness of most, if not all, of these diseases. Although mutations

in single genes have in some cases been identified as causal - notably in the thalassemias and sickle cell anemia - disorders of the bone marrow are, for the most part, believed to have polygenic etiologies.

5 For example, cancers that originate in the bone marrow and lymphatic tissues such as the lymphomas, leukemias, and myeloma have been recognized as a major health concern. An estimated 632,000 Americans are presently living with lymphoma, leukemia or myeloma, and
10 over 110,000 new cases are anticipated each year. The new cases alone account for 11% of all cancer cases reported in the United States.

 Lymphoma is a general term for a group of cancers of lymphocytes that manifest in the tissues of the
15 lymphatic system. Eventually, monoclonal proliferation crowds out healthy cells and creates tumors which enlarge lymph nodes. Approximately 450,000 members of the U.S. population are living with lymphoma: 160,000 with Hodgkin disease (HD) and 290,000 with non-Hodgkin lymphoma.

20 Hodgkin disease (HD) is a specialized form of lymphoma, and represent about 8% of all lymphomas. HD can be distinguish in tissues by the presence of an abnormal cell called the Reed-Sternberg cell. Incidence rates of HD are higher in adolescents and young adults, but HD is
25 considered to be one of the most curable forms of cancer. Symptoms of HD include painless swelling of lymph glands, fatigue, recurrent high fever, sweating at night, skin irritations and loss of weight.

 Although an infectious etiology has been proposed
30 to account for the disproportionate incidence of HD among siblings reared together - particularly an association with Epstein Barr Virus (EBV) - multiple genetic contributions have also been suggested.

 As early as 1986, linkage to HLA was suggested,
35 with Klitz et al., Am. J. Hum. Genet. 54: 497-505 (1994)

reporting an overall association of the nodular sclerosing (NSHD) group with the HLA class II region. Results of the study suggested that susceptibility to NSHD is influenced by more than 1 locus within the class II region. Through a literature search, Shugart and Collins (2000), *Europ. J. Hum. Genet.* 8: 460-463 (2000), performed a combined segregation and linkage analysis on 59 nuclear families with HD and concluded that HD is most likely determined by both an HLA-associated major gene and other non-HLA genetic factors, in conjunction with environmental effects.

Non-Hodgkin lymphoma (NHL) is a malignant monoclonal proliferation of the lymphoid cells in the immune system, including bone marrow, spleen, liver and GI tract. The pathologic classification of NHL continues to evolve, reflecting new insights into the cells of origin and the biologic bases of these heterogeneous diseases. The course of NHL varies from indolent and initially well tolerated to rapidly fatal. Furthermore, common clinical symptoms of NHL, but rare in HD, are congestion and edema of the face and neck and ureteral compression.

Non-Hodgkin lymphoma (NHL) has been linked to a variety of specific genetic defects, including 26 mutated genes and at least 9 identified chromosomal translocations. Among the mutated genes are: ALK (2p23); API2 (MIHC, cIAP2) (11q22-q23); API4 (survivin, SVV) (17q25(?)); ATM (ATA, ATC) (11q22.3); BCL1 (11q13.3); BCL10 (CLAP, CIPER) (1p22); BCL2 (18q21.3); BCL6 (LAZ3, ZNF51) (3q27); BLYM (1p32); BMI1 (10p13); CCND1 (D11S287E, Cyclin D, PRAD1) (11q13); CD44 (MDU3, HA, MDU2) (11pter-p13); FRAT1 (10q23-q24(?)); FRAT2 (GBP) (10(?)); IL6 (IFNB2) (7p21); IRF4 (MUM1, LSIRF) (6p25-p23); LCP1 (PLS2) (13q14.1-q14.3); MALT1 (MLT) (18q21); MUC1 (PUM, PEM) (1q21); MYBL1 (AMYB, A-MYB) (8q22); MYC (CMYC, C-MYC) (8q24.12-q24.13); NBS1 (8q21); NPM1 (B23) (5q35); PCNA (20p12); TIAM1 (21q22.1); and TP53 (p53, P53) (17q13.1).

Among the chromosomal abnormalities are: t(1;14)

(p22;q32); t(14;18)(q32;q21); t(3;14)(q27;q32);
t(6;14)(p25;q32); t(11;18)(q21;q21); t(1;14)(q21;q32);
t(2;5)(p23;q35); add(14q32) / dup(14p32); and
t(11;14)(q13;q32).

5 Additional genetic loci, as yet undiscovered, are
believed to account for other occurrences of NHL.

As another example, acute leukemia is a malignant
disease of blood-forming tissues such as the bone marrow.
It is characterized by the uncontrolled growth of white
10 blood cells. As a result, immature myeloid cells (in acute
myelogenous leukemia (AML)) or lymphoid cells (in acute
lymphocytic leukemia (ALL)) rapidly accumulate and
progressively replace the bone marrow; diminished
production of normal red cells, white cells, and platelets
15 ensues. This loss of normal marrow function in turn gives
rise to the typical clinical complications of leukemia:
anemia, infection, and bleeding.

If untreated, ALL is rapidly fatal; most patients
die within several months of diagnosis. With appropriate
20 therapy, many patients can be cured. The survival rate for
patients diagnosed with AML or ALL is 14% and 58%
respectively. However, the incidences of AML is expected
to be greater than ALL: an estimated 10,000 new cases of
AML, predominantly in older adults, is anticipated in the
25 U.S. alone, whereas 3,100 new cases of ALL are expected,
with 1,500 of these new cases occurring among children.

The etiology of acute leukemia is not known.
Although human T-cell lymphotropic virus type I (HTLV-I), a
causative agent of adult T-cell leukemia, and HTLV-II,
30 obtained from several patients with a syndrome resembling
hairy cell leukemia, have been isolated, the etiologic link
between HTLV and malignancy is uncertain. There is,
however, evidence which suggests a genetic predisposition
to incidences of acute leukemia.

35 For example, genetic disorders such as Fanconi

anemia and Down syndrome appear to increase risk of acute leukemia, specifically, AML. Evidence supporting a chromosome 21 locus for acute myelogenous leukemia (AML) includes the finding of linkage to 21q22.1-q22.2 in a family with a platelet disorder and propensity to develop AML (Ho et al., Blood 87: 5218-5224 (1996), an increased incidence of leukemia in Down syndrome, and frequent somatic translocation in leukemia involving the CBFA gene on 21q22.3. In addition, Horwitz et al., Am. J. Hum. Genet. 61:873-881 (1997), suggest that a gene on 16q22 may be a second cause of acute myelogenous leukemia. Nonparametric linkage analysis gave a P-value of 0.00098 for the conditional probability of linkage. Mutational analysis excluded expansion of the AT-rich minisatellite repeat FRA16B fragile site and the CAG trinucleotide repeat in the E2F-4 transcription factor. Large CAG repeat expansion was excluded as a cause of leukemia in this family.

Similarly, acute lymphoblastic leukemia (ALL) has been suggested to have a genetic predisposition. In particular, linkage to chromosome 9p has been reported by a number of groups. Chilcote et al., New Eng. J. Med. 313: 286-291 (1985), found that 6 of 8 patients with clinical features of lymphomatous ALL (LALL), a distinct category of ALL of T-cell lineage, had karyotypic abnormalities leading to loss of bands 9p22-p21. The mechanisms varied and included deletions, unbalanced translocations, and loss of the entire chromosome; only 1 of 57 patients without LALL had an abnormality of chromosome 9 at diagnosis. Kowalczyk et al., Cancer Genet. Cytogenet. 9:383-385 (1981), had earlier found changes in 9p in a subgroup of ALL cases. Chilcote et al. (1985) pointed out that there is a fragile site at 9p21 and raised the question of familial predisposition on this basis. This fragile site is the breakpoint in the translocation t(9;11)(p21-22;q23), which

is associated with acute nonlymphocytic leukemia with monocytic features, ANLL-AMoL-M5a. In a large series, Murphy et al., New Eng. J. Med. 313:1611 (1985), confirmed an abnormality of 9p in 10 to 11% of cases (33 out of more than 300) of acute lymphoblastic leukemia. The breakpoints in 9p clustered in the p22-p21 region. They could not, however, corroborate the specific association with T-cell origin or so-called lymphomatous clinical features. In addition, Taki et al., Proc. Natl. Acad. Sci. USA 96:14535 (1999), recently identified AF5q31, a new AF4-related gene, fused to MLL in infant ALL with ins(5;11)(q31;q13q23), and suspects that AF5q31 and AF4 might define a new family particularly involved in the pathogenesis of 11q23-associated-ALL.

As yet a further example of a disease affecting bone marrow with likely polygenic etiology is multiple myeloma (MM).

MM is a cancer of plasma cells, the final differentiated stage of B lymphocyte maturation. The malignant clone proliferates in the bone marrow and frequently invades the adjacent bone, producing extensive skeletal destruction that results in bone pain and fractures. Anemia, hypercalcemia, and renal failure are some clinical manifestations associated with MM.

MM causes 1% of all cancer deaths in Western countries. A genetic component to its etiology is suggested by disparate incidence among various groups in the country. Its incidence is higher in men than in women, in people of African descent relative to the U.S. population at large, and in older adults as compared to the young. It has been estimated that 14,000 new cases of myeloma will be diagnosed in the U.S., and over 11,000 persons will die from MM within the year.

Although, Kaposi's sarcoma-associated herpes virus has been associated with MM (Retig et al., Science

276:1851 (1997)), there is evidence that chromosomal abnormalities, such as the deletion of 13q14 and rearrangements of 14q increase the proliferation of myeloma cells.

5 Up to 30% of patients who suffer with MM have a balanced translocation, t(4;14)(p16.3;q32), that places the fibroblast growth factor receptor 3 (FGFR3) gene under the control of IgH promoter elements (Chesi et al., Nat. Genet. 16:260 (1997)). This results in increased expression of
10 FGFR3, a member of a family of tyrosine kinase receptors implicated in control of cellular proliferation.

According to Zoger et al., Blood 95:1925 (2000), monoallelic deletions of the retinoblastoma-1 (rb-1) gene and the D13S319 locus were observed in 48 of 104 patients
15 (46.2%) and in 28 of 72 (38.9%) patients, respectively, with newly diagnosed MM. Fluorescence in situ hybridization (FISH) studies found that 13q14 was deleted in all 17 patients with karyotypic evidence of monosomy 13 or deletion of 13q but also in 9 of 19 patients with
20 apparently normal karyotypes. Patients with a 13q14 deletion were more likely to have higher serum levels of beta(2)-microglobulin (P=0.059) and a higher percentage of bone marrow plasma cells (P=0.085) than patients with a normal 13q14 status on FISH analysis. In patients with a
25 deletion of 13q14, myeloma cell proliferation was markedly increased. The presence of a 13q14 deletion on FISH analysis was associated with a significantly lower rate of response to conventional-dose chemotherapy (40.8% compared with 78.6%; P =.009) and a shorter overall
30 survival (24.2 months compared with > 60 months; P <.005) than in patients without the deletion.

There are numerous other mutated genes and chromosomal abnormalities that may predispose to MM. Examples of such genes are: B2M (15q21-q22); CCND1
35 (D11S287E, Cyclin D, PRAD1)(11q13); CD19 (16p11.2); HGF

(HPTA) (7q21.1); IL6 (IFNB2) (7p21); IRF4 (MUM1, LSIRF) (6p25-p23); LTA (TNFB, LT) (6p21.3); SDC1 (2p24.1); and TNF (TNFA, TNFSF2, DIF) (6p21.3). Examples of chromosomal abnormalities include: t(6;14) (p25;q32) and
5 t(11;14) (q13;q32).

Other significant diseases or disorders of the bone marrow are also believed, or likely to have, a genetic, typically polygenic, etiologic component. These diseases include, for example, chronic myeloid leukemia,
10 chronic lymphoid leukemia, polycythemia vera, myelofibrosis, primary thrombocythemia, myelodysplastic syndromes, Wiskott-Aldrich, lymphoproliferative syndrome, aplastic anemia, Fanconi anemia, Down syndrome, sickle cell disease, thalassemia, granulocyte disorders, Kostmann
15 syndrome, chronic granulomatous disease, Chediak-Higashi syndrome, platelet disorders, Glanzmann thrombasthenia, Bernard-Soulier syndrome, metabolic storage diseases, osteoporosis, congenital hemophagocytic syndrome.

The human genome-derived single exon nucleic acid
20 probes and microarrays of the present invention are useful for predicting, diagnosing, grading, staging, monitoring and prognosing diseases of human bone marrow, particularly those diseases with polygenic etiology. With each of the single exon probes described herein shown to be expressed
25 at detectable levels in human bone marrow, and with about 2/3 of the probes identifying novel genes, the single exon microarrays of the present invention provide exceptionally high informational content for such studies.

For example, diagnosis, grading, and/or staging
30 of a disease can be based upon the quantitative relatedness of a patient gene expression profile to one or more reference expression profiles known to be characteristic of a given bone marrow disease, or to specific grades or stages thereof.

35 In one embodiment, the patient gene expression

profile is generated by hybridizing nucleic acids obtained directly or indirectly from transcripts expressed in the patient's bone marrow (or cells cultured therefrom) to the genome-derived single exon microarray of the present invention. Reference profiles are obtained similarly by hybridizing nucleic acids obtained directly or indirectly from transcripts expressed in the bone marrow of individuals with known disease. Methods for quantitatively relating gene expression profiles, without regard to the function of the protein encoded by the gene, are disclosed in WO 99/58720, incorporated herein by reference in its entirety.

In another approach, the genome-derived single exon probes and microarrays of the present invention can be used to interrogate genomic DNA, rather than pools of expressed message; this latter approach permits predisposition to and/or prognosis of diseases of bone marrow to be assessed through the massively parallel determination of altered copy number, deletion, or mutation in the patient's genome of exons known to be expressed in human bone marrow. The algorithms set forth in WO 99/58720 can be applied to such genomic profiles without regard to the function of the protein encoded by the interrogated gene.

The utility is specific to the probe; at sufficiently high hybridization stringency, which stringencies are well known in the art — see Ausubel et al. and Maniatis et al. — each probe reports the level of expression of message specifically containing that ORF.

It should be appreciated, however, that the probes of the present invention, for which expression in the bone marrow has been demonstrated are useful for both measurement in the bone marrow and for survey of expression in other tissues.

Significant among such advantages is the presence

of probes for novel genes.

As mentioned above and further detailed in Examples 1 and 2, the methods described enable ORFs which are not present in existing expression databases to be
5 identified. And the fewer the number of tissues in which the ORF can be shown to be expressed, the more likely the ORF will prove to be part of a novel gene: as further discussed in Example 2, ORFs whose expression was measurable in only a single of the tested tissues were
10 represented in existing expression databases at a rate of only 11%, whereas 36% of ORFs whose expression was measurable in 9 tissues were present in existing expression databases, and fully 45% of those ORFs expressed in all ten tested tissues were present in existing expressed sequence
15 databases.

Either as tools for measuring gene expression or tools for surveying gene expression, the genome-derived single exon probes of the present invention have significant advantages over the cDNA or EST-based probes
20 that are currently available for achieving these utilities.

The genome-derived single exon probes of the present invention are useful in constructing genome-derived single exon microarrays; the genome-derived single exon microarrays, in turn, are useful devices for measuring and
25 for surveying gene expression in the human.

Gene expression analysis using microarrays - conventionally using microarrays having probes derived from expressed message - is well-established as useful in the biological research arts (see Lockhart et al. Nature 405,
30 827-836).

Microarrays have been used to determine gene expression profiles in cells in response to drug treatment (see, for example, Kaminski et al., "Global Analysis of Gene Expression in Pulmonary Fibrosis Reveals Distinct
35 Programs Regulating Lung Inflammation and Fibrosis," *Proc.*

- Natl. Acad. Sci. USA 97(4):1778-83 (2000); Bartosiewicz et al., "Development of a Toxicological Gene Array and Quantitative Assessment of This Technology," *Arch. Biochem. Biophys.* 376(1):66-73 (2000)), viral infection (see for
5 example, Geiss et al., "Large-scale Monitoring of Host Cell Gene Expression During HIV-1 Infection Using cDNA Microarrays," *Virology* 266(1):8-16 (2000)) and during cell processes such as differentiation, senescence and apoptosis (see, for example, Shelton et al., "Microarray Analysis of
10 Replicative Senescence," *Curr. Biol.* 9(17):939-45 (1999); Voehringer et al., "Gene Microarray Identification of Redox and Mitochondrial Elements That Control Resistance or Sensitivity to Apoptosis," *Proc. Natl. Acad. Sci. USA* 97(6):2680-5 (2000)).
- 15 Microarrays have also been used to determine abnormal gene expression in diseased tissues (see, for example, Alon et al., "Broad Patterns of Gene Expression Revealed by Clustering Analysis of Tumor and Normal Colon Tissues Probed by Oligonucleotide Arrays," *Proc. Natl.*
20 *Acad. Sci. USA* 96(12):6745-50 (1999); Perou et al., "Distinctive Gene Expression Patterns in Human Mammary Epithelial Cells and Breast Cancers," *Proc. Natl. Acad. Sci. USA* 96(16):9212-7 (1999); Wang et al., "Identification of Genes Differentially Over-expressed in Lung Squamous Cell
25 Carcinoma Using Combination of cDNA Subtraction and Microarray Analysis," *Oncogene* 19(12):1519-28 (2000); Whitney et al., "Analysis of Gene Expression in Multiple Sclerosis Lesions Using cDNA Microarrays," *Ann. Neurol.* 46(3):425-8 (1999)), in drug discovery screens (see, for
30 example, Scherf et al., "A Gene Expression Database for the Molecular Pharmacology of Cancer," *Nat. Genet.* 24(3):236-44 (2000)) and in diagnosis to determine appropriate treatment strategies (see, for example, Sgroi et al., "In vivo Gene Expression Profile Analysis of Human Breast Cancer

Progression," *Cancer Res.* 59(22):5656-61 (1999)).

In microarray-based gene expression screens of pharmacological drug candidates upon cells, each probe provides specific useful data. In particular, it should be appreciated that even those probes that show no change in expression are as informative as those that do change, serving, in essence, as negative controls.

For example, where gene expression analysis is used to assess toxicity of chemical agents on cells, the failure of the agent to change a gene's expression level is evidence that the drug likely does not affect the pathway of which the gene's expressed protein is a part.

Analogously, where gene expression analysis is used to assess side effects of pharmacological agents - whether in lead compound discovery or in subsequent screening of lead compound derivatives - the inability of the agent to alter a gene's expression level is evidence that the drug does not affect the pathway of which the gene's expressed protein is a part.

WO 99/58720 provides methods for quantifying the relatedness of a first and second gene expression profile and for ordering the relatedness of a plurality of gene expression profiles. The methods so described permit useful information to be extracted from a greater percentage of the individual gene expression measurements from a microarray than methods previously used in the art.

Other uses of microarrays are described in Gerhold et al., *Trends Biochem. Sci.* 24(5):168-173 (1999) and Zweiger, *Trends Biotechnol.* 17(11):429-436 (1999); Schena et al.

The invention particularly provides genome-derived single-exon probes known to be expressed in bone marrow. The individual single exon probes can be provided in the form of substantially isolated and purified nucleic acid, typically, but not necessarily, in a quantity

sufficient to perform a hybridization reaction.

Such nucleic acid can be in any form directly hybridizable to the message that contains the probe's ORF, such as double stranded DNA, single-stranded DNA
5 complementary to the message, single-stranded RNA complementary to the message, or chimeric DNA/RNA molecules so hybridizable. The nucleic acid can alternatively or additionally include either nonnative nucleotides, alternative internucleotide linkages, or both, so long as
10 complementary binding can be obtained. For example, probes can include phosphorothioates, methylphosphonates, morpholino analogs, and peptide nucleic acids (PNA), as are described, for example, in U.S. Patent Nos. 5,142,047; 5,235,033; 5,166,315; 5,217,866; 5,184,444; 5,861,250.

15 Usefully, however, such probes are provided in a form and quantity suitable for amplification, where the amplified product is thereafter to be used in the hybridization reactions that probe gene expression. Typically, such probes are provided in a form and quantity
20 suitable for amplification by PCR or by other well known amplification technique. One such technique additional to PCR is rolling circle amplification, as is described, *inter alia*, in U.S. Patent Nos. 5,854,033 and 5,714,320 and international patent publications WO 97/19193 and
25 WO 00/15779. As is well understood, where the probes are to be provided in a form suitable for amplification, the range of nucleic acid analogues and/or internucleotide linkages will be constrained by the requirements and nature of the amplification enzyme.

30 Where the probe is to be provided in form suitable for amplification, the quantity need not be sufficient for direct hybridization for gene expression analysis, and need be sufficient only to function as an amplification template, typically at least about 1, 10 or
35 100 pg or more.

Each discrete amplifiable probe can also be packaged with amplification primers, either in a single composition that comprises probe template and primers, or in a kit that comprises such primers separately packaged therefrom. As earlier mentioned, the ORF-specific 5' primers used for genomic amplification can have a first common sequence added thereto, and the ORF-specific 3' primers used for genomic amplification can have a second, different, common sequence added thereto, thus permitting, in this embodiment, the use of a single set of 5' and 3' primers to amplify any one of the probes. The probe composition and/or kit can also include buffers, enzyme, etc., required to effect amplification.

As mentioned earlier, when intended for use on a genome-derived single exon microarray of the present invention, the genome-derived single exon probes of the present invention will typically average at least about 100, 200, 300, 400 or 500 bp in length, including (and typically, but not necessarily centered about) the ORF. Furthermore, when intended for use on a genome-derived single exon microarray of the present invention, the genome-derived single exon probes of the present invention will typically not contain a detectable label.

When intended for use in solution phase hybridization, however — that is, for use in a hybridization reaction in which the probe is not first bound to a support substrate (although the target may indeed be so bound) — length constraints that are imposed in microarray-based hybridization approaches will be relaxed, and such probes will typically be labeled.

In such case, the only functional constraint that dictates the minimum size of such probe is that each such probe must be capable of specifically identifying in a hybridization reaction the exon from which it is drawn. In theory, a probe of as little as 17 nucleotides is capable

of uniquely identifying its cognate sequence in the human genome. For hybridization to expressed message - a subset of target sequence that is much reduced in complexity as compared to genomic sequence - even fewer nucleotides are
5 required for specificity.

Therefore, the probes of the present invention can include as few as 20, 25 or 50 bp or ORF, or more. In particular embodiments, the ORF sequences are given in SEQ ID NOS. 13,115 - 26,012, respectively, for probe SEQ ID
10 NOS. 1 - 13,114. The minimum amount of ORF required to be included in the probe of the present invention in order to provide specific signal in either solution phase or microarray-based hybridizations can readily be determined for each of ORF SEQ ID NOS. 13,115 - 26,012 individually
15 by routine experimentation using standard high stringency conditions.

Such high stringency conditions are described, *inter alia*, in Ausubel et al. and Maniatis et al. For microarray-based hybridization, standard high stringency
20 conditions can usefully be 50% formamide, 5X SSC, 0.2 µg/µl poly(dA), 0.2 µg/µl human c₀t1 DNA, and 0.5 % SDS, in a humid oven at 42°C overnight, followed by successive washes of the microarray in 1X SSC, 0.2% SDS at 55°C for 5 minutes, and then 0.1X SSC, 0.2% SDS, at 55°C for 20
25 minutes. For solution phase hybridization, standard high stringency conditions can usefully be aqueous hybridization at 65°C in 6X SSC. Lower stringency conditions, suitable for cross-hybridization to mRNA encoding structurally- and functionally-related proteins, can usefully be the same as
30 the high stringency conditions but with reduction in temperature for hybridization and washing to room temperature (approximately 25°C).

When intended for use in solution phase hybridization, the maximum size of the single exon probes
35 of the present invention is dictated by the proximity of

other expressed exons in genomic DNA: although each single exon probe can include intergenic and/or intronic material contiguous to the ORF in the human genome, each probe of the present invention will include portions of only one
5 expressed exon.

Thus, each single exon probe will include no more than about 25 kb of contiguous genomic sequence, more typically no more than about 20 kb of contiguous genomic sequence, more usually no more than about 15 kb, even more
10 usually no more than about 10 kb. Usually, probes that are maximally about 5 kb will be used, more typically no more than about 3 kb.

It will be appreciated that the Sequence Listing appended hereto presents, by convention, only that strand
15 of the probe and ORF sequence that can be directly translated reading from 5' to 3' end. As would be well understood by one of skill in the art, single stranded probes must be complementary in sequence to the ORF as present in an mRNA; it is well within the skill in the art
20 to determine such complementary sequence. It will further be understood that double stranded probes can be used in both solution-phase hybridization and microarray-based hybridization if suitably denatured.

Thus, it is an aspect of the present invention to
25 provide single-stranded nucleic acid probes that have sequence complementary to those described herein above and below, and double-stranded probes one strand of which has sequence complementary to the probes described herein.

The probes can, but need not, contain intergenic
30 and/or intronic material that flanks the ORF, on one or both sides, in the same linear relationship to the ORF that the intergenic and/or intronic material bears to the ORF in genomic DNA. The probes do not, however, contain nucleic acid derived from more than one expressed ORF.

35 And when intended for use in solution

hybridization, the probes of the present invention can usefully have detectable labels. Nucleic acid labels are well known in the art, and include, *inter alia*, radioactive labels, such as ^3H , ^{32}P , ^{33}P , ^{35}S , ^{125}I , ^{131}I ; fluorescent
5 labels, such as Cy3, Cy5, Cy5.5, Cy7, SYBR[®]

Green and other labels described in Haugland, *Handbook of Fluorescent Probes and Research Chemicals*, 7th ed., Molecular Probes Inc., Eugene, OR (2000), or fluorescence resonance energy transfer tandem conjugates
10 thereof; labels suitable for chemiluminescent and/or enhanced chemiluminescent detection; labels suitable for ESR and NMR detection; and labels that include one member of a specific binding pair, such as biotin, digoxigenin, or the like.

15 The probes, either in quantity sufficient for hybridization or sufficient for amplification, can be provided in individual vials or containers.

Alternatively, such probes can usefully be packaged as a plurality of such individual genome-derived
20 single exon probes.

When provided as a collection of plural individual probes, the probes are typically made available in amplifiable form in a spatially-addressable ordered set, typically one per well of a microtiter dish. Although a 96
25 well microtiter plate can be used, greater efficiency is obtained using higher density arrays.

If, as earlier mentioned, the ORF-specific 5' primers used for genomic amplification had a first common sequence added thereto, and the ORF-specific 3'
30 primers used for genomic amplification had a second, different, common sequence added thereto, a single set of 5' and 3' primers can be used to amplify all of the probes from the amplifiable ordered set.

Such collections of genome-derived single exon
35 probes can usefully include a plurality of probes chosen

for the common attribute of expression in the human bone marrow.

In such defined subsets, typically at least 50, 60, 75, 80, 85, 90 or 95% or more of the probes will be
5 chosen by their expression in the defined tissue or cell type.

The single exon probes of the present invention, as well as fragments of the single exon probes comprising selectively hybridizable portions of the probe ORF, can be
10 used to obtain the full length cDNA that includes the ORF by (i) screening of cDNA libraries; (ii) rapid amplification of cDNA ends ("RACE"); or (iii) other conventional means, as are described, *inter alia*, in Ausubel et al. and Maniatis et al.

15 It is another aspect of the present invention to provide genome-derived single exon nucleic acid microarrays useful for gene expression analysis, where the term "microarray" has the meaning given in the definitional section of this description, *supra*.

20 The invention particularly provides genome-derived single-exon nucleic acid microarrays comprising a plurality of probes known to be expressed in human bone marrow. In preferred embodiments, the present invention provides human genome-derived single exon microarrays
25 comprising a plurality of probes drawn from the group consisting of SEQ ID NOS.: 1 - 13,114.

When used for gene expression analysis, the genome-derived single exon microarrays provide greater physical informational density than do the genome-derived
30 single exon microarrays that have lower percentages of probes known to be expressed commonly in the tested tissue. At a fixed probe density, for example, a given microarray surface area of the defined subset genome-derived single exon microarray can yield a greater number of expression
35 measurements. Alternatively, at a given probe density, the

same number of expression measurements can be obtained from a smaller substrate surface area. Alternatively, at a fixed probe density and fixed surface area, probes can be provided redundantly, providing greater reliability in
5 signal measurement for any given probe. Furthermore, with a higher percentage of probes known to be expressed in the assayed tissue, the dynamic range of the detection means can be adjusted to reveal finer levels discrimination among the levels of expression.

10 Although particularly described with respect to their utility as probes of gene expression, particularly as probes to be included on a genome-derived single exon microarray, each of the nucleic acids having SEQ ID NOS.: 1 - 13,114 contains an open-reading frame, set forth
15 respectively in SEQ ID NOS.: 13,115 - 26,012, that encodes a protein domain. Thus, each of SEQ ID NOS. 1 - 13,114 can be used, or that portion thereof in SEQ ID NOS. 13,115 - 26,012 used, to express a protein domain by standard *in vitro* recombinant techniques. See Ausubel et al. and
20 Maniatis et al.

Additionally, kits are available commercially that readily permit such nucleic acids to be expressed as protein in bacterial cells, insect cells, or mammalian cells, as desired (e.g., HAT™ Protein Expression &
25 Purification System, ClonTech Laboratories, Palo Alto, CA; Adeno-X™ Expression System, ClonTech Laboratories, Palo Alto, CA; Protein Fusion & Purification (pMAL™) System, New England Biolabs, Beverley, MA)

Furthermore, shorter peptides can be chemically
30 synthesized using commercial peptide synthesizing equipment and well known techniques. Procedures are described, *inter alia*, in Chan et al. (eds.), Fmoc Solid Phase Peptide Synthesis: A Practical Approach (Practical Approach Series, (Paper)), Oxford Univ. Press (March 2000) (ISBN:
35 0199637245); Jones, Amino Acid and Peptide Synthesis

(Oxford Chemistry Primers, No 7) , Oxford Univ. Press
(August 1992) (ISBN: 0198556683); and Bodanszky, Principles
of Peptide Synthesis (Springer Laboratory), Springer Verlag
(December 1993) (ISBN: 0387564314).

5 It is, therefore, another aspect of the invention
to provide peptides comprising an amino acid sequence
translated from SEQ ID NOS.: 13,115 - 26,012. Such amino
acid sequences are set out in SEQ ID NOS: 26,013 - 38,628.
Any such recombinantly-expressed or synthesized peptide of
10 at least 8, and preferably at least about 15, amino acids,
can be conjugated to a carrier protein and used to generate
antibody that recognizes the peptide. Thus, it is a
further aspect of the invention to provide peptides that
have at least 8, preferably at least 15, consecutive amino
15 acids.

The following examples are offered by way of
illustration and not by way of limitation.

20 EXAMPLE 1

Preparation of Single Exon Microarrays from ORFs Predicted
in Human Genomic Sequence

Bioinformatics Results

25 All human BAC sequences in fewer than 10 pieces
that had been accessioned in a five month period
immediately preceding this study were downloaded from
GenBank. This corresponds to ~2200 clones, totaling ~350
MB of sequence, or approximately 10% of the human genome.

30 After masking repetitive elements using the
program CROSS_MATCH, the sequence was analyzed for open
reading frames using three separate gene finding programs.
The three programs predict genes using independent
algorithmic methods developed on independent training sets:
35 GRAIL uses a neural network, GENEFINDER uses a hidden

Markoff model, and DICTION, a program proprietary to Genetics Institute, operates according to a different heuristic. The results of all three programs were used to create a prediction matrix across the segment of genomic
5 DNA.

The three gene finding programs yielded a range of results. GRAIL identified the greatest percentage of genomic sequence as putative coding region, 2% of the data analyzed. GENEFINDER was second, calling 1%, and DICTION
10 yielded the least putative coding region, with 0.8% of genomic sequence called as coding region.

The consensus data were as follows. GRAIL and GENEFINDER agreed on 0.7% of genomic sequence, GRAIL and DICTION agreed on 0.5% of genomic sequence, and the three
15 programs together agreed on 0.25% of the data analyzed. That is, 0.25% of the genomic sequence was identified by all three of the programs as containing putative coding region.

ORFs predicted by any two of the three programs
20 ("consensus ORFs") were assorted into "gene bins" using two criteria: (1) any 7 consecutive exons within a 25 kb window were placed together in a bin as likely contributing to a single gene, and (2) all ORFs within a 25 kb window were placed together in a bin as likely contributing to a single
25 gene if fewer than 7 exons were found within the 25 kb window.

PCR

The largest ORF from each gene bin that did not
30 span repetitive sequence was then chosen for amplification, as were all consensus ORFs longer than 500 bp. This method approximated one exon per gene; however, a number of genes were found to be represented by multiple elements.

Previously, we had determined that DNA fragments
35 fewer than 250 bp in length do not bind well to the amino-

modified glass surface of the slides used as support substrate for construction of microarrays; therefore, amplicons were designed in the present experiments to approximate 500 bp in length.

5 Accordingly, after selecting the largest ORF per gene bin, a 500 bp fragment of sequence centered on the ORF was passed to the primer picking software, PRIMER3 (available online for use at <http://www-genome.wi.mit.edu/cgi-bin/primer/>). A first
10 additional sequence was commonly added to each ORF-unique 5' primer, and a second, different, additional sequence was commonly added to each ORF-unique 3' primer, to permit subsequent reamplification of the amplicon using a single set of "universal" 5' and 3' primers, thus immortalizing
15 the amplicon. The addition of universal priming sequences also facilitates sequence verification, and can be used to add a cloning site should some ORFs be found to warrant further study.

The ORFs were then PCR amplified from genomic
20 DNA, verified on agarose gels, and sequenced using the universal primers to validate the identity of the amplicon to be spotted in the microarray.

Primers were supplied by Operon Technologies (Alameda, CA). PCR amplification was performed by standard
25 techniques using human genomic DNA (Clontech, Palo Alto, CA) as template. Each PCR product was verified by SYBR[®] green (Molecular Probes, Inc., Eugene, OR) staining of agarose gels, with subsequent imaging by Fluorimager (Molecular Dynamics, Inc., Sunnyvale, CA). PCR
30 amplification was classified as successful if a single band appeared.

The success rate for amplifying ORFs of interest directly from genomic DNA using PCR was approximately 75%. FIG. 5 graphs the distribution of predicted ORF (exon)
35 length and distribution of amplified PCR products, with ORF

length shown in red and PCR product length shown in blue (which may appear black in the figure). Although the range of ORF sizes is readily seen to extend to beyond 900 bp, the mean predicted exon size was only 229 bp, with a median
5 size of 150 bp (n=9498). With an average amplicon size of 475 ± 25 bp, approximately 50% of the average PCR amplification product contained predicted coding region, with the remaining 50% of the amplicon containing either intron, intergenic sequence, or both.

10 Using a strategy predicated on amplifying about 500 bp, it was found that long exons had a higher PCR failure rate. To address this, the bioinformatics process was adjusted to amplify 1000, 1500 or 2000 bp fragments from exons larger than 500 bp. This improved the rate of
15 successful amplification of exons exceeding 500 bp, constituting about 9.2% of the exons predicted by the gene finding algorithms.

Approximately 75% of the probes disposed on the array (90% of those that successfully PCR amplified) were
20 sequence-verified by sequencing in both the forward and reverse direction using MegaBACE sequencer (Molecular Dynamics, Inc., Sunnyvale, CA), universal primers, and standard protocols.

Some genomic clones (BACs) yielded very poor PCR
25 and sequencing results. The reasons for this are unclear, but may be related to the quality of early draft sequence or the inclusion of vector and host contamination in some submitted sequence data.

Although the intronic and intergenic material
30 flanking coding regions could theoretically interfere with hybridization during microarray experiments, subsequent empirical results demonstrated that differential expression ratios were not significantly affected by the presence of noncoding sequence. The variation in exon size was
35 similarly found not to affect differential expression

ratios significantly; however, variation in exon size was observed to affect the absolute signal intensity (data not shown).

The 350 MB of genomic DNA was, by the above-
5 described process, reduced to 9750 discrete probes, which were spotted in duplicate onto glass slides using commercially available instrumentation (MicroArray GenII Spotter and/or MicroArray GenIII Spotter, Molecular Dynamics, Inc., Sunnyvale, CA). Each slide additionally
10 included either 16 or 32 *E. coli* genes, the average hybridization signal of which was used as a measure of background biological noise.

Each of the probe sequences was BLASTed against the human EST data set, the NR data set, and SwissProt
15 GenBank (May 7, 1999 release 2.0.9).

One third of the probe sequences (as amplified) produced an exact match (BLAST Expect ("E") values less than $1 e^{-100}$) to either an EST (20% of sequences) or a known mRNA (13% of sequences). A further 22% of the probe
20 sequences showed some homology to a known EST or mRNA (BLAST E values from $1 e^{-5}$ to $1 e^{-99}$). The remaining 45% of the probe sequences showed no significant sequence homology to any expressed, or potentially expressed, sequences present in public databases.

25 All of the probe sequences (as amplified) were then analyzed for protein similarities with the SwissProt database using BLASTX, Gish et al., *Nature Genet.* 3:266 (1993). The predicted functional breakdowns of the 2/3 of probes identical or homologous to known sequences are
30 presented in Table 1.

Table 1

Function of Predicted ORFs As Deduced From Comparative Sequence Analysis
--

Total	V6 chip	V7 chip	Function Predicted from Comparative Sequence Analysis
211	96	115	Receptor
120	43	77	Zinc Finger
30	11	19	Homeobox
25	9	16	Transcription Factor
17	11	7	Transcription
118	57	61	Structural
95	39	56	Kinase
36	18	18	Phosphatase
83	31	52	Ribosomal
45	19	26	Transport
21	17	14	Growth Factor
17	12	5	Cytochrome
50	33	17	Channel

As can be seen, the two most common types of genes were transcription factors and receptors, making up 2.2% and 1.8% of the arrayed elements, respectively.

5

EXAMPLE 2

Gene Expression Measurements From Genome-Derived Single Exon Microarrays

10

The two genome-derived single exon microarrays prepared according to Example 1 were hybridized in a series of simultaneous two-color fluorescence experiments to (1) 15 Cy3-labeled cDNA synthesized from message drawn individually from each of brain, heart, liver, fetal liver, placenta, lung, bone marrow, HeLa, BT 474, or HBL 100 cells, and (2) Cy5-labeled cDNA prepared from message

pooled from all ten tissues and cell types, as a control in each of the measurements. Hybridization and scanning were carried out using standard protocols and Molecular Dynamics equipment.

5 Briefly, mRNA samples were bought from commercial sources (Clontech, Palo Alto, CA and Amersham Pharmacia Biotech (APB)). Cy3-dCTP and Cy5-dCTP (both from APB) were incorporated during separate reverse transcriptions of 1 µg of polyA⁺ mRNA performed using 1 µg oligo(dT)12-18 primer
10 and 2 µg random 9mer primers as follows. After heating to 70°C, the RNA:primer mixture was snap cooled on ice. After snap cooling on ice, added to the RNA to the stated final concentration was: 1X Superscript II buffer, 0.01 M DTT, 100µM dATP, 100 µM dGTP, 100 µM dTTP, 50 µM dCTP, 50 µM
15 Cy3-dCTP or Cy5-dCTP 50 µM, and 200 U Superscript II enzyme. The reaction was incubated for 2 hours at 42°C. After 2 hours, the first strand cDNA was isolated by adding 1 U Ribonuclease H, and incubating for 30 minutes at 37°C. The reaction was then purified using a Qiagen PCR cleanup
20 column, increasing the number of ethanol washes to 5. Probe was eluted using 10 mM Tris pH 8.5.

Using a spectrophotometer, probes were measured for dye incorporation. Volumes of both Cy3 and Cy5 cDNA corresponding to 50 pmoles of each dye were then dried in a
25 Speedvac, resuspended in 30 µl hybridization solution containing 50% formamide, 5X SSC, 0.2 µg/µl poly(dA), 0.2 µg/µl human c₀t1 DNA, and 0.5 % SDS.

Hybridizations were carried out under a coverslip, with the array placed in a humid oven at 42°C
30 overnight. Before scanning, slides were washed in 1X SSC, 0.2% SDS at 55°C for 5 minutes, followed by 0.1X SSC, 0.2% SDS, at 55°C for 20 minutes. Slides were briefly dipped in water and dried thoroughly under a gentle stream of nitrogen.

35 Slides were scanned using a Molecular Dynamics

Gen3 scanner, as described. Schena (ed.), Microarray Biochip: Tools and Technology, Eaton Publishing Company/BioTechniques Books Division (2000) (ISBN: 1881299376).

5 Although the use of pooled cDNA as a reference permitted the survey of a large number of tissues, it attenuates the measurement of relative gene expression, since every highly expressed gene in the tissue/cell type-specific fluorescence channel will be present to a level of
10 at least 10% in the control channel. Because of this fact, both signal and expression ratios (the latter hereinafter, "expression" or "relative expression") for each probe were normalized using the average ratio or average signal, respectively, as measured across the whole slide.

15 Data were accepted for further analysis only when signal was at least three times greater than biological noise, the latter defined by the average signal produced by the *E. coli* control genes.

 The relative expression signal for these probes
20 was then plotted as function of tissue or cell type, and is presented in FIG. 6.

 FIG. 6 shows the distribution of expression across a panel of ten tissues. The graph shows the number of sequence-verified products that were either not
25 expressed ("0"), expressed in one or more but not all tested tissues ("1" - "9"), and expressed in all tissues tested ("10").

 Of 9999 arrayed elements on the two microarrays (including positive and negative controls and "failed"
30 products), 2353 (51%) were expressed in at least one tissue or cell type. Of the gene elements showing significant signal - where expression was scored as "significant" if the normalized Cy3 signal was greater than 1, representing signal 5-fold over biological noise (0.2) - 39% (991) were
35 expressed in all 10 tissues. The next most common class

(15%) consisted of gene elements expressed in only a single tissue.

The genes expressed in a single tissue were further analyzed, and the results of the analyses are
5 compiled in FIG. 7.

FIG. 7A is a matrix presenting the expression of all verified sequences that showed expression greater than 3 in at least one tissue. Each clone is represented by a column in the matrix. Each of the 10 tissues assayed is
10 represented by a separate row in the matrix, and relative expression of a clone in that tissue is indicated at the respective node by intensity of green shading, with the intensity legend shown in panel B. The top row of the matrix ("EST Hit") contains "bioinformatic" rather than
15 "physical" expression data - that is, presents the results returned by query of EST, NR and SwissProt databases using the probe sequence. The legend for "bioinformatic expression" (i.e., degree of homology returned) is presented in panel C. Briefly, white is known, black is
20 novel, with gray depicting nonidentical with significant homology (white: E values < 1e-100; gray: E values from 1e-05 to 1e-99; black: E values > 1e-05).

As FIG. 7 readily shows, heart and brain were demonstrated to have the greatest numbers of genes that
25 were shown to be uniquely expressed in the respective tissue. In brain, 200 uniquely expressed genes were identified; in heart, 150. The remaining tissues gave the following figures for uniquely expressed genes: liver, 100; lung, 70; fetal liver, 150; bone marrow, 75; placenta, 100;
30 HeLa, 50; HBL, 100; and BT474, 50.

It was further observed that there were many more "novel" genes among those that were up-regulated in only one tissue, as compared with those that were down-regulated in only one tissue. In fact, it was found that ORFs whose
35 expression was measurable in only a single of the tested

tissues were represented in sequencing databases at a rate of only 11%, whereas 36% of the ORFs whose expression was measurable in 9 of the tissues were present in public databases. As for those ORFs expressed in all ten tissues, 5 fully 45% were present in existing expressed sequence databases. These results are not unexpected, since genes expressed in a greater number of tissues have a higher likelihood of being, and thus of having been, discovered by EST approaches.

10

Comparison of Signal from Known and Unknown Genes

The normalized signal of the genes found to have high homology to genes present in the GenBank human EST database were compared to the normalized signal of those 15 genes not found in the GenBank human EST database. The data are shown in FIG. 8.

FIG. 8 shows the normalized Cy3 signal intensity for all sequence-verified products with a BLAST Expect ("E") value of greater than $1e-30$ (designated "unknown") 20 upon query of existing EST, NR and SwissProt databases, and shows in blue the normalized Cy3 signal intensity for all sequence-verified products with a BLAST Expect value of less than $1e-30$ ("known"). Note that biological background noise has an averaged normalized Cy3 signal intensity of 25 0.2.

As expected, the most highly expressed of the ORFs were "known" genes. This is not surprising, since very high signal intensity correlates with very commonly-expressed genes, which have a higher likelihood of being 30 found by EST sequence.

However, a significant point is that a large number of even the high expressers were "unknown". Since the genomic approach used to identify genes and to confirm their expression does not bias exons toward either the 3' 35 or 5' end of a gene, many of these high expression genes

will not have been detected in an end-sequenced cDNA library.

The significant point is that presence of the gene in an EST database is *not* a prerequisite for incorporation into a genome-derived microarray, and further, that arraying such "unknown" exons can help to assign function to as-yet undiscovered genes.

Verification of Gene Expression

10 To ascertain the validity of the approach described above to identify genes from raw genomic sequence, expression of two of the probes was assayed using reverse transcriptase polymerase chain reaction (RT PCR) and northern blot analysis.

15 Two microarray probes were selected on the basis of exon size, prior sequencing success, and tissue-specific gene expression patterns as measured by the microarray experiments. The primers originally used to amplify the two respective ORFs from genomic DNA were used in RT PCR
20 against a panel of tissue-specific cDNAs (Rapid-Scan gene expression panel 24 human cDNAs) (OriGene Technologies, Inc., Rockville, MD).

Sequence AL079300_1 was shown by microarray hybridization to be present in cardiac tissue, and sequence
25 AL031734_1 was shown by microarray experiment to be present in placental tissue (data not shown). RT-PCR on these two sequences confirmed the tissue-specific gene expression as measured by microarrays, as ascertained by the presence of a correctly sized PCR product from the respective tissue
30 type cDNAs.

Clearly, all microarray results cannot, and indeed should not, be confirmed by independent assay methods, or the high throughput, highly parallel advantages of microarray hybridization assays will be lost. However,
35 in addition to the two RT-PCR results presented above, the

observation that 1/3 of the arrayed genes exist in expression databases provides powerful confirmation of the power of our methodology – which combines bioinformatic prediction with expression confirmation using genome-derived single exon microarrays – to identify novel genes from raw genomic data.

To verify that the approach further provides correct characterization of the expression patterns of the identified genes, a detailed analysis was performed of the microarrayed sequences that showed high signal in brain.

For this latter analysis, sequences that showed high (normalized) signal in brain, but which showed very low (normalized) signal (less than 0.5, determined to be biological noise) in all other tissues, were further studied. There were 82 sequences that fit these criteria, approximately 2% of the arrayed elements. The 10 sequences showing the highest signal in brain in microarray hybridizations are detailed in Table 2, along with assigned function, if known or reasonably predicted.

20

Table 2

Function of the Most Highly Expressed Genes Expressed Only in Brain				
Microarray Sequence Name	Normalized Signal	Expression Ratio	Homology to EST present in GenBank	Gene Function as described by GenBank
AP000217-1	5.2	+7.7	High	S-100 protein, b-chain, Ca ²⁺ binding protein expressed in central nervous

				system
AP000047-1	2.3		High	Unknown Function
AC006548-9	1.7		High	Similar to mouse membrane glyco-protein M6, expressed in central nervous system
AC007245-5	1.5		High	Similar to amphiphysin, a synaptic vesicle- associated protein. Ref 21
L44140-4	1.2	+2.0	High	Endothelial actin-binding protein found in nonmuscle filamin
AC004689-9	1.2	+3.5	High	Protein Phosphatase PP2A, neuronal/ downregulates activated protein kinases
AL031657-1	1.2	+3.0	High	Unknown function/ Contains the anhyrin motif, a common protein sequence motif
AC009266-2	1.1	+3.7	Low	Low homology to

				the Synaptotagmin I protein in rat/present at low levels throughout rat brain
AP000086-1	1.0	+2.7	Low	Unknown, very poor homology to collagen
AC004689-3	1.0		High	Protein Phosphatase PP2A, neuronal/ downregulates activated protein kinases

Of the ten sequences studied by these latter confirmatory approaches, eight were previously known. Of these eight, six had previously been reported to be
5 important in the central nervous system or brain. The exon giving the highest signal (AP00217-1) was found to be the gene encoding an S100B Ca^{2+} binding protein, reported in the literature to be highly and uniquely expressed in the central nervous system. Heizmann, *Neurochem. Res.* 9:1097
10 (1997).

A number of the brain-specific probe sequences (including AC006548-9, AC009266-2) did not have homology to any known human cDNAs in GenBank but did show homology to rat and mouse cDNAs. Sequences AC004689-9 and AC004689-3
15 were both found to be phosphatases present in neurons (Millward et al., *Trends Biochem. Sci.* 24(5):186-191 (1999)). Two microarray sequences, AP000047-1 and AP000086-1 have unknown function, with AP000086-1 being absent from GenBank. Functionality can now be narrowed

down to a role in the central nervous system for both of these genes, showing the power of designing microarrays in this fashion.

Next, the function of the chip sequences with the highest (normalized) signal intensity in brain, regardless of expression in other tissues, was assessed. In this latter analysis, we found expression of many more common genes, since the sequences were not limited to those expressed only in brain. For example, looking at the 20 highest signal intensity spots in brain, 4 were similar to tubulin (AC00807905; AF146191-2; AC007664-4; AF14191-2), 2 were similar to actin (AL035701-2; AL034402-1), and 6 were found to be homologous to glyceraldehyde-3-phosphate dehydrogenase (GAPDH) (AL035604-1; Z86090-1; AC006064-L, AC006064-K; AC035604-3; AC006064-L). These genes are often used as controls or housekeeping genes in microarray experiments of all types.

Other interesting genes highly expressed in brain were a ferritin heavy chain protein, which is reported in the literature to be found in brain and liver (Joshi et al., *J. Neurol. Sci.* 134(Suppl):52-56 (1995)), a result duplicated with the array. Other highly expressed chip sequences included a translation elongation factor 1 α (AC007564-4), a DEAD-box homolog (AL023804-4), and a Y-chromosome RNA-binding motif (Chai et al., *Genomics* 49(2):283-89 (1998)) (AC007320-3). A low homology analog (AP00123-1/2) to a gene, DSCR1, thought to be involved in trisomy 21 (Down's syndrome), showed high expression in both brain and heart, in agreement with the literature (Fuentes et al., *Mol. Genet.* 4(10):1935-44 (1995)).

As a further validation of the approach, we selected the BAC AC006064 to be included on the array. This BAC was known to contain the GAPDH gene, and thus could be used as a control for the ORF selection process. The gene finding and exon selection algorithms resulted in

choosing 25 exons from BAC AC006064 for spotting onto the array, of which four were drawn from the GAPDH gene. Table 3 shows the comparison of the average expression ratio for the 4 exons from BAC006064 compared with the average expression ratio for 5 different dilutions of a commercially available GAPDH cDNA (Clontech).

Table 3

Comparison of Expression Ratio, for each tissue, of GAPDH		
	AC006064 (n = 4)	Control (n = 5)
Bone Marrow	-1.81 \pm 0.11	-1.85 \pm 0.08
Brain	-1.41 \pm 0.11	-1.17 \pm 0.05
BT474	1.85 \pm 0.09	1.66 \pm 0.12
Fetal Liver	-1.62 \pm 0.07	-1.41 \pm 0.05
HBL100	1.32 \pm 0.05	2.64 \pm 0.12
Heart	1.16 \pm 0.09	1.56 \pm 0.10
HeLa	1.11 \pm 0.06	1.30 \pm 0.15
Liver	-1.62 \pm 0.22	-2.07 \pm
Lung	-4.95 \pm 0.93	-3.75 \pm 0.21
Placenta	-3.56 \pm 0.25	-3.52 \pm 0.43

10

Each tissue shows excellent agreement between the experimentally chosen exons and the control, again demonstrating the validity of the present exon mining approach. In addition, the data also show the variability of expression of GAPDH within tissues, calling into question its classification as a housekeeping gene and utility as a housekeeping control in microarray experiments.

20 EXAMPLE 3

Representation of Sequence and Expression Data as a
"Mondrian"

For each genomic clone processed for microarray
5 as above-described, a plethora of information was
accumulated, including full clone sequence, probe sequence
within the clone, results of each of the three gene finding
programs, EST information associated with the probe
sequences, and microarray signal and expression for
10 multiple tissues, challenging our ability to display the
information.

Accordingly, we devised a new tool for visual
display of the sequence with its attendant annotation
which, in deference to its visual similarity to the
15 paintings of Piet Mondrian, is hereinafter termed a
"Mondrian". FIGS. 3 and 4 present the key to the
information presented on a Mondrian.

FIG. 9 presents a Mondrian of BAC AC008172 (bases
25,000 to 130,000 shown), containing the carbamyl phosphate
20 synthetase gene (AF154830.1). Purple background within the
region shown as field 81 in FIG. 3 indicates all 37 known
exons for this gene.

As can be seen, GRAIL II successfully identified
27 of the known exons (73%), GENEFINDER successfully
25 identified 37 of the known exons (100%), while DICTION
identified 7 of the known exons (19%).

Seven of the predicted exons were selected for
physical assay, of which 5 successfully amplified by PCR
and were sequenced. These five exons were all found to be
30 from the same gene, the carbamyl phosphate synthetase gene
(AF154830.1).

The five exons were arrayed, and gene expression.
measured across 10 tissues. As is readily seen in the
Mondrian, the five chip sequences on the array show
35 identical expression patterns, elegantly demonstrating the

reproducibility of the system..

FIG. 10 is a Mondrian of BAC AL049839. We selected 12 exons from this BAC, of which 10 successfully sequenced, which were found to form between 5 and 6 genes. Interestingly, 4 of the genes on this BAC are protease inhibitors. Again, these data elegantly show that exons selected from the same gene show the same expression patterns, depicted below the red line. From this figure, it is clear that our ability to find known genes is very good. A novel gene is also found from 86.6 kb to 88.6 kb, upon which all the exon finding programs agree. We are confident we have two exons from a single gene since they show the same expression patterns and the exons are proximal to each other. Backgrounds in the following colors indicate a known gene (top to bottom): red = kallistatin protease inhibitor (P29622); purple = plasma serine protease inhibitor (P05154); turquoise = α 1 anti-chymotrypsin (P01011); mauve = 40S ribosomal protein (P08865). Note that chip sequence 8 and 12 did not sequence verify.

EXAMPLE 4

Genome-Derived Single Exon Probes Useful For Measuring Human Gene Expression

The protocols set forth in Examples 1 and 2, *supra*, were applied to additional human genomic sequence as it became newly available in GenBank to identify unique exons in the human genome that could be shown to be expressed at significant levels in bone marrow tissue.

These unique exons are within longer probe sequences. Each probe was completely sequenced on both strands prior to its use on a genome-derived single exon microarray; sequencing confirms the exact chemical

structure of each probe. An added benefit of sequencing is that it placed us in possession of a set of single base-incremented fragments of the sequenced nucleic acid, starting from the sequencing primer 3' OH. (Since the
5 single exon probes were first obtained by PCR amplification from genomic DNA, we were of course additionally in possession of an even larger set of single base incremented fragments of each of the 13,114 single exon probes, each fragment corresponding to an extension product from one of
10 the two amplification primers.)

The structures of the 13,114 unique single exon probes are clearly presented in the Sequence Listing as SEQ ID Nos.: 1 - 13,114. The 16 nt 5' primer sequence and 16 nt 3' primer sequence present on the amplicon are not
15 included in the sequence listing. The sequences of the exons present within each of these probes is presented in the Sequence Listing as SEQ ID Nos.: 13,115 - 26,012, respectively. It will be noted that some amplicons have more than one exon, some exons are contained in more than
20 one amplicon.

As detailed in Example 2, expression was demonstrated by disposing the amplicons as single exon probes on nucleic acid microarrays and then performing two-color fluorescent hybridization analysis; significant
25 expression is based on a statistical confidence that the signal is significantly greater than negative biological control spots. The negative biological control is formed from spotted DNA sequences from a different species. Here, 32 sequences from E.Coli were spotted in duplicate to give
30 a total of 64 spots.

For each hybridisation (each slide, each colour) the median value of the signal from all of the spots is determined. The normalised signal value is the arithmetic mean of the signal from duplicate spots divided by the
35 population median.

Control spots are eliminated if there is more than a five-fold difference between each one of the duplicate spots raw signals.

The median of the signal from the remaining
5 control spots is calculated and all subsequent calculations are done with normalised signals.

Control spots having a signal of greater than median + 2.4 (the value 2.4 is roughly 12 times the observed standard deviation of control spot populations)
10 are eliminated. Spots with such high signals are considered to be "outliers".

The mean and standard deviation of the modified control spot populations are calculated.

The mean + 3x the standard deviation (mean +
15 (3*SD)) is used as the signal threshold qualifier for that particular hybridisation. Thus, individual thresholds are determined for each channel and each hybridisation.

This means that, assuming that the data is distributed normally, there is a 99% confidence that any
20 signal exceeding the threshold is significant.

The probes and their expression data are presented in Table 4, set forth respectively in Example 5. Example 5 presents the subset of probes that is significantly expressed in the human bone marrow and thus
25 presents the subset of probes that was recognized to be useful for measuring expression of their cognate genes in human bone marrow tissue.

The sequence of each of the exon probes identified by SEQ ID NOS.: 13,115 - 26,012 was individually
30 used as a BLAST (or, for SWISSPROT, BLASTX) query to identify the most similar sequence in each of dbEST, SwissProt (BLASTX), and NR divisions of GenBank. Because the query sequences are themselves derived from genomic sequence in GenBank, only nongenic hits from NR were
35 scored.

The smallest in value of the BLAST (or BLASTX) expect ("E") scores for each query sequence across the three database divisions was used as a measure of the "expression novelty" of the probe's ORF. Table 4 is sorted
5 in descending order based on this measure, reported as "Most Similar (top) Hit BLAST E Value". Those sequences for which no "Hit E Value" is listed are those exons which were found to have no similar sequences.

As sorted, Table 4 thus lists its respective
10 probes (by "AMPLICON SEQ ID NO.:" and additionally by the SEQ ID NO.: of the exon contained within the probe:"EXON SEQ ID NO.:") from least similar to sequences known to be expressed (i.e., highest BLAST E value), at the beginning of the table, to most similar to sequences known to be
15 expressed (i.e., lowest BLAST E value), at the bottom of the table.

Table 4 further provides, for each listed probe, the accession number of the database sequence that yielded the "Most Similar (top) Hit BLAST E Value", along with the
20 name of the database in which the database sequence is found ("Top Hit Database Source").

Table 4 further provides SEQ ID NOS.
corresponding to the predicted amino acid sequences where they have been determined for the probe and exon nucleotide
25 sequences. These are set out as PEPTIDE SEQ ID NOS.:. The peptide sequences for a given exon are predicted as follows: Since each chip exon is a consensus sequence drawn from predictions from various exon finding programs (i.e. Grail, GeneFinder and GenScan), the multiple initial ORFs
30 are first determined in a uniform way according to each prediction. In particular, the reading frame for predicting the first amino acid in the peptide sequence always starts with the first base of any codon and ends with the last base of non-termination codon. Next, for each strand of the
35 exon, initial ORFs are merged into one or more final ORFs

in an exhaustive process based on the following criteria:

1) the merging ORFs must be overlapping, and 2) the merging ORFs must be in the same frame.

The Sequence Listing, which is a superset of all
5 of the data presented in Table 4, further includes, for each probe, the most similar hit, with accession number and BLAST E value, from the each of the three queried databases.

Table 4 further lists, for each probe, a portion
10 of the descriptor for the top hit ("Top Hit Descriptor") as provided in the sequence database. For those ORFs that are similar in sequence, but nonidentical to known sequences (e.g., those with BLAST E values between about $1e-05$ and $1e-100$), the descriptor reveals the likely function of the
15 protein encoded by the probe's ORF.

Using BLAST E value cutoffs of $1e-05$ (i.e., 1×10^{-5}) and $1e-100$ (i.e., 1×10^{-100}) as evidence of similarity to sequences known to be expressed is of course arbitrary: in Example 2, *supra*, a BLAST E value of $1e-30$ was used as
20 the boundary when only two classes were to be defined for analysis (unknown, $>1e-30$; known $<1e-30$) (see also FIG. 8). Furthermore, even when the "Most Similar (Top) Hit BLAST E Value" is low, e.g., less than about $1e-100$ — which is probative evidence that the query sequence has previously
25 been shown to be expressed — the top hit is highly unlikely exactly to match the probe sequence.

First, such expression entries typically will not have the intronic and/or intergenic sequence present within the single exon probes listed in the Table. Second, even
30 the ORF itself is unlikely in such cases to be present identically in the databases, since most of the EST and mRNA clones in existing databases include multiple exons, without any indication of the location of exon boundaries.

As noted, the data presented in Table 4 represent
35 a proper subset of the data present within the attached

sequence listing. For each amplicon probe (SEQ ID NOs.: 1 - 13,114) and probe exon (SEQ ID NOs.: 13,115 - 26,012, respectively), the sequence listing further provides, through iterated annotation fields <220> and <223>:

5 (a) the accession number of the BAC from which the sequence was derived ("MAP TO"), thus providing a link to the chromosomal map location and other information about the genomic milieu of the probe sequence;

 (b) the most similar sequence provided by BLAST
10 query of the EST database, with accession number and BLAST E value for the "hit";

 (c) the most similar sequence provided by BLAST query of the GenBank NR database, with accession number and BLAST E value for the "hit"; and

15 (d) the most similar sequence provided by BLASTX query of the SWISSPROT database, with accession number and BLAST E value for the "hit".

20 EXAMPLE 5

Genome-Derived Single Exon Probes Useful For Measuring Expression of Genes in Human Bone marrow

Table 4 (546 pages) presents expression, homology, and
25 functional information for the genome-derived single exon probes that are expressed significantly in human bone marrow.

30

CLAIMS

1. A spatially-addressable set of single exon nucleic acid probes for measuring gene expression in a sample derived
5 from human bone marrow comprising a plurality single exon nucleic probes, said probes comprising any one of the nucleotide sequences set out in SEQ ID NOS: 1 - 13,114 or a complementary sequence, or a portion of such a sequence.
- 10 2. A spatially-addressable set of single exon nucleic acid probes as claimed in claim 1 wherein each of said plurality of probes is separately and addressably amplifiable.
3. A spatially-addressable set of single exon nucleic acid
15 probes as claimed in claim 1 wherein each of said plurality of probes is separately and addressably isolatable from said plurality.
4. A spatially-addressable set of single exon nucleic acid
20 probes as claimed in any of claims 1 to 3 wherein said probes comprise any one of the nucleotide sequences set out in SEQ ID NOS.: 13,115 - 26,012.
5. A spatially-addressable set of single exon nucleic acid
25 probes as claimed in any of claims 1 to 4, wherein each of said plurality of probes is amplifiable using at least one common primer.
6. A spatially-addressable set of single exon nucleic acid
30 probes as claimed in any of claims 1 to 5 wherein the set comprises between 50 - 20,000 single exon nucleic acid probes.
7. A spatially-addressable set of single exon nucleic acid
35 probes as claimed in any of claims 1 to 6, wherein the

average length of the single exon nucleic acid probes is between 200 and 500 bp.

8. A spatially-addressable set of single exon nucleic acid probes as claimed in any of claims 1 to 7, wherein at least 50% of said single exon nucleic acid probes lack prokaryotic and bacteriophage vector sequence.

9. A spatially-addressable set of single exon nucleic acid probes as claimed in any of claims 1 to 8, wherein at least 50% of said single exon nucleic acid probes lack homopolymeric stretches of A or T.

10. A spatially-addressable set of single exon nucleic acid probes as claimed in any of claims 1 - 9 characterised in that said set of probes is addressably disposed upon a substrate.

11. A spatially-addressable set of single exon nucleic acid probes as claimed in claim 10 wherein said substrate is selected from glass, amorphous silicon, crystalline silicon and plastic.

12. A microarray comprising a spatially addressable set of single exon nucleic acid probes as claimed in any of claims 1 - 11.

13. A single exon nucleic acid probe for measuring human gene expression in a sample derived from human bone marrow comprising a nucleotide sequence as set out in any of SEQ ID NOs.: 1 - 13,114 or a complementary sequence or a fragment thereof wherein said probe hybridizes at high stringency to a nucleic acid molecule expressed in the human bone marrow.

35

14. A single exon nucleic acid probe as claimed in claim 13 comprising a nucleotide sequence as set out in any of SEQ ID NOs.: 13,115 - 26,012 or a complementary sequence or a fragment thereof.
- 5
15. A single exon nucleic acid probe for measuring human gene expression in a sample derived from human bone marrow which is a nucleic acid molecule having a sequence encoding a peptide comprising a peptide sequence as set out in any
- 10 of SEQ ID NOs.: 26,013 - 38,628, or a complementary sequence or a fragment thereof wherein said probe hybridizes at high stringency to a nucleic acid expressed in the human bone marrow.
- 15 16. A single exon nucleic acid probe as claimed in any one of claims 13 to 15 wherein said single exon nucleic acid probe comprises between 15 and 25 contiguous nucleotides of said SEQ ID NO.
- 20 17. A single exon nucleic acid probe as claimed in any one of claims 13 to 15, wherein said probe is between 3 - 25 kb in length.
18. A single exon nucleic acid probe as claimed in any one
- 25 of claims 13 - 17, wherein said probe is DNA, RNA or PNA.
19. A single exon nucleic acid probe as claimed in any one of claims 13 - 18, wherein said probe is detectably labeled.
- 30
20. A single exon nucleic acid probe as claimed in any one of claims 13 - 19, wherein said probe lacks prokaryotic and bacteriophage vector sequence.
- 35 21. A single exon nucleic acid probe as claimed in any one

of claims 13 - 20, wherein said probe lacks homopolymeric stretches of A or T.

22. A method of measuring gene expression in a sample
5 derived from human bone marrow, comprising:
 contacting the microarray of claim 12, with a first
 collection of detectably labeled nucleic acids,
 said first collection of nucleic acids derived
 from mRNA of human bone marrow; and then
10 measuring the label detectably bound to each probe of
 said microarray.

23. A method of identifying exons in a eukaryotic genome,
comprising:
15 algorithmically predicting at least one exon from
 genomic sequence of said eukaryote; and then
 detecting specific hybridization of detectably labeled
 nucleic acids to a single exon probe,
wherein said detectably labeled nucleic acids are derived
20 from mRNA from the bone marrow of said eukaryote, said
probe is a single exon probe having a fragment identical in
sequence to, or complementary in sequence to, said
predicted exon, said probe is included within a microarray
according to claim 12, and said fragment is selectively
25 hybridizable at high stringency.

24. A method of assigning exons to a single gene,
comprising:
 identifying a plurality of exons from genomic
30 sequence according to the method of claim 23; and
 then
 measuring the expression of each of said exons in a
 plurality of tissues and/or cell types using
 hybridization to single exon microarrays having a
35 probe with said exon,

wherein a common pattern of expression of said exons in said plurality of tissues and/or cell types indicates that the exons should be assigned to a single gene.

5 25. A nucleic acid sequence as set out in any of SEQ ID Nos: 1 - 26,012 which encodes a peptide.

26. A peptide encoded by a sequence as set out in any of SEQ ID Nos: 1 - 26,012.

10

27. A peptide comprising a sequence as set out in any of SEQ ID Nos: 26,013 - 38,628.

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Table 4
Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
450	13523	26455	4.57				
850	13943	26903	10.46				
1046	14092		3.86				
1305	14341	27305	7.19				
1818	14650	27926	4.21				
1642	14674	27647	6.05				
1738	14768	27753	2.88				
1764	14783	27778	1.27				
1770	14799	27785	9.04				
1608	14832	27928	1.24				
1995	15016	28023	2.44				
2175	15191	28212	2.92				
2287	15300	28324	2.97				
3200	16255	29175	3.13				
3464	16510	29431	1.32				
3527	16573	29486	10.05				
3574	16619		0.85				
3938	17008		1.15				
4225	17254	30141	1.68				
4290	17319	30198	6.25				
4310	17339	30218	0.83				
4310	17339	30219	0.83				
4364	17391		1.03				
4420	17447	30338	0.53				
4874	17891	30760	1.27				
4958	17974	30885	0.74				
5053	18093	30959	5.95				
5095	18105	30980	1.42				
5329	18435	31187	1.78				
5329	18435	31188	1.78				
5496	18595		4.07				
5678	18773		7.77				
5762	18566		3.48				
5824	18514	32037	0.55				

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Table 4
Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5830	18920	32103	3.19				
6138	26655	32443	1.58				
6167	19242	32473	2.11				
6556	19816		1.24				
6700	19757	33034	0.89				
6700	19757	33035	0.89				
7332	20303	33647	1.52				
7332	20303	33848	1.52				
7642	20602	33966	1.45				
7642	20602	33967	1.45				
8114	21051		0.61				
8396	21365	34774	1.55				
8830	21797	35218	1.21				
9212	22178	35608	0.57				
9212	22178	35609	0.57				
9892	22845	36302	5.61				
10124	23050	36528	0.69				
10241	23186	36653	1.44				
10383	23305	36782	0.91				
10675	23597	37093	0.49				
10675	23597	37094	0.49				
10784	23715	37216	0.6				
10784	23715	37217	0.6				
11043	24007		2.14				
11366	24314		1.61				
11687	24653	38232	1.82				
11829	24712		1.94				
12600	25302		1.5				
12888	25476	31730	1.34				
6170	19245	32477	15.3	9.9E+00 AJ236028.1	NT		Homo sapiens LSS gene, partial, exons 15, 16, 17 and 18
8339	21308	34723	1.75	9.8E+00 U32716.1	NT		Haemophilus influenzae Rd section 31 of 163 of the complete genome
10100	23026	36502	0.47	9.8E+00 Y18930.1	NT		Sulfolobus solfataricus 281 kb genomic DNA fragment, strain P2
10100	23026	36503	0.47	9.8E+00 Y18930.1	NT		Sulfolobus solfataricus 281 kb genomic DNA fragment, strain P2
7194	20218	33549	0.66	9.6E+00 AF066630.1	NT		Gallus gallus ornithine transcarbamylase (OTC) gene, exon 1

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7194	20218	33550	0.66	9.6E+00	AF065630.1	NT	Gallus gallus ornithine transcarbamylase (OTC) gene, exon 1
10787	23708	37209	1.19	9.6E+00	AF242432.1	NT	Mus musculus Naip3 gene, exon 1; neuronal apoptosis inhibitory protein 1 (Naip1) and general transcription factor 1LH polypeptide 2 (Gr2h2) genes, complete cds
10787	23708	37210	1.19	9.6E+00	AF242432.1	NT	Mus musculus Naip3 gene, exon 1; neuronal apoptosis inhibitory protein 1 (Naip1) and general transcription factor 1LH polypeptide 2 (Gr2h2) genes, complete cds
2835	15993	28913	3.21	9.4E+00	AB043785.1	NT	Mus musculus At3 gene for antithrombin, complete cds
6457	19522	32773	0.54	9.4E+00	P75130	SWISSPROT	HYPOTHETICAL PROTEIN MG447 HOMOLOG
11911	24792	38381	2.45	9.4E+00	O98825	SWISSPROT	NADH-UBIQUINONE OXIDOREDUCTASE CHAIN 4
11911	24792	38382	2.45	9.4E+00	O98825	SWISSPROT	NADH-UBIQUINONE OXIDOREDUCTASE CHAIN 4
8435	21404	34817	0.86	9.3E+00	AF130990.1	NT	Homo sapiens ectodysplasin-A receptor protein (EDAR) gene, exons 2, 3, and 4
9356	22321	35748	3.15	9.3E+00	P11210	SWISSPROT	IMMEDIATE-EARLY PROTEIN 1 (IE1) (IMMEDIATE-EARLY PHOSPHOPROTEIN PP89)
5369	18474	31346	2.66	9.1E+00	AF095609.1	NT	Leuciscus cephalus orientalis cytochrome b (cyt b) gene, partial cds; mitochondrial gene for mitochondrial product
5369	18474	31347	2.66	9.1E+00	AF095609.1	NT	Leuciscus cephalus orientalis cytochrome b (cyt b) gene, partial cds; mitochondrial gene for mitochondrial product
9785	22726		0.95	9.0E+00	P09241	SWISSPROT	RHODOPSIN
6152	19227	32456	5.62	8.9E+00	BE971806.1	EST_HUMAN	601651038R1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:3934592 3'
6517	19580	32837	2.21	8.7E+00	AB019788.1	NT	Cynops pyrrhogaster CpTbx3 premature mRNA, partial cds
6517	19580	32838	2.21	8.7E+00	AB019788.1	NT	Cynops pyrrhogaster CpTbx3 premature mRNA, partial cds
440	13514	26445	1.03	8.4E+00	5031804	NT	Homo sapiens insulin receptor substrate 1 (IRS1) mRNA
9810	21133	34536	3.58	8.1E+00	AL131719.1	NT	Zea mays mRNA for legumain-like protease (see2a)
11504	24446		1.54	8.0E+00	P41820	SWISSPROT	BREFELDIN A RESISTANCE PROTEIN
8491	21459		0.82	7.6E+00	Z21499.1	NT	African swine fever virus NP1450L gene encoding RNA polymerase largest subunit
7669	20532		2.17	7.5E+00	AL445065.1	NT	Thermoplasma acidophilum complete genome; segment 3/5
8704	21672	35095	1.58	7.5E+00	P35441	SWISSPROT	THROMBOSPONDIN 1 PRECURSOR
8704	21672	35096	1.58	7.5E+00	P35441	SWISSPROT	THROMBOSPONDIN 1 PRECURSOR
5898	18985	32176	3.53	7.4E+00	BF700517.1	EST_HUMAN	602128876F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4285506 5'
9106	22072	35498	2.72	7.4E+00	P04929	SWISSPROT	HISTIDINE-RICH GLYCOPROTEIN PRECURSOR
9106	22072	35499	2.72	7.4E+00	P04929	SWISSPROT	HISTIDINE-RICH GLYCOPROTEIN PRECURSOR
2990	16048	28968	4.7	7.2E+00	L12051.1	NT	Lycopodium esculentum Mill. GTPase (SAR2) mRNA, complete cds
2990	16048	28969	4.7	7.2E+00	L12051.1	NT	Lycopodium esculentum Mill. GTPase (SAR2) mRNA, complete cds
7230	20252	33598	1.12	7.2E+00	BE179090.1	EST_HUMAN	RC0-HT0613-200300-031-407 HT0613 Homo sapiens cDNA
7356	20328	33673	1.1	7.1E+00	P28166	SWISSPROT	ZINC-FINGER PROTEIN 1 (ZINC-FINGER HOMEODOMAIN PROTEIN 1)
7356	20328	33674	1.1	7.1E+00	P28166	SWISSPROT	ZINC-FINGER PROTEIN 1 (ZINC-FINGER HOMEODOMAIN PROTEIN 1)

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Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9957	22884		6.86	7.1E+00	AL161595.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 91
11715	24678	38256	2.96	7.1E+00	P05860	SWISSPROT	HYPOTHETICAL 17.3 KDA PROTEIN IN MRDA-PHPB INTERGENIC REGION
11909	24790	38379	4.81	7.1E+00	P06106	SWISSPROT	MET17 PROTEIN [INCLUDES: O-ACETYLHOMOSERINE SULFHYDRYLASE (OAH SULFHYDRYLASE); O-ACETYL SERINE SULFHYDRYLASE (OAS SULFHYDRYLASE)]
10341	23265	38744	3.43	7.0E+00	P48610	SWISSPROT	ARGININE KINASE (AK)
11580	24518	38074	1.7	7.0E+00	O22469	SWISSPROT	WD-40 REPEAT PROTEIN MS13
8626	21594	35014	3.94	6.9E+00	P35679	SWISSPROT	60S RIBOSOMAL PROTEIN L4 (L2)
10716	23638	37131	1.32	6.9E+00	P44834	SWISSPROT	DNA MISMATCH REPAIR PROTEIN MUTS
10734	23658	37149	0.44	6.9E+00	P34226	SWISSPROT	SKT5 PROTEIN
8240	21209	34613	1.31	6.8E+00	W03412.1	EST_HUMAN	z07c11.17 Soares melanocyte 2NbhM Homo sapiens cDNA clone IMAGE:291860 5'
8240	21209	34614	1.31	6.8E+00	W03412.1	EST_HUMAN	z07c11.17 Soares melanocyte 2NbhM Homo sapiens cDNA clone IMAGE:291860 5'
							OUTER CAPSID PROTEIN VP4 (HEMAGGLUTININ) (OUTER LAYER PROTEIN VP4) [CONTAINS:
							OUTER CAPSID PROTEINS VP5 AND VP8]
9488	22452		1.35	6.8E+00	P36307	SWISSPROT	HYPOTHETICAL 157.0 KDA PROTEIN C38C10.5 IN CHROMOSOME III
10569	23491	36983	3.31	6.8E+00	Q03570	SWISSPROT	CATECHOL-O-METHYLTRANSFERASE, SOLUBLE FORM (S-COMT)
6356	18461		0.74	6.6E+00	Q99028	SWISSPROT	602152573F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4293427 5'
6695	19752	33029	0.72	6.6E+00	BF672121.1	EST_HUMAN	URIDYLATE KINASE (UK) (URIDINE MONOPHOSPHATE KINASE) (UMP KINASE)
10434	23356	36842	1.87	6.6E+00	Q9ZE07	SWISSPROT	URIDYLATE KINASE (UK) (URIDINE MONOPHOSPHATE KINASE) (UMP KINASE)
10434	23356	36843	1.87	6.6E+00	Q9ZE07	SWISSPROT	PROBABLE CATION-TRANSPORTING ATPASE O8C3.05C
11463	24406		2.49	6.6E+00	Q10309	SWISSPROT	ENV POLYPROTEIN [CONTAINS: COAT PROTEIN GP52; COAT PROTEIN GP36]
9535	22498	36946	7.17	6.5E+00	P03374	SWISSPROT	601678435F1 NIH_MGC_53 Homo sapiens cDNA clone IMAGE:3660969 5'
10667	23589	37086	0.47	6.5E+00	BE866001.1	EST_HUMAN	Schizaphyllum commune unknown mRNA
10099	23025	36501	1.17	6.2E+00	AY010901.1	NT	Mus musculus mannosidase 2, alpha B1 (Man2b1), mRNA
10927	23947	37362	0.65	6.2E+00	6754621	NT	601468031F1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:3671303 5'
7236	20257	33591	1.36	6.0E+00	BE790163.1	EST_HUMAN	Pyrococcus horikoshii OT3 genomic DNA, 1166001-1485000 nt, position (677)
10175	23100	36580	0.46	6.0E+00	AP000006.1	NT	Deinococcus radiodurans R1 section 1 of 2 of the complete chromosome 2
10880	23900	37302	0.63	6.0E+00	AE001862.1	NT	Deinococcus radiodurans R1 section 1 of 2 of the complete chromosome 2
10880	23800	37303	0.63	6.0E+00	AE001862.1	NT	Mus musculus mixed lineage kinase 3 (MLK3) and two pore domain K+ channel subunit (Kcnk6) genes, complete cds
6670	19727	33003	6.7	5.9E+00	AF155142.1	NT	Homo sapiens DESC1 protein (DESC1), mRNA
3536	16982		0.88	5.8E+00	7661557	NT	Mus musculus immunoglobulin scavenger receptor IgSR mRNA, complete cds
7369	20339	33690	0.65	5.7E+00	AF302046.1	NT	Mus musculus immunoglobulin scavenger receptor IgSR mRNA, complete cds
7369	20339	33691	0.65	5.7E+00	AF302046.1	NT	Mus musculus immunoglobulin scavenger receptor IgSR mRNA, complete cds
7819	20768		1.5	5.6E+00	P75080	SWISSPROT	DNA POLYMERASE III, ALPHA CHAIN POLC-TYPE (POLIII)
11805	23960	37485	2.98	5.6E+00	Q55276	SWISSPROT	LYCOPENE BETA CYCLASE

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6380	19448	32689	0.78	5.6E+00	P47447	SWISSPROT	HEAT-INDUCIBLE TRANSCRIPTION REPRESSOR HRCA
10138	23084		0.47	5.6E+00	P13983	SWISSPROT	EXTENSIN PRECURSOR (CELL WALL HYDROXYPROLINE-RICH GLYCOPROTEIN)
11803	23958	37482	2.35	5.9E+00	P11990	SWISSPROT	PNEUMOLYSIN (THIOL-ACTIVATED CYTOLYSIN)
7115	20049	33351	1.1	5.4E+00	XQ2212.1	NT	Chicken alpha-cardiac actin gene
7115	20049	33352	1.1	5.4E+00	XQ2212.1	NT	Chicken alpha-cardiac actin gene
7552	20515		0.84	5.4E+00	Q89435	SWISSPROT	NEL PROTEIN PRECURSOR (NEL-RELATED PROTEIN 2)
8143	21080	34480	0.6	5.4E+00	P50391	SWISSPROT	NEUROPEPTIDE Y RECEPTOR TYPE 4 (NPY4-R) (PANCREATIC POLYPEPTIDE RECEPTOR 1) (PP1)
							VITELLOGENIN PRECURSOR (VTG) [CONTAINS: LIPOVITELLIN LV-1N; LIPOVITELLIN LV-1C;
8202	21172		1.72	5.4E+00	Q81062	SWISSPROT	LIPOVITELLIN LV-2J
9151	22117	35543	0.73	5.4E+00	P40379	SWISSPROT	REP1 PROTEIN
9151	22117	35544	0.73	5.4E+00	P40379	SWISSPROT	REP1 PROTEIN
10396	23318	36799	1.41	5.4E+00	Q17094	SWISSPROT	RHODOPSIN
10396	23318	36800	1.41	5.4E+00	Q17094	SWISSPROT	RHODOPSIN
4824	17941	30739	1.22	5.3E+00	L43126.1	NT	Bovine immunodeficiency-like virus surface envelope gene, 5' end of cds
6635	19693		0.6	5.3E+00	P41779	SWISSPROT	HOMEBOX PROTEIN CEH-20
8415	21384		3.9	5.3E+00	P54098	SWISSPROT	DNA POLYMERASE GAMMA (MITOCHONDRIAL DNA POLYMERASE CATALYTIC SUBUNIT)
9335	22300		0.53	5.3E+00	AB034990.1	NT	Homo sapiens HERPUD1 gene for stress protein Herp, complete cds
11950	24829	38425	1.84	5.3E+00	Q27605	SWISSPROT	PROBABLE ANTIBACTERIAL PEPTIDE POLYPROTEIN PRECURSOR
12093	24964	38559	2.34	5.3E+00	Z72683.1	NT	S. cerevisiae chromosome VII reading frame ORF YGL141w
12093	24964	38560	2.34	5.3E+00	Z72683.1	NT	S. cerevisiae chromosome VII reading frame ORF YGL141w
5539	18636		1.22	5.2E+00	BE184840.1	EST_HUMAN	Q14-H10691-270400-186-09 H10691 Homo sapiens cDNA
10738	23660		0.78	5.2E+00	AF248070.1	NT	Drosophila orientacea R1B retrotransposable element reverse transcriptase gene, partial cds
11527	24468		1.46	5.2E+00	Q10136	SWISSPROT	HYPOTHETICAL 61.1 KD PROTEIN C23E2.03C IN CHROMOSOME I
9313	22278	35709	0.85	5.1E+00	Q16005	SWISSPROT	RHODOPSIN
10184	23109	36592	1.07	5.1E+00	P09182	SWISSPROT	COLICIN N IMMUNITY PROTEIN (MICROGICIN N IMMUNITY PROTEIN)
11617	24555	38117	3.01	5.1E+00	P56200	SWISSPROT	ZINC FINGER PROTEIN HRX (ALL-1)
6418	19485	32734	0.65	5.0E+00	BF310443.1	EST_HUMAN	601894910F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4124114 5'
10554	23476		0.65	5.0E+00	BF308561.1	EST_HUMAN	601890420F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4131509 5'
10796	23717	37219	3.79	5.0E+00	AF162445.2	NT	Canis familiaris skeletal muscle chloride channel CIC-1 (CLCN1) mRNA, complete cds
11622	24560	38122	6.39	5.0E+00	Z83860.1	NT	Mycobacterium tuberculosis H37Rv complete genome, segment 103/162
							Human hereditary haemochromatosis region, histone 2A-like protein gene, hereditary haemochromatosis (HLA-H) gene, Rofet gene, and sodium phosphate transporter (NPT3) gene, complete cds
10592	23514		0.63	4.9E+00	U91328.1	NT	Human hereditary haemochromatosis region, histone 2A-like protein gene, hereditary haemochromatosis (HLA-H) gene, Rofet gene, and sodium phosphate transporter (NPT3) gene, complete cds
4090	17124		9.81	4.8E+00	AF185255.1	NT	Eunice australis histone H3 (H3) gene, partial cds

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8494	21462	34878	0.53	4.8E+00	BF367909.1	EST_HUMAN	RC3-GN0042-100800-011-c10 GN0042 Homo sapiens cDNA
8888	21852		5.15	4.8E+00	AW750087.1	EST_HUMAN	PMO-BT0547-310100-002-p04 BT0547 Homo sapiens cDNA
288	13384	26311	2.03	4.7E+00	BF240552.1	EST_HUMAN	601876654F1 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:4099716 5'
290	13384	26311	1.89	4.7E+00	BF240552.1	EST_HUMAN	601876654F1 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:4099716 5'
3287	16341	29260	1.66	4.7E+00	AL163280.2	NT	Homo sapiens chromosome 21 segment HS21C080
8084	21001	34397	0.55	4.6E+00	U67689.1	NT	Methanococcus jannaschii section 111 of 150 of the complete genome
9551	22513	35983	1.12	4.6E+00	BE848437.1	EST_HUMAN	7e86g10.x1 NCI_CGAP_CLL1 Homo sapiens cDNA clone IMAGE:3292098 3' similar to TR:O75140 O75140
9551	22513	35984	1.12	4.6E+00	BE848437.1	EST_HUMAN	KIAA0845 PROTEIN, contains element PTR5 repetitive element ;
10755	23677		0.8	4.6E+00	AF240786.1	NT	7e86g10.x1 NCI_CGAP_CLL1 Homo sapiens cDNA clone IMAGE:3292098 3' similar to TR:O75140 O75140
8047	20984		0.61	4.5E+00	AF126177.1	NT	KIAA0845 PROTEIN, contains element PTR5 repetitive element ;
11830	24811	38406	2.19	4.5E+00	AE001044.1	NT	KIAA0845 PROTEIN, contains element PTR5 repetitive element ;
12055	24928	38528	1.67	4.5E+00	BF688841.1	EST_HUMAN	genes, complete cds
3053	16110	29024	0.76	4.4E+00	BF530893.1	EST_HUMAN	Isaiahenklia orientalis inositolphosphorylceramide synthase (IPC1) gene, complete cds
3053	16110	29025	0.76	4.4E+00	BF530893.1	EST_HUMAN	Archaeoglobus fulgidus section 63 of 172 of the complete genome
6326	18386		1.69	4.4E+00	X13414.1	NT	602123238F1 NCI_CGAP_Bm87 Homo sapiens cDNA clone IMAGE:4280216 5'
6394	19462	32709	0.59	4.4E+00	AF156696.1	NT	602072585F1 NCI_CGAP_Bm87 Homo sapiens cDNA clone IMAGE:4215284 5'
6240	19313		0.71	4.3E+00	AF059878.1	NT	602072585F1 NCI_CGAP_Bm87 Homo sapiens cDNA clone IMAGE:4215284 5'
7872	20630	33984	3.53	4.3E+00	Y13402.1	NT	Murine l gene for MHC class II(a) associated invariant chain
7874	20818	34196	0.81	4.3E+00	AE001222.1	NT	Nicotiana tabacum inorganic phosphate transporter (PT1) mRNA, complete cds
11210	24164	37694	7.01	4.3E+00	AF240786.1	NT	Homo sapiens neutrophil collagenase (CLGNA) gene, promoter region and 5'UTR
11278	24230		1.93	4.3E+00	11526311	NT	Pleurodium falciparum R28R+var1 gene, exon 1
5595	18991		3.57	4.2E+00	P16444	SWISSPROT	Treponema pallidum section 38 of 87 of the complete genome
5675	18770	31942	1.35	4.2E+00	P51826	SWISSPROT	Homo sapiens glutathione S-transferase theta 2 (GSTT2) and glutathione S-transferase theta 1 (GSTT1) genes, complete cds
5854	18945		0.58	4.2E+00	O27830	SWISSPROT	Homo sapiens DiGeorge syndrome critical region gene 2 (DGCR2), mRNA
6938	20162	33483	1.69	4.2E+00	P13983	SWISSPROT	MICROSOMAL DIPEPTIDASE PRECURSOR (MDP) (DEHYDROPEPTIDASE-I) (RENAL DIPEPTIDASE) (RDP)
6938	20162	33484	1.69	4.2E+00	P13983	SWISSPROT	LAF-4 PROTEIN (LYMPHOID NUCLEAR PROTEIN)
9311	22276	35708	5.1	4.2E+00	AI809013.1	EST_HUMAN	PUTATIVE ATP-DEPENDENT HELICASE MTH1802
10278	23203	36688	1.1	4.2E+00	P31368	SWISSPROT	EXTENSIN PRECURSOR (CELL WALL HYDROXYPROLINE-RICH GLYCOPROTEIN)
10508	23430		0.53	4.2E+00	P40886	SWISSPROT	EXTENSIN PRECURSOR (CELL WALL HYDROXYPROLINE-RICH GLYCOPROTEIN)
							wf67g03.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2360692 3'
							NUBBIN PROTEIN (TWIN PROTEIN) (POU DOMAIN PROTEIN 1) (PDM-1) (DPOU-19) (DOCT1)
							HEXOSE TRANSPORTER HXT8

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6046	25652	32334	0.64	4.1E+00	O09185	SWISSPROT	CELLULAR TUMOR ANTIGEN P53
6046	25652	32335	0.64	4.1E+00	O09185	SWISSPROT	CELLULAR TUMOR ANTIGEN P53
7319	20290	33633	0.78	4.1E+00	BE253668.1	EST_HUMAN	601110727F1 NIH_MGC_18 Homo sapiens cDNA clone IMAGE:3351534 5'
7420	20387	33738	0.55	4.1E+00	BF247939.1	EST_HUMAN	60185030F1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:4069758 5'
7923	20886	34254	7.87	4.1E+00	Q23810	SWISSPROT	YY1 PROTEIN PRECURSOR
8081	20998		0.64	4.1E+00	AB041523.1	NT	Pathogen yersinia mRNA for calcineurin A, complete cds
8085	21002	34398	3.95	4.1E+00	P28964	SWISSPROT	GENE 68 PROTEIN
8085	21002	34399	3.95	4.1E+00	P28964	SWISSPROT	GENE 68 PROTEIN
8249	21218	34628	2.5	4.1E+00	U57503.1	NT	Pan troglodytes novel repetitive solo LTR element in the RNU2 locus
9898	22851	36310	0.52	4.1E+00	P11253	SWISSPROT	50S RIBOSOMAL PROTEIN L4
10031	22958	36428	2.43	4.1E+00	BF62425.1	EST_HUMAN	602247938F1 NIH_MGC_62 Homo sapiens cDNA clone IMAGE:4333209 5'
10689	23591		0.45	4.1E+00	P46414	SWISSPROT	CYCLIN-DEPENDENT KINASE INHIBITOR 1B (CYCLIN-DEPENDENT KINASE INHIBITOR P27)
10981	23901	37414	0.47	4.1E+00	O84242	SWISSPROT	3-OXOACYL-[ACYL-CARRIER-PROTEIN] SYNTHASE III (BETA-KETOACYL-ACP SYNTHASE III) (KAS III)
11231	24184		2.3	4.1E+00	P09716	SWISSPROT	HYPOTHEICAL PROTEIN HVLF1
11317	24267		13.22	4.1E+00	BE885880.1	EST_HUMAN	601607510F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3909051 5'
3556	16602		0.7	4.0E+00	P38229	SWISSPROT	GLC7-INTERACTING PROTEIN 1
5534	20057	33361	0.94	4.0E+00	O62653	SWISSPROT	SUCRASE-ISOMALTASE, INTESTINAL [CONTAINS: SUCRASE; ISOMALTASE]
5534	20057	33362	0.94	4.0E+00	O62653	SWISSPROT	SUCRASE-ISOMALTASE, INTESTINAL [CONTAINS: SUCRASE; ISOMALTASE]
7123	20057	33361	1.01	4.0E+00	O62653	SWISSPROT	SUCRASE-ISOMALTASE, INTESTINAL [CONTAINS: SUCRASE; ISOMALTASE]
7123	20057	33362	1.01	4.0E+00	O62653	SWISSPROT	SUCRASE-ISOMALTASE, INTESTINAL [CONTAINS: SUCRASE; ISOMALTASE]
7395	20363	33715	1.47	4.0E+00	Q33010	SWISSPROT	CELL DIVISION PROTEIN FTSY HOMOLOG
9225	22191	35621	0.44	4.0E+00	Q14157	SWISSPROT	HYPOTHEICAL PROTEIN KIAA0144
10303	23228	36711	0.43	4.0E+00	O61309	SWISSPROT	NITRIC-OXIDE SYNTHASE (NOS, TYPE I) (NEURONAL NOS) (NNOS)
10526	23448	36946	0.6	4.0E+00	AE002132.1	NT	Ureaplasma urealyticum section 33 of 59 of the complete genome
10620	23542	37041	0.49	4.0E+00	Q00511	SWISSPROT	URICASE (URATE OXIDASE)
10620	23542	37042	0.49	4.0E+00	Q00511	SWISSPROT	URICASE (URATE OXIDASE)
11802	23957	37451	1.67	4.0E+00	P14546	SWISSPROT	CYTOCHROME C OXIDASE POLYPEPTIDE III
11875	24757	38340	2.88	4.0E+00	P07564	SWISSPROT	GENOME POLYPEPTIDE [CONTAINS: CAPSID PROTEIN C (CORE PROTEIN); MATRIX PROTEIN (ENVELOPE GLYCOPROTEIN M); MAJOR ENVELOPE PROTEIN E; NONSTRUCTURAL PROTEINS (NS1, NS2A, NS2B, NS4A AND NS4B); HELICASE (NS3); RNA-DIRECTED RNA POLYMERASE (NS5)]

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Table 4
Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
11875	24757	38341	2.88	4.0E+00	P07584	SWISSPROT	GENOME POLYPROTEIN [CONTAINS: CAPSID PROTEIN C (CORE PROTEIN); MATRIX PROTEIN (ENVELOPE GLYCOPROTEIN M); MAJOR ENVELOPE PROTEIN E; NONSTRUCTURAL PROTEINS NS1, NS2A, NS2B, NS4A AND NS4B; HELICASE (NS3); RNA-DIRECTED RNA POLYMERASE (NS5)]
3513	16559	29483	4.65	3.9E+00	X64518.1	NT	N. tabacum chitinase gene 50 for class I chitinase C
4349	17376		0.96	3.9E+00	AF055466.1	NT	Mus musculus seminal vesicle secretory protein 99 (MSV/SP99) gene, promoter region
5741	18835	32015	2.98	3.9E+00	BE814357.1	EST_HUMAN	MRO-BN0070-300500-028-h05 BN0070 Homo sapiens cDNA
5741	18835	32016	2.98	3.9E+00	BE814357.1	EST_HUMAN	MRO-BN0070-300500-028-h05 BN0070 Homo sapiens cDNA
6791	19845	33129	0.95	3.9E+00	AF298209.1	NT	Dictyostelium discoideum non-LTR retrotransposon TRE5-B, polyprotein (gag) and group-specific antigen (pc) genes, complete cds
6848	19901	33185	0.67	3.9E+00	U91328.1	NT	Human hereditary haemochromatosis region, histone 2A-like protein gene, hereditary haemochromatosis (HLA-H) gene, RoRet gene, and sodium phosphate transporter (NPT3) gene, complete cds
7057	20079	33388	4.24	3.9E+00	P39289	SWISSPROT	HYPOTHETICAL TRANSCRIPTIONAL REGULATOR IN AIDB-RPSF INTERGENIC REGION
7587	20548	33908	4.15	3.9E+00	M23907.1	NT	Human MHC class II lymphocyte antigen (DPw4-beta-1) gene, exon 2
8660	21628	35049	2.34	3.9E+00	X65865.1	NT	X. laevis mRNA for M4 muscarinic receptor
11720	23917	37434	2.93	3.9E+00	Y18000.1	NT	Homo sapiens NF2 gene
11742	24627	38206	1.89	3.9E+00	AA661489.1	EST_HUMAN	nr18a12.s1 NCL CGAP_Ew1 Homo sapiens cDNA clone IMAGE:1188318 similar to gb:A10416
2637	15636		1.27	3.8E+00	AE001562.1	NT	METALLOPROTEINASE INHIBITOR 1 PRECURSOR (HUMAN);
6630	19593	32854	0.93	3.8E+00	Q57830	SWISSPROT	Helicobacter pylori, strain J99 section 123 of 132 of the complete genome
6937	20161	33482	0.59	3.8E+00	AI493849.1	EST_HUMAN	HYPOTHETICAL PROTEIN MJ0385
8775	21742	35164	1.03	3.8E+00	D44725.1	EST_HUMAN	q25107.x1 NCL CGAP Kid11 Homo sapiens cDNA clone IMAGE:2030437 3'
10154	23079		0.59	3.8E+00	AJ390961.1	NT	HUMSUPY135 Human brain cDNA Homo sapiens cDNA clone 148
12119	24989		15.21	3.8E+00	9631294	NT	Streptococcus oralis partial xpl gene for xanthine phosphoribosyltransferase, strain NCTC7884.
4049	17086	29982	9.75	3.7E+00	AL161539.2	NT	Melanoplus sanguinipes entomopoxvirus, complete genome
7372	20342		0.9	3.7E+00	AL445065.1	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 39
9056	22022		0.49	3.7E+00	4503950	NT	Thermoplasma acidophilum complete genome; segment 3/5
9532	22495	35943	0.92	3.7E+00	U43541.1	NT	Homo sapiens glucokinase (hexokinase 4, maturity onset diabetes of the young 2) (GCK), nuclear gene encoding mitochondrial protein, mRNA
11760	24688	38269	1.73	3.7E+00	BF689279.1	EST_HUMAN	Mus musculus laminin beta 2 gene, exons 17-33, and complete cds
11760	24688	38270	1.73	3.7E+00	BF689279.1	EST_HUMAN	602120551F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4277748 5'
12266	25082		2.5	3.7E+00	AB013746.3	NT	602120551F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4277748 5'
595	13662	26576	4.04	3.6E+00	AV761055.1	EST_HUMAN	Gallus gallus mRNA for hypoxia-inducible factor-1 alpha, complete cds
							AV761055 MDS Homo sapiens cDNA clone MDSBUE10 5'

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Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5286	18292	31153	0.63	3.6E+00	Z89109.1	NT	Bacillus subtilis complete genome (section 6 of 21): from 999501 to 1209940
5327	18433	31185	0.73	3.6E+00	BF316316.1	EST_HUMAN	601901866F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4131018 5'
8897	21863	35285	0.93	3.6E+00	D12367.1	EST_HUMAN	HUM0007B08 Liver HepG2 cell line. Homo sapiens cDNA clone lb08
8897	21863	35286	0.93	3.6E+00	D12367.1	EST_HUMAN	HUM0007B08 Liver HepG2 cell line. Homo sapiens cDNA clone lb08
8992	21958	35383	4.21	3.6E+00	AE004447.1	NT	Pseudomonas aeruginosa PA01, section 8 of 529 of the complete genome
8992	21958	35384	4.21	3.6E+00	AE004447.1	NT	Pseudomonas aeruginosa PA01, section 8 of 529 of the complete genome
10022	22949	36416	0.44	3.6E+00	U72775.1	NT	Ciconia episcopus cytochrome b gene, mitochondrial gene encoding mitochondrial protein, partial cds
10022	22949	36417	0.44	3.6E+00	U72775.1	NT	Ciconia episcopus cytochrome b gene, mitochondrial gene encoding mitochondrial protein, partial cds
11200	24155		3.18	3.6E+00	M96795.1	NT	Escherichia coli glycerophosphate dehydrogenase (gpd) gene, partial cds; and the translation start site has been verified (gdpE), the translation start site has been verified (gdpG), and repressor protein (gdpR) genes, complete cds
6115	19193		1.1	3.5E+00	L42898.1	NT	Borrelia burgdorferi (strain 25015) outer surface protein (ospC) gene, partial cds
6337	19406	32647	0.96	3.5E+00	R19745.1	EST_HUMAN	Y94008.1 Soares infant brain 1N1B Homo sapiens cDNA clone IMAGE:34940 5'
8087	21023	34422	0.5	3.5E+00	P97808	SWISSPROT	5-OXOPROLINASE (5-OXO-L-PROLINASE) (PYROGLUTAMASE) (5-OPASE)
8094	21030	34428	0.54	3.5E+00	AA992102.1	EST_HUMAN	037710.s1 Soares_besit_NHT Homo sapiens cDNA clone IMAGE:1618987 3' similar to gb:J04213
8124	21081	34459	0.56	3.5E+00	4505264	NT	CELLULAR RETINALDEHYDE-BINDING PROTEIN (HUMAN);
8829	21796		0.6	3.5E+00	P24567	SWISSPROT	Homo sapiens macrophage stimulating 1 receptor (G-met-related tyrosine kinase) (MST1R) mRNA
9387	22352	35782	0.91	3.5E+00	AA190998.1	EST_HUMAN	THROMBOXANE-A SYNTHASE (TXA SYNTHASE) (TXS)
9387	22352	35783	0.91	3.5E+00	AA190998.1	EST_HUMAN	zp86604.s1 Stratagene HeLa cell s3 937216 Homo sapiens cDNA clone IMAGE:627055 3' similar to contains Alu repetitive element; contains element MSR1 repetitive element;
9850	22786	36240	0.96	3.5E+00	AL161563.2	NT	contains Alu repetitive element; contains element MSR1 repetitive element;
1514	14546	27517	5.3	3.4E+00	AF254577.1	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 53
6893	19845	33241	0.49	3.4E+00	U77617.1	NT	Brassica napus RPB5d mRNA, complete cds
7986	20547	33907	2.99	3.4E+00	P04052	SWISSPROT	Chlorate-Aster yellows phytoplasma acetate kinase gene, complete cds
7968	20607	34298	0.9	3.4E+00	P04052	SWISSPROT	DNA-DIRECTED RNA POLYMERASE II LARGEST SUBUNIT
9025	21981		0.68	3.4E+00	U65406.1	NT	DNA-DIRECTED RNA POLYMERASE II LARGEST SUBUNIT
9428	22392	36831	0.73	3.4E+00	AJ229042.1	NT	Human alternatively spliced potassium channels ROM-K1, ROM-K2, ROM-K3, ROM-K4, ROM-K5, and ROM-K6 (KCNJ1) gene, complete cds
9467	22431	35889	0.55	3.4E+00	AJ250567.1	NT	Homo sapiens 959 kb contig between AML1 and CBR1 on chromosome 21q22, segment 2/3
10627	23549	37049	2.59	3.4E+00	AF013167.1	NT	Homo sapiens partial TM4SF2 gene for tetraspanin protein, exon 6
							Saccharomyces cerevisiae MSS1 gene, complete cds

Table 4

Single Exon Probes Expressed In Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
11861	24743	38327	2.86	3.4E+00	L77570.1	NT	Homo sapiens DiGeorge syndrome critical region, centromeric end
6186	19281	32496	1.03	3.3E+00	Q09669	SWISSPROT	PUTATIVE IRON ALCOHOL DEHYDROGENASE
6186	19281	32497	1.03	3.3E+00	Q09669	SWISSPROT	PUTATIVE IRON ALCOHOL DEHYDROGENASE
8225	21194	34601	0.9	3.3E+00	AF111188.2	NT	Homo sapiens serine palmitoyl transferase, subunit II gene, complete cds; and unknown genes
10830	23751	37250	0.9	3.3E+00	AP001511.1	NT	Bacillus halodurans genomic DNA, section 5/14
10830	23751	37251	0.9	3.3E+00	AP001511.1	NT	Bacillus halodurans genomic DNA, section 5/14
501	13573	26495	1.85	3.2E+00	X96422.1	NT	D. rerio zp-50 POU gene
4056	13573	26495	0.89	3.2E+00	X96422.1	NT	D. rerio zp-50 POU gene
4759	17779	30674	1.35	3.2E+00	4502404	NT	Homo sapiens carcinoembryonic antigen-related cell adhesion molecule 1 (biliary glycoprotein) (CEACAM1), mRNA
5648	18744	31910	1.2	3.2E+00	P54924	SWISSPROT	SQUALENE-HOPENE CYCLASE
5648	18744	31911	1.2	3.2E+00	P54924	SWISSPROT	SQUALENE-HOPENE CYCLASE
5683	18778	31950	2.79	3.2E+00	P12783	SWISSPROT	PHOSPHOGLYCERATE KINASE, CYTOSOLIC
5683	18778	31951	2.78	3.2E+00	P12783	SWISSPROT	PHOSPHOGLYCERATE KINASE, CYTOSOLIC
6439	19504	32754	1.66	3.2E+00	P18931	SWISSPROT	NADH-UBIQUINONE OXIDOREDUCTASE CHAIN 4
6439	19504	32755	1.66	3.2E+00	P18931	SWISSPROT	NADH-UBIQUINONE OXIDOREDUCTASE CHAIN 4
7863	20807	34185	0.71	3.2E+00	P04275	SWISSPROT	VON WILLEBRAND FACTOR PRECURSOR (VWF)
8052	20989	34386	2.47	3.2E+00	Y13655.1	NT	Chlamydomonas reinhardtii chloroplast DNA for rps9, ycf4, ycf3, rps18 genes
8052	20989	34387	2.47	3.2E+00	Y13655.1	NT	Chlamydomonas reinhardtii chloroplast DNA for rps9, ycf4, ycf3, rps18 genes
9385	22350	36921	4.78	3.2E+00	P13061	SWISSPROT	PERIPLASMIC [NIFE] HYDROGENASE SMALL SUBUNIT (NIFE HYDROGENLYASE SMALL CHAIN)
8888	22841	36298	1.87	3.2E+00	M36383.1	NT	S. cerevisiae threonine deaminase (LV1) gene, complete cds
10500	23422	36921	2	3.2E+00	AB016081.2	NT	Oryzias latipes CIGC6 gene for guanlyl cyclase C, complete cds
12217	25055		2.84	3.2E+00	L39836.1	NT	Sus scrofa choline acetyltransferase gene, promoter region
5976	19080	32261	2.25	3.1E+00	Q10135	SWISSPROT	HYPOTHETICAL_142.5 KD PROTEIN C23E2.02 IN CHROMOSOME I
7618	20578	33941	0.9	3.1E+00	P52178	SWISSPROT	TRIOSE PHOSPHATE/PHOSPHATE TRANSLOCATOR, NON-GREEN PLASTID PRECURSOR (CTPT)
7999	20638		1	3.1E+00	AF303225.1	NT	Bacillus alcalophilus pectate lyase (pelE) gene, complete cds
8424	21393	34804	0.43	3.1E+00	P40985	SWISSPROT	PROBABLE UBIQUITIN-PROTEIN LIGASE HUL4
8949	21915	35338	4.37	3.1E+00	P49894	SWISSPROT	TYPE I IODOTHYRONINE DEIODINASE (TYPE I 5DEIODINASE) (DIOI) (TYPE I DIO) (5DI)
8949	21915	35339	4.37	3.1E+00	P49894	SWISSPROT	TYPE I IODOTHYRONINE DEIODINASE (TYPE I 5DEIODINASE) (DIOI) (TYPE I DIO) (5DI)
9614	22618		3.9	3.1E+00	Q14957	SWISSPROT	GLUTAMATE (NMDA) RECEPTOR SUBUNIT EPSILON 3 PRECURSOR (N-METHYL D-ASPARTATE RECEPTOR SUBTYPE 2C) (NR2C) (NMDAR2C)
9680	22633	36089	0.48	3.1E+00	Q01149	SWISSPROT	COLLAGEN ALPHA 2(I) CHAIN PRECURSOR
10256	23181	36668	0.86	3.1E+00	7524759	NT	Chlorella vulgaris chloroplast, complete genome
10347	23271		0.61	3.1E+00	Q10125	SWISSPROT	HYPOTHETICAL_56.3 KD PROTEIN F52C9.5 IN CHROMOSOME III

Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10700	23622	37118	5.2	3.1E+00	P49365	SWISSPROT	DEOXYHYDROLYSINE SYNTHASE (DHS)
11791	23946		1.98	3.1E+00	P33515	SWISSPROT	GENOME POLYPROTEIN [CONTAINS: CAPSID PROTEIN C (CORE PROTEIN); MATRIX PROTEIN (ENVELOPE PROTEIN M); MAJOR ENVELOPE PROTEIN E; NONSTRUCTURAL PROTEINS NS1, NS2A, NS2B, NS4A AND NS4B; HELICASE (NS3); RNA-DIRECTED RNA POLYMERASE (NS5)] retinoid acid nuclear receptor isoform beta 2 [rat, embryonal carcinoma cell line, PCC7-MZ1, mRNA, 2971 nt]
11811	24896		2.76	3.1E+00	S56680.1	NT	
2849	15909	28833	1.5	3.0E+00	8923984	NT	Homo sapiens hypothetical protein PR00889 (PRO0889), mRNA
5411	18514	31392	1.33	3.0E+00	X53086.1	NT	S. aureus genes encoding Sau961 DNA methyltransferase and Sau961 restriction endonuclease
6708	19764	33043	0.79	3.0E+00	X56037.1	NT	Corynebacterium glutamicum thrC gene for threonine synthase (EC 4.2.99.2)
6708	19764	33044	0.79	3.0E+00	X56037.1	NT	Corynebacterium glutamicum thrC gene for threonine synthase (EC 4.2.99.2)
7363	20333		9.66	3.0E+00	P18406	SWISSPROT	CYR61 PROTEIN PRECURSOR (3CH61)
7402	20370		0.59	3.0E+00	Q13201	SWISSPROT	ENDOTHELIAL CELL MULTIMERIN PRECURSOR
9258	22224		1.21	3.0E+00	X67838.1	NT	B. napus DNA for myosinase
10657	23579	37076	0.54	3.0E+00	Q58605	SWISSPROT	S-ADENOSYLMETHIONINE SYNTHETASE (METHIONINE ADENOSYLTTRANSFERASE) (ADOMET SYNTHETASE)
11008	23973	37497	1.65	3.0E+00	Q18181	SWISSPROT	CDC10 PROTEIN HOMOLOG
11351	24301	37827	4.64	3.0E+00	P51842	SWISSPROT	RETINAL GUANYLYL CYCLASE 2 PRECURSOR (GUANYLYL CYCLASE 2F, RETINAL) (RETGC-2) (ROD OUTER SEGMENT MEMBRANE GUANYLYL CYCLASE 2) (ROS-GC2) (GUANYLYL CYCLASE F) (GC-F)
11351	24301	37828	4.64	3.0E+00	P51842	SWISSPROT	RETINAL GUANYLYL CYCLASE 2 PRECURSOR (GUANYLYL CYCLASE 2F, RETINAL) (RETGC-2) (ROD OUTER SEGMENT MEMBRANE GUANYLYL CYCLASE 2) (ROS-GC2) (GUANYLYL CYCLASE F) (GC-F)
2028	18046	28059	2.33	2.9E+00	AE002225.2	NT	Chlamydia pneumoniae AR39, section 53 of 84 of the complete genome
6192	19266		0.6	2.9E+00	AB026033.1	NT	Bonapartia pediculus mitochondrial DNA for 16S ribosomal RNA
7094	20028	33332	1.97	2.9E+00	Z36879.1	NT	F. pringlei gdsA gene for P-protein of the glycine cleavage system
7418	20385	33734	5.15	2.9E+00	O14514	SWISSPROT	BRAIN-SPECIFIC ANGIOGENESIS INHIBITOR 1 PRECURSOR
7418	20385	33735	5.15	2.9E+00	O14514	SWISSPROT	BRAIN-SPECIFIC ANGIOGENESIS INHIBITOR 1 PRECURSOR
7689	20647	34011	5.32	2.9E+00	P46589	SWISSPROT	ADHERENCE FACTOR (ADHESION AND AGGREGATION MEDIATING SURFACE ANTIGEN)
8200	21170	34580	0.61	2.9E+00	P05844	SWISSPROT	STRUCTURAL POLYPEPTIDE [CONTAINS: MAJOR STRUCTURAL PROTEIN VP2; NONSTRUCTURAL PROTEIN VP4; MINOR STRUCTURAL PROTEIN VP3]
8200	21170	34581	0.61	2.9E+00	P05844	SWISSPROT	STRUCTURAL POLYPEPTIDE [CONTAINS: MAJOR STRUCTURAL PROTEIN VP2; NONSTRUCTURAL PROTEIN VP4; MINOR STRUCTURAL PROTEIN VP3]
8434	21403	34816	0.82	2.9E+00	BF344171.1	EST_HUMAN	802017413FT NCI CGAP Bm64 Homo sapiens cDNA clone IMAGE:4153059 5'
1451	14484	27460	4.16	2.8E+00	AF186398.1	NT	Buxus harlandi maturase K (mark) gene, partial cds; chloroplast gene for chloroplast product

Table 4

Single Exon Probes Expressed In Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1637	14669		2.57	2.8E+00	AL161552.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 52
7529	20492	33854	4.93	2.8E+00	8393724	NT	Mus musculus endomucin (LOC53423), mRNA
8972	22899		0.56	2.8E+00	BE566182.1	EST_HUMAN	601342758F1 NIH_MGC_53 Homo sapiens cDNA clone IMAGE:3684807 5'
11048	20492	33854	1.73	2.8E+00	8393724	NT	Mus musculus endomucin (LOC53423), mRNA
233	13333	28256	13.36	2.7E+00	6679306	NT	Mus musculus per-hexamer repeat gene 3 (Phx3), mRNA
233	13333	28257	13.36	2.7E+00	6679306	NT	Mus musculus per-hexamer repeat gene 3 (Phx3), mRNA
5631	18727	31888	1.11	2.7E+00	L14005.1	NT	Homo sapiens apoA polymorphism Kringle IV gene, exons 1 and 2
8485	21453		0.66	2.7E+00	U15947.1	NT	Ipomoea purpurea chalcone synthase (CHS) gene including complete 5'UTR and complete cds
9319	22284		1.69	2.7E+00	AL116459.1	NT	Botrytis cinerea strain T4 cDNA library under conditions of nitrogen deprivation
9787	21110	34510	0.64	2.7E+00	AW088191.1	EST_HUMAN	xc88e12.x1 NC1_CGAP_Brn35 Homo sapiens cDNA clone IMAGE:2591374 3' similar to gb:M17733
10866	23786		1.69	2.7E+00	BE033527.1	EST_HUMAN	THYMOSIN BETA-4 (HUMAN)
4701	17722	30615	6.29	2.6E+00	AF088749.1	NT	CMO-BT0281-031199-087-H04 BT0281 Homo sapiens cDNA
5827	18723	31883	2.06	2.6E+00	6755601	NT	Mus musculus sphingosine kinase (SPHK1b) mRNA, complete cds
5827	18723	31884	2.06	2.6E+00	6755601	NT	Mus musculus SRY-box containing gene 13 (Sox13), mRNA
5925	19011		3.9	2.6E+00	Y17062.1	NT	Mus musculus SRY-box containing gene 13 (Sox13), mRNA
7803	26002		0.7	2.6E+00	AJ224639.1	NT	Mycobacterium fortuitum furA II gene
7987	20906		32.15	2.6E+00	AF235502.1	NT	Homo sapiens Surf-5 and Surf-6 genes
8394	21363	34770	1.12	2.6E+00	AJ132180.1	NT	Mus musculus SH2-containing histidyl 5-phosphatase (Ship) gene, exons 16 through 27, and complete cds
8394	21363	34771	1.12	2.6E+00	AJ132180.1	NT	faba bean necrotic yellows virus C2-Eg gene, isolate Egyptian EV1-93
10015	22942	36408	3.12	2.6E+00	AL161540.2	NT	faba bean necrotic yellows virus C2-Eg gene, isolate Egyptian EV1-93
10720	23642		1.61	2.6E+00	9055193	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 40
12841	25877		2.58	2.6E+00	11419220	NT	Mus musculus cleavage and polyadenylation specificity factor 3 (Ops3), mRNA
1460	14493	27466	3.73	2.5E+00	AJ271844.1	NT	Homo sapiens ATP-binding cassette, sub-family B (MDR/TAP), member 4 (ABCB4), mRNA
1460	14493	27467	3.73	2.5E+00	AJ271844.1	NT	Aspergillus nidulans recQ gene for DNA helicase, exons 1-4
5911	18997	32186	2.32	2.5E+00	P13485	SWISSPROT	Aspergillus nidulans recQ gene for DNA helicase, exons 1-4
5911	18997	32187	2.32	2.5E+00	P13485	SWISSPROT	TEICHOIC ACID BIOSYNTHESIS PROTEIN F
6601	18997	32186	1.49	2.5E+00	P13485	SWISSPROT	TEICHOIC ACID BIOSYNTHESIS PROTEIN F
6601	18997	32187	1.49	2.5E+00	P13485	SWISSPROT	TEICHOIC ACID BIOSYNTHESIS PROTEIN F
6882	19944	33240	0.66	2.5E+00	D30052.1	NT	TEICHOIC ACID BIOSYNTHESIS PROTEIN F
7960	20901	34293	0.55	2.5E+00	P17568	SWISSPROT	Vibrio cholerae ctxA gene and ctxB gene for cholera toxins, complete cds
8035	20972	34366	0.97	2.5E+00	AW949158.1	EST_HUMAN	LATENCY-RELATED PROTEIN 1
8095	21031	34429	0.51	2.5E+00	4502302	NT	QV4-FT0005-110500-205-g07 FT0005 Homo sapiens cDNA
							Homo sapiens clathrin, heavy polypeptide-like 1 (GLTCL1) mRNA

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Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9459	22423	35861	1.49	2.5E+00	D50307.1	NT	Rice DNA for aldolase C-1, complete cds
10211	23136	36623	0.73	2.5E+00	BE297758.1	EST_HUMAN	601175779F1 NIH_MGC 17 Homo sapiens cDNA clone IMAGE:3631090 5'
12214	25053		2.5	2.5E+00	AF289665.1	NT	Mus musculus EIF4H gene, partial cds; LIMK1 gene, complete cds; and ELN gene, partial cds
3026	16083	28006	1.1	2.4E+00	M24282.1	NT	Chicken alpha-3 collagen type VI mRNA, 3' end
4944	17960	30851	5.31	2.4E+00	4503352	NT	Homo sapiens double C2-like domains, alpha (DOC2A) mRNA
6126	19204	32427	3.62	2.4E+00	P02843	SWISSPROT	VITELLOGENIN 1 PRECURSOR (YOLK PROTEIN 1)
7606	20567	33927	0.71	2.4E+00	BF667502.1	EST_HUMAN	602120856F1 NIH_MGC 56 Homo sapiens cDNA clone IMAGE:4278012 5'
7606	20567	33928	0.71	2.4E+00	BF667502.1	EST_HUMAN	602120856F1 NIH_MGC 56 Homo sapiens cDNA clone IMAGE:4278012 5'
8479	21448	34864	2.08	2.4E+00	P28842	SWISSPROT	OD27L RECEPTOR PRECURSOR (T-CELL ACTIVATION ANTIGEN CD27) (T14)
8479	21448	34865	2.08	2.4E+00	P28842	SWISSPROT	OD27L RECEPTOR PRECURSOR (T-CELL ACTIVATION ANTIGEN CD27) (T14)
8554	21522		2.92	2.4E+00	AE001486.1	NT	Helicobacter pylori, strain J99 section 47 of 132 of the complete genome
8998	21964		1.46	2.4E+00	AW875126.1	EST_HUMAN	RC2-PT0004-031299-011-805 PT0004 Homo sapiens cDNA
9180	22146	35573	9.52	2.4E+00	P24091	SWISSPROT	ENDOCHITINASE B PRECURSOR (CHN-B)
10398	23320	36803	2.34	2.4E+00	P13673	SWISSPROT	SKIN GRANULE PROTEIN PRECURSOR
10398	23320	36804	2.34	2.4E+00	P13673	SWISSPROT	SKIN GRANULE PROTEIN PRECURSOR
10468	23388	36882	2.1	2.4E+00	X92511.1	NT	H. sapiens CTGF gene and promoter region
10604	23526		6.1	2.4E+00	P09096	SWISSPROT	XYLULOSE KINASE (XYLUKINASE)
10685	23607	37100	1.67	2.4E+00	BE326702.1	EST_HUMAN	hr63106.x1 NCI CGAP Kid11 Homo sapiens cDNA clone IMAGE:3133187 3'
10685	23607	37101	1.67	2.4E+00	BE326702.1	EST_HUMAN	hr63106.x1 NCI CGAP Kid11 Homo sapiens cDNA clone IMAGE:3133187 3'
10955	23875	37389	1.14	2.4E+00	Q51481	SWISSPROT	DENITRIFICATION REGULATORY PROTEIN NIRQ
11415	24359	37894	2.2	2.4E+00	Y14079.1	NT	Bacillus subtilis chromosomal DNA, region 75 degrees: glpPKD operon and downstream
11517	24458		1.66	2.4E+00	AF096872.1	NT	Capra hircus alphaS2-casein type C gene, intron 15
11696	24652	38231	2.14	2.4E+00	AF158862.2	NT	Fragaria x ananassa cytosolic ascorbate peroxidase (ApxSC) gene, ApxSC-c allele, complete cds
1258	14293	27257	11.33	2.3E+00	Z46724.1	NT	G. domesticus artificial single chain antibody gene (L3)
4147	17178		1.45	2.3E+00	AJ401081.1	NT	Bos taurus partial cyto gene for cytochrome b
5934	19020		0.99	2.3E+00	N86245.1	EST_HUMAN	J7340F Human fetal heart, Lambda ZAP Express Homo sapiens cDNA clone J7340 5' similar to
7687	20545	34009	2.42	2.3E+00	6978554	NT	PROLYLCARBOXYPEPTIDASE
7853	26003		2.79	2.3E+00	P07199	SWISSPROT	Rattus norvegicus ATPase, Ca++ transporting, ubiquitous (Atp2a3), mRNA
8059	20996	34392	1.12	2.3E+00	X60265.1	NT	MAJOR CENTROMERE AUTOANTIGEN B (CENTROMERE PROTEIN B) (CENP-B)
9465	22429	35868	0.54	2.3E+00	5835317	NT	M. maezi dnaK and dnaJ genes homologues coding for DnaK and DnaJ
9525	22488	35938	2.03	2.3E+00	Q11127	SWISSPROT	Polymerase ornithinyl transferase, complete genome ALPHA(1,3)-FUCOSYLTRANSFERASE (GALACTOSIDE 3-L-FUCOSYLTRANSFERASE) (FUCOSYLTRANSFERASE 4) (FUCT-IV)

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Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10958	23878	37390	0.45	2.3E+00	P02461	SWISSPROT	COLLAGEN ALPHA 1(III) CHAIN PRECURSOR
11153	24113	37638	7.84	2.3E+00	Q07076	SWISSPROT	ANNEXIN VII (SYNEXIN)
11897	24778	38364	1.59	2.3E+00	P45931	SWISSPROT	HYPOTHETICAL 171.0 KD PROTEIN IN SPOIIIC-OWLA INTERGENIC REGION
12072	24945	38539	2.34	2.3E+00	BF541987.1	EST_HUMAN	602069121F1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:4068173 5'
12072	24945	38540	2.34	2.3E+00	BF541987.1	EST_HUMAN	602069121F1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:4068173 5'
12443	25205	31828	6.31	2.3E+00	BE895237.1	EST_HUMAN	601433673F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3918643 5'
13077	25609		1.3	2.3E+00	AF281862.1	NT	Neurospora crassa G protein alpha subunit GNA-3 (gna-3) gene, complete cds
4046	17084	29981	1.42	2.2E+00	AF020628.1	NT	Magnaporthe grisea Class IV chitin synthase (chs4) gene, complete cds
4342	17369	30251	3.8	2.2E+00	D67071.1	NT	Rat gene for regucalcin, exon1 (non-coding exon)
4342	17369	30252	3.8	2.2E+00	D67071.1	NT	Rat gene for regucalcin, exon1 (non-coding exon)
5415	18518	31395	11.02	2.2E+00	O88307	SWISSPROT	SORTILIN-RELATED RECEPTOR PRECURSOR (SORTING PROTEIN-RELATED RECEPTOR CONTAINING LDLR CLASS A REPEATS) (MSORLA) (SORLA-1) (LOW-DENSITY LIPOPROTEIN RECEPTOR RELATIVE WITH 11 LIGAND-BINDING REPEATS) (LDLR RELATIVE WITH 11 LIGAND-BINDING REPEATS) (LR11) (>
5415	18518	31396	11.02	2.2E+00	O88307	SWISSPROT	SORTILIN-RELATED RECEPTOR PRECURSOR (SORTING PROTEIN-RELATED RECEPTOR CONTAINING LDLR CLASS A REPEATS) (MSORLA) (SORLA-1) (LOW-DENSITY LIPOPROTEIN RECEPTOR RELATIVE WITH 11 LIGAND-BINDING REPEATS) (LDLR RELATIVE WITH 11 LIGAND-BINDING REPEATS) (LR11) (>
5953	19038	32234	1.83	2.2E+00	BE927220.1	EST_HUMAN	RC3-CT0264-300800-022-e06 CT0264 Homo sapiens cDNA
5953	19038	32235	1.83	2.2E+00	BE927220.1	EST_HUMAN	RC3-CT0264-300800-022-e06 CT0264 Homo sapiens cDNA
6180	19255	32488	8.78	2.2E+00	BE250383.1	EST_HUMAN	600943401T1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:2959777 3'
6489	19554	32804	3.91	2.2E+00	Q00335	SWISSPROT	MINOR VIRION STRUCTURAL PROTEIN MU-2
6750	19804	33085	3.14	2.2E+00	P51459	SWISSPROT	INSULIN-LIKE GROWTH FACTOR II PRECURSOR (IGF-II) (SOMATOMEDIN A)
7149	18381		3.5	2.2E+00	AA694574.1	EST_HUMAN	nl95b02.st NCI CGAP Co10 Homo sapiens cDNA clone IMAGE:1058379 3'
7539	20502	33861	0.95	2.2E+00	AA137027.1	EST_HUMAN	zn9704.r1 Stralagene fetal retina 937202 Homo sapiens cDNA clone IMAGE:566143 5'
7865	20809	34187	18.24	2.2E+00	AA449012.1	EST_HUMAN	z05g10.r1 Soares fetal testis Nb2HF8_gw Homo sapiens cDNA clone IMAGE:785634 5'
7863	20894	34287	0.68	2.2E+00	P54918	SWISSPROT	ALANINE RACEMASE
8439	21408	34820	0.69	2.2E+00	BE301560.1	EST_HUMAN	bb17h12.x1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:2963207 3' similar to gb:D45836 Mouse mRNA for nuclear pore-targeting-complex component of (MOUSE);
8439	21408	34821	0.69	2.2E+00	BE301560.1	EST_HUMAN	bb17h12.x1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:2963207 3' similar to gb:D45836 Mouse mRNA for nuclear pore-targeting-complex component of (MOUSE);
9897	22650		11.22	2.2E+00	BE741678.1	EST_HUMAN	601694733F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3948561 5'
9827	25698		2.53	2.2E+00	Q04706	SWISSPROT	TRANSPONIN TY1 PROTEIN A

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Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10413	23335	36819	1.57	2.2E+00	AI290373.1	EST_HUMAN	qm89b03.x1 Soares_placenta_8to9weeks_2NBHP8b0W Homo sapiens cDNA clone IMAGE:1893965 3' similar to gb:Y00433 GLUTATHIONE PEROXIDASE (HUMAN);
10413	23335	36820	1.57	2.2E+00	AI290373.1	EST_HUMAN	qm89b03.x1 Soares_placenta_8to9weeks_2NBHP8b0W Homo sapiens cDNA clone IMAGE:1893965 3' similar to gb:Y00433 GLUTATHIONE PEROXIDASE (HUMAN);
10456	23378	36871	2.22	2.2E+00	BF246782.1	EST_HUMAN	qm89b03.x1 Soares_placenta_8to9weeks_2NBHP8b0W Homo sapiens cDNA clone IMAGE:1893965 3' similar to gb:Y00433 GLUTATHIONE PEROXIDASE (HUMAN);
10822	23743	37244	3.06	2.2E+00	AF180416.1	NT	601855591F1 NIH_MGC_37 Homo sapiens cDNA clone IMAGE:4075391 5'
11788	23923	37442	3.23	2.2E+00	P07911	SWISSPROT	Homo sapiens ovarian granulosa cell 13.0 kDa protein hGR74 homolog mRNA, complete cds
11937	24818	38415	6.31	2.2E+00	P10407	SWISSPROT	UROMODULIN PRECURSOR (TAMM-HORSFALL URINARY GLYCOPROTEIN) (THP)
571	15844	26555	12.39	2.1E+00	AF132612.2	NT	EARLY E1A 28 KD PROTEIN
3601	16646		0.83	2.1E+00	AW449366.1	EST_HUMAN	Mus musculus pre-T cell receptor alpha gene, enhancer region and upstream region
6255	19328		0.86	2.1E+00	P75357	SWISSPROT	UI-HB18-alk-e-08-0-UI.s1 NCI_CGAP_Sub5 Homo sapiens cDNA clone IMAGE:2734550 3'
6980	20203	33532	3.45	2.1E+00	O70159	SWISSPROT	HYPOTHEICAL PROTEIN MG302 HOMOLOG
7225	20247	33581	0.61	2.1E+00	4503430	NT	ALPHA-2HS-GLYCOPROTEIN PRECURSOR (FETUIN-A)
7246	19981	33278	5.97	2.1E+00	N29575.1	EST_HUMAN	Homo sapiens dysferlin, limb girdle muscular dystrophy 2B (autosomal recessive) (DYSF) mRNA, and translated products
8842	21809		1.92	2.1E+00	AU123630.1	EST_HUMAN	yy08a10.s1 Soares_melanocyte 2NBHM Homo sapiens cDNA clone IMAGE:270618 3' similar to gb:M55654 TRANSCRIPTION INITIATION FACTOR TFIIID (HUMAN);
1201	14240	27197	1.39	2.0E+00	AF180527.1	NT	AU123630 NT2RM2 Homo sapiens cDNA clone NT2RM2000671 5'
1201	14240	27198	1.39	2.0E+00	AF180527.1	NT	Homo sapiens p22Dokdel (DOKDEL) mRNA, complete cds
1338	14372	27342	1.19	2.0E+00	AF204927.1	NT	Homo sapiens p22Dokdel (DOKDEL) mRNA, complete cds
1578	14611		3.42	2.0E+00	P25592	SWISSPROT	Oryctolagus cuniculus Na ⁺ /K ⁺ -ATPase beta 1 subunit mRNA, complete cds
2159	15175	28195	4.98	2.0E+00	Z78279.1	NT	PUTATIVE RRNA METHYLTRANSFERASE SPB1
2159	15175	28196	4.98	2.0E+00	Z78279.1	NT	R.norvegicus mRNA for collagen alpha1 type I
4127	17160	30048	2.24	2.0E+00	AW664496.1	EST_HUMAN	R.norvegicus mRNA for collagen alpha1 type I
4127	17160	30049	2.24	2.0E+00	AW664496.1	EST_HUMAN	hi13c05.x1 NCI_CGAP_GU1 Homo sapiens cDNA clone IMAGE:2972188 3' similar to gb:X01677 GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE, LIVER (HUMAN);
7798	20750		0.85	2.0E+00	P07566	SWISSPROT	hi13c05.x1 NCI_CGAP_GU1 Homo sapiens cDNA clone IMAGE:2972188 3' similar to gb:X01677 GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE, LIVER (HUMAN);
8358	21327	34738	3.84	2.0E+00	AB008676.1	NT	STRUCTURAL POLYPROTEIN [CONTAINS: NUCLEOCAPSID PROTEIN C; MEMBRANE GLYCOPROTEINS E1 AND E2]
8358	21327	34739	3.84	2.0E+00	AB008676.1	NT	Escherichia coli 0157 DNA, map position at 46 min., complete cds
8358	21327	34740	3.84	2.0E+00	AB008676.1	NT	Escherichia coli 0157 DNA, map position at 46 min., complete cds
9274	22240	35668	3.22	2.0E+00	F31500.1	EST_HUMAN	Escherichia coli 0157 DNA, map position at 46 min., complete cds
12756	25538	31427	4.52	2.0E+00	5834843	NT	HSPD22703 HM3 Homo sapiens cDNA clone s4000117B08
							Gallus gallus mitochondrion, complete genome

Table 4

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4829	17948	30746	0.98	1.9E+00	AF209468.1	NT	Danio rerio Rh50-like protein mRNA, complete cds
5679	18774	31945	4.52	1.9E+00	0754389	NT	Mus musculus inositol 1,4,5-triphosphate receptor 1 (Itpr1), mRNA
5679	18774	31945	4.52	1.9E+00	0754389	NT	Mus musculus inositol 1,4,5-triphosphate receptor 1 (Itpr1), mRNA
6219	19293	32527	1.05	1.9E+00	BE909595.1	EST_HUMAN	601870638F1 NIH_MGC_78 Homo sapiens cDNA clone IMAGE:3949881 5'
6810	19864		1.19	1.9E+00	AW845689.1	EST_HUMAN	MRO-CT0063-071059-002-902 CT0063 Homo sapiens cDNA
6912	19864		2.37	1.9E+00	Q63027	SWISSPROT	CTD-BINDING SR-LIKE PROTEIN RA4
8802	21769	35193	1.72	1.9E+00	P02467	SWISSPROT	COLLAGEN ALPHA 2(I) CHAIN PRECURSOR
8802	21769	35194	1.72	1.9E+00	P02467	SWISSPROT	COLLAGEN ALPHA 2(I) CHAIN PRECURSOR
9006	21972		3.6	1.9E+00	BF360206.1	EST_HUMAN	GM3-MT0114-010800-323-112 MT0114 Homo sapiens cDNA
9245	22211		1.52	1.9E+00	O51781	SWISSPROT	ARGININE DEIMINASE (ADI) (ARGININE DIHYDROLASE) (ADI)
9988	22915	36380	0.53	1.9E+00	AA669125.1	EST_HUMAN	ab94a04.s1 Stratagene lung (#937210) Homo sapiens cDNA clone IMAGE:854574 3' similar to contains Alu repetitive element/contains element L1 L1 repetitive element ;
10929	23849	37364	0.63	1.9E+00	AF248269.1	NT	Homo sapiens gag-pro-pol precursor protein gene, partial cds
3109	16166	29077	1.5	1.8E+00	P21004	SWISSPROT	PROTEIN B8 PRECURSOR
3137	16194	29103	10.81	1.8E+00	U04356.1	NT	Synechococcus sp. PCC7942 copper transporting P-ATPase (ctaA) and ATP synthase epsilon subunit (atpE) genes, complete cds
3137	16194	29104	10.81	1.8E+00	U04356.1	NT	Synechococcus sp. PCC7942 copper transporting P-ATPase (ctaA) and ATP synthase epsilon subunit (atpE) genes, complete cds
5967	19052		1.84	1.8E+00	P18502	SWISSPROT	HEDGEHOG RECEPTOR (PATCHED PROTEIN)
6224	19298	32532	2.2	1.8E+00	BF311969.1	EST_HUMAN	601897854F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4127364 5'
6538	19600		1.19	1.8E+00	BF683327.1	EST_HUMAN	602139470F1 NIH_MGC_46 Homo sapiens cDNA clone IMAGE:4298272 5'
6804	19656	33253	1.02	1.8E+00	BF305652.1	EST_HUMAN	601893489F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4139038 5'
7260	19995	33292	1.07	1.8E+00	P21249	SWISSPROT	MAJOR ANTIGEN
7476	20442		0.7	1.8E+00	P27127	SWISSPROT	LIPOPOLYSACCHARIDE 1,6-GALACTOSYLTRANSFERASE (UDP-D-GALACTOSE--(GLUCOSYL)LIPOPOLYSACCHARIDE-ALPHA-1,3-D-GALACTOSYLTRANSFERASE)
8454	21423	34838	0.9	1.8E+00	P11369	SWISSPROT	RETROVIRUS-RELATED POLYPROTEIN [CONTAINS: REVERSE TRANSCRIPTASE ; ENDONUCLEASE]
8454	21423	34839	0.9	1.8E+00	P11369	SWISSPROT	RETROVIRUS-RELATED POLYPROTEIN [CONTAINS: REVERSE TRANSCRIPTASE ; ENDONUCLEASE]
8812	21779	35204	0.46	1.8E+00	P48634	SWISSPROT	LARGE PROLINE-RICH PROTEIN BAT2 (HLA-B-ASSOCIATED TRANSCRIPT 2)
8812	21779	35205	0.46	1.8E+00	P48634	SWISSPROT	LARGE PROLINE-RICH PROTEIN BAT2 (HLA-B-ASSOCIATED TRANSCRIPT 2)
8812	21779	35206	0.46	1.8E+00	P48634	SWISSPROT	LARGE PROLINE-RICH PROTEIN BAT2 (HLA-B-ASSOCIATED TRANSCRIPT 2)
9206	22172	35603	2.21	1.8E+00	O43281	SWISSPROT	EMBRYONAL FYN-ASSOCIATED SUBSTRATE (HEFS)
9330	22493	35941	0.66	1.8E+00	R31042.1	EST_HUMAN	Yn72c08.r Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:135278 5'

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Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9617	22561	36009	0.64	1.8E+00	AW890004.1	EST_HUMAN	QV0-OT0030-070300-148-a03 OT0030 Homo sapiens cDNA
10208	23133	36620	0.93	1.8E+00	P27050	SWISSPROT	CHITINASE D PRECURSOR
10846	23568		2.88	1.8E+00	AF111849.1	NT	Homo sapiens PRO0530 mRNA, complete cds
10919	23839		0.75	1.8E+00	P44325	SWISSPROT	CYTIDINE DEAMINASE (CYTIDINE AMINOHYDROLASE) (ODA)
12563	25808		8.17	1.8E+00	AF314254.1	NT	Chlamydomonas reinhardtii alternative oxidase 1 (AOX1) gene, nuclear gene encoding mitochondrial protein
12842	25326		5.53	1.8E+00	9506404	NT	Rattus norvegicus Actin-related protein complex 1b (Arp1b), mRNA
1110	14154	27104	2.43	1.7E+00	Q60114	SWISSPROT	LEVANSUCRASE (BETA-D-FRUCTOFURANOSYL TRANSFERASE) (SUCROSE 6-FRUCTOSYL TRANSFERASE)
2279	15292	28317	3.08	1.7E+00	AL163280.2	NT	Homo sapiens chromosome 21 segment HS21C080
2382	15390	28415	1.67	1.7E+00	AI141067.1	EST_HUMAN	oz43n05.x1 Soares_NihMPu_S1 Homo sapiens cDNA clone IMAGE:1678137 3'
4487	17512	30400	0.9	1.7E+00	Q60114	SWISSPROT	LEVANSUCRASE (BETA-D-FRUCTOFURANOSYL TRANSFERASE) (SUCROSE 6-FRUCTOSYL TRANSFERASE)
5694	18789	31959	1.66	1.7E+00	BE063546.1	EST_HUMAN	GM0-BT0282-171299-127-a05 BT0282 Homo sapiens cDNA
5694	18789	31960	1.66	1.7E+00	BE063546.1	EST_HUMAN	GM0-BT0282-171299-127-a05 BT0282 Homo sapiens cDNA
5955	19040	32238	0.49	1.7E+00	R38748.1	EST_HUMAN	G4946 Fetal heart Homo sapiens cDNA clone G4846 5' and
6133	19210	32436	3.14	1.7E+00	Q9T1R8	SWISSPROT	COUP TRANSCRIPTION FACTOR 1 (COUP-TF1) (COUP-TF1)
6703	19759	33038	0.59	1.7E+00	P35816	SWISSPROT	(PYRUVATE DEHYDROGENASE (LIPOAMIDE) PHOSPHATASE, MITOCHONDRIAL PRECURSOR
7428	20395	33746	1.01	1.7E+00	Q03703	SWISSPROT	(PDP) (PYRUVATE DEHYDROGENASE PHOSPHATASE, CATALYTIC SUBUNIT) (PDPC)
7428	20395	33747	1.01	1.7E+00	Q03703	SWISSPROT	HYPOTHETICAL 38.0 KD PROTEIN IN CAT2-AMDT INTERGENIC REGION
8187	21157	34566	0.81	1.7E+00	AF021335.1	NT	HYPOTHETICAL 38.0 KD PROTEIN IN CAT2-AMDT INTERGENIC REGION
8367	21336	34748	1.21	1.7E+00	6755715	NT	Mus musculus T cell receptor gamma locus, TCR gamma 2 and gamma 4 gene clusters
8397	21366	34775	0.54	1.7E+00	BF530630.1	EST_HUMAN	Mus musculus T-cell acute lymphocytic leukemia 1 (Tall), mRNA
8887	21853	35273	0.45	1.7E+00	AF245513.1	NT	602071917F1 NCL CGAP_Bm67 Homo sapiens cDNA clone IMAGE:4214669 5'
8974	21940		1.92	1.7E+00	BF308000.1	EST_HUMAN	Hippoglossus hippoglossus interferon inducible Mx protein (Mx) mRNA, complete cds
9052	22018	35442	0.51	1.7E+00	X69033.1	NT	601894255F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4140084 5'
9052	22018	35443	0.51	1.7E+00	X69033.1	NT	M. musculus Ank-1 mRNA for erythroid ankyrin
9166	22132	35558	0.43	1.7E+00	U19832.1	NT	M. musculus Ank-1 mRNA for erythroid ankyrin
9504	25697	35909	2.37	1.7E+00	O60479	SWISSPROT	Rattus norvegicus SA gene, partial cds
9504	25697	35910	2.37	1.7E+00	O60479	SWISSPROT	HOMEOBOX PROTEIN DLX-3
9965	22892		1.4	1.7E+00	AF161380.1	NT	HOMEOBOX PROTEIN DLX-3
10332	23454		0.5	1.7E+00	AW953681.1	EST_HUMAN	Homo sapiens HSPC262 mRNA, partial cds
							EST1365751 IMAGE: ressequences, MAGC Homo sapiens cDNA

Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
12518	25249	31803	1.78	1.7E+00	AI678443.1	EST_HUMAN	tu82d07.x1 NCI_CGAP_Gas4 Homo sapiens cDNA clone IMAGE:2257649 3' similar to contains MSR1.11 (MSR1) repetitive element.
2049	15068	28088	14.89	1.6E+00	AF199339.1	NT	Homo sapiens lens epithelium-derived growth factor gene, alternatively spliced, complete cds
2059	15078	28097	3.29	1.6E+00	AF077374.1	NT	Homo sapiens small proline-rich protein (SPRR3) gene, exons 1, 2, and 3 and complete cds
2065	15083	28102	1.62	1.6E+00	Y11344.1	NT	Mus musculus ST6GalNAcII gene, exon 2
2292	15304		1.33	1.6E+00	X98373.1	NT	B. napus gene encoding endo-polygalacturonase
2972	16030	28953	1.88	1.6E+00	W58426.1	EST_HUMAN	zid25f01.1 Soares, fetal heart, NBH19W Homo sapiens cDNA clone IMAGE:341689 5' similar to
4063	17099		7.07	1.6E+00	BF570077.1	EST_HUMAN	gb:D29805 N-ACETYLACTOSAMINE SYNTHASE (HUMAN);
4378	17407	30287	1.29	1.6E+00	AF155827.1	NT	60218609511 NIH_MGC_45 Homo sapiens cDNA clone IMAGE:4310591 3'
4378	17407	30288	1.29	1.6E+00	AF155827.1	NT	Homo sapiens proliferation-associated SNF2-like protein (SMARCA6) mRNA, complete cds
5120	18130	31006	2.98	1.6E+00	Y11344.1	NT	Homo sapiens proliferation-associated SNF2-like protein (SMARCA6) mRNA, complete cds
5120	18130	31007	2.98	1.6E+00	Y11344.1	NT	Mus musculus ST6GalNAcII gene, exon 2
5926	19012	32204	2.21	1.6E+00	LO4808.1	NT	Mus musculus ST6GalNAcII gene, exon 2
6020	19103	32305	0.82	1.6E+00	AF005931.1	NT	Brachydanio rerio MHC class II DA-beta-2*01 gene, 3' end
6814	19872	32950	0.83	1.6E+00	BF380703.1	EST_HUMAN	Homo sapiens transglutaminase type 1 (Tgase1) gene, promoter region
6868	19921	33217	0.97	1.6E+00	AW294881.1	EST_HUMAN	IL2-UT0073-060900-145-E02 UT0073 Homo sapiens cDNA
7456	20422	33777	2.47	1.6E+00	BE697267.1	EST_HUMAN	UI-HB12-ahr-b-04-0-U1.s1 NCI_CGAP_Sub4 Homo sapiens cDNA clone IMAGE:2727511 3'
8364	21333		1.1	1.6E+00	Q46378	SWISSPROT	RCQ-CT0415-200700-032-c10 CT0415 Homo sapiens cDNA
8722	21690	35117	3.42	1.6E+00	AI297131.1	NT	VIRULENCE FACTOR MVIN HOMOLOG
9251	22217	35647	0.9	1.6E+00	11437222	NT	Mus musculus SIL_MAP_17, CYP_a, SOL & CYP_b genes
9251	22217	35648	0.9	1.6E+00	11437222	NT	Homo sapiens hypothetical protein PRO0971 (PRO0971), mRNA
9815	25695	34540	1.54	1.6E+00	X52046.1	NT	Homo sapiens hypothetical protein PRO0971 (PRO0971), mRNA
9815	25695	34541	1.54	1.6E+00	X52046.1	NT	M.musculus COL3A1 gene for collagen alpha-1
9945	22872		0.48	1.6E+00	AF043466.1	NT	M.musculus COL3A1 gene for collagen alpha-1
10091	23017	36493	1.23	1.6E+00	T41280.1	EST_HUMAN	Thermotoga maritima D-xylose-binding protein (xyf) gene, complete cds
10506	23428	36925	0.48	1.6E+00	AF121381.1	NT	ph6b6_19/1TV Outward Alu-primed hncDNA library Homo sapiens cDNA clone ph6b6_19/1TV
10545	23467	36961	1.12	1.6E+00	AW835644.1	EST_HUMAN	Drosophila melanogaster signal transducing adaptor protein (STAM), serine threonine kinase Ial (IAL), and
10545	23467	36962	1.12	1.6E+00	AW835644.1	EST_HUMAN	zinc finger protein (DNZ1) genes, complete cds
10709	23631	37126	0.78	1.6E+00	AF037352.1	NT	QV4-LT0016-090200-100-407 LT0016 Homo sapiens cDNA
11123	24083	37808	1.73	1.6E+00	PE4817	SWISSPROT	QV4-LT0016-090200-100-407 LT0016 Homo sapiens cDNA
11192	19103	32305	5.78	1.6E+00	AF005693.1	NT	Mus musculus T cell receptor gamma locus, TCR gamma 1 and gamma 3 gene clusters
12017	24894	38491	2.83	1.6E+00	AF104313.1	NT	CAPSID PROTEIN P40 [CONTAINS: ASSEMBLIN (PROTEASE); CAPSID ASSEMBLY PROTEIN]
							Homo sapiens transglutaminase type 1 (Tgase1) gene, promoter region
							Homo sapiens unknown mRNA

Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
35	13155	26056	3.54	1.5E+00	U53449.1	NT	Rattus norvegicus jun dimerization protein 2 (jdp-2) mRNA, complete cds
234	13334	26258	2.63	1.5E+00	AE002201.2	NT	Chlamydomonas reinhardtii AR39, section 32 of 94 of the complete genome
622	13687		2.04	1.5E+00	6752961	NT	Mus musculus a disintegrin and metalloproteinase domain (ADAM) 15 (metargidin) (Adam15), mRNA
2420	15427	28450	3.2	1.5E+00	AJ131402.1	NT	Potato virus A RNA complete genome, isolate U
2522	15427	28547	2.17	1.5E+00	6678350	NT	Mus musculus T-cell lymphoma invasion and metastasis 1 (Tiam1), mRNA
3155	15427	28450	2.96	1.5E+00	AJ131402.1	NT	Potato virus A RNA complete genome, isolate U
3386	16435	29362	0.92	1.5E+00	AE001945.1	NT	Deinococcus radiodurans R1 section 82 of 229 of the complete chromosome 1
5817	18907	32090	0.82	1.5E+00	AI655301.1	EST_HUMAN	hK1F.1.;
5817	18907	32091	0.82	1.5E+00	AI655301.1	EST_HUMAN	hK1F.1.;
6546	19607	32869	2.71	1.5E+00	R17879.1	EST_HUMAN	yg10602.1f Soares infant brain 1N1B Homo sapiens cDNA clone IMAGE:31893 5'
7335	20306		1.48	1.5E+00	BE783356.1	EST_HUMAN	601478745F1 NIH_MGC 58 Homo sapiens cDNA clone IMAGE:3881555 5'
7368	20338	33688	16.72	1.5E+00	P47179	SWISSPROT	HYPOTHETICAL 118.4 KD PROTEIN IN BAT2-DALS INTERGENIC REGION PRECURSOR
7368	20338	33689	16.72	1.5E+00	P47179	SWISSPROT	HYPOTHETICAL 118.4 KD PROTEIN IN BAT2-DALS INTERGENIC REGION PRECURSOR
7588	20531	33890	0.6	1.5E+00	AA88259.1	EST_HUMAN	ak2610.s1 Soares testis_NHT Homo sapiens cDNA clone IMAGE:1407115 3'
7850	20796	34172	0.73	1.5E+00	AI003254.1	EST_HUMAN	an07b11.s1 Stralagene schizo brain S11 Homo sapiens cDNA clone IMAGE:1684893 3' similar to gb:S95936 SEROTRANSFERRIN PRECURSOR (HUMAN);
8144	21081		0.67	1.5E+00	AB039887.1	NT	Homo sapiens WDR4 gene for WD repeat protein, complete cds
8459	21428	34845	0.91	1.5E+00	BE887448.1	EST_HUMAN	601509586F1 NIH_MGC 71 Homo sapiens cDNA clone IMAGE:3911181 5'
8514	21482	34856	0.48	1.5E+00	AB040887.1	NT	Homo sapiens mRNA for KIAA1454 protein, partial cds
8991	21957	35382	1.08	1.5E+00	K02138.1	NT	Mouse germline IgM chain gene, mu-delta region
9370	22335		0.47	1.5E+00	AB038516.1	NT	Homo sapiens hGPIb alpha gene for platelet glycoprotein Ib alpha, complete cds
9489	22453	35893	0.55	1.5E+00	BF217818.1	EST_HUMAN	601882662F1 NIH_MGC 57 Homo sapiens cDNA clone IMAGE:4095135 5'
9838	22774	36229	0.91	1.5E+00	R81928.1	EST_HUMAN	y03h01.1f Soares placenta N2b4HR Homo sapiens cDNA clone IMAGE:147697 5'
9893	22920	36387	1.09	1.5E+00	AW375897.1	EST_HUMAN	QV3-CT0192-281099-008-d09 CT0192 Homo sapiens cDNA
10219	23144	36833	6.14	1.5E+00	BF376754.1	EST_HUMAN	RC0-TN0078-150900-034-g05 TN0078 Homo sapiens cDNA
10412	23334		1.42	1.5E+00	BF337944.1	EST_HUMAN	602035771F1 NCI_CGAP_Brm64 Homo sapiens cDNA clone IMAGE:4183865 5'
10556	23478	36972	2.92	1.5E+00	AA017689.1	EST_HUMAN	ze38g06.1f Soares retina N2b4HR Homo sapiens cDNA clone IMAGE:361306 5'
10556	23478	36973	2.92	1.5E+00	AA017689.1	EST_HUMAN	ze38g06.1f Soares retina N2b4HR Homo sapiens cDNA clone IMAGE:361306 5'
11727	24613	38190	5.98	1.5E+00	AL134197.1	EST_HUMAN	DKFZp547P243_s1 547 (synonym: hbr1) Homo sapiens cDNA clone DKFZp547P243 3'
11869	24751		6.39	1.5E+00	X07380.1	NT	Mus musculus mitochondrial rRNA-Sar gene and rRNA-Phe pseudogene
12112	24982	38583	1.53	1.5E+00	BE257552.1	EST_HUMAN	601109621F1 NIH_MGC 16 Homo sapiens cDNA clone IMAGE:3350477 5'

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
12362	25151		1.87	1.5E+00	8753287	NT	Mus musculus caspase 8 associated protein 2 (Casp8ap2), mRNA
12510	25899	31420	1.51	1.5E+00	D63480.1	NT	Human mRNA for KIAA0148 gene, partial cds
12723	25376		4.94	1.5E+00	AL445085.1	NT	Thermoplasma acidophilum complete genome; segment 3/5
12821	25443		1.33	1.5E+00	6978492	NT	Rattus norvegicus 5 - Lipoxigenase (Alox5), mRNA
32	13152	26052	1.41	1.4E+00	7561685	NT	Homo sapiens DKFZP586M0122 protein (DKFZP586M0122), mRNA
32	13152	26053	1.41	1.4E+00	7561685	NT	Homo sapiens DKFZP586M0122 protein (DKFZP586M0122), mRNA
2285	15298		0.9	1.4E+00	AF053357.1	NT	Helicobacter pylori glutamine synthetase (glnA) gene, complete cds
2341	15351		8.77	1.4E+00	U67922.1	NT	Ovis aries prion protein gene, complete cds
2877	15673	28693	1.83	1.4E+00	X74463.1	NT	Human papillomavirus type 7 genomic DNA
2784	15776	28794	2.75	1.4E+00	AF064584.2	NT	Fugu rubripes neurofibromatosis type 1 (NF1), A-kinase anchor protein (AKAP84), BAW protein (BAW), and WSB1 protein (WSB1) genes, complete cds
2784	15776	28795	2.75	1.4E+00	AF064584.2	NT	Fugu rubripes neurofibromatosis type 1 (NF1), A-kinase anchor protein (AKAP84), BAW protein (BAW), and WSB1 protein (WSB1) genes, complete cds
3345	16396		0.63	1.4E+00	5453733	NT	WSB1 protein (WSB1) genes, complete cds
4284	17313	30191	1.38	1.4E+00	AW900455.1	EST_HUMAN	Homo sapiens Mad4 homolog (MAD4) mRNA
4284	17313	30192	1.38	1.4E+00	AW900455.1	EST_HUMAN	CMV-NN1005-140300-286-106 NN1005 Homo sapiens cDNA
4590	16144	29056	0.92	1.4E+00	AE002324.2	NT	CMV-NN1005-140300-286-106 NN1005 Homo sapiens cDNA
4590	16144	29057	0.92	1.4E+00	AE002324.2	NT	Chlamydia muridarum, section 55 of 85 of the complete genome
4615	17636		1.71	1.4E+00	BF691547.1	EST_HUMAN	Chlamydia muridarum, section 55 of 85 of the complete genome
5446	18548	31461	1.58	1.4E+00	AW054978.1	EST_HUMAN	602156687F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4297556 5'
5606	18702		5.52	1.4E+00	AB032983.1	NT	wt45g07.x1 NCL_CGAP_Pan1 Homo sapiens cDNA clone IMAGE:2510460 3'
6410	19478	32725	3.06	1.4E+00	Q13472	SWISSPROT	Homo sapiens mRNA for KIAA1157 protein, partial cds
6427	25996		4.2	1.4E+00	AB020712.1	NT	DNA TOPOISOMERASE III ALPHA
6552	19613	32875	2.65	1.4E+00	Q92777	SWISSPROT	Homo sapiens mRNA for KIAA0905 protein, complete cds
6552	19613	32876	2.65	1.4E+00	Q92777	SWISSPROT	SYNAPSIN II
6781	19836	33119	0.56	1.4E+00	BE007870.1	EST_HUMAN	SYNAPSIN II
6781	19836	33120	0.56	1.4E+00	BE007870.1	EST_HUMAN	QV0-BN0148-050500-215-511 BN0148 Homo sapiens cDNA
6996	20122	33436	0.86	1.4E+00	AW893057.1	EST_HUMAN	QV0-BN0148-050500-215-511 BN0148 Homo sapiens cDNA
7503	20468	33829	2.02	1.4E+00	AJ133269.1	NT	QV0-BN0148-050500-215-511 BN0148 Homo sapiens cDNA
7521	20486	33848	1.15	1.4E+00	AW467760.1	EST_HUMAN	QV0-BN0148-050500-215-511 BN0148 Homo sapiens cDNA
7682	20544	33904	0.58	1.4E+00	P55288	SWISSPROT	QV0-BN0148-050500-215-511 BN0148 Homo sapiens cDNA
7582	20544	33905	0.58	1.4E+00	P55288	SWISSPROT	QV0-BN0148-050500-215-511 BN0148 Homo sapiens cDNA
							CMV-NN0006-300300-132-612 NN0006 Homo sapiens cDNA
							Homo sapiens caveolin-1/2 locus, Contig1, D7S622, genes CAV2 (exons 1, 2a, and 2b), CAV1 (exons 1 and 2)
							he23f05.x1 NCL_CGAP_QML1 Homo sapiens cDNA clone IMAGE:2919873 3' similar to contains Alu repetitive element;
							LAMININ BETA-2 CHAIN PRECURSOR (S-LAMININ)
							LAMININ BETA-2 CHAIN PRECURSOR (S-LAMININ)

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Table 4
Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7611	20571	33935	0.66	1.4E+00	Q80905	SWISSPROT	MINOR CAPSID PROTEIN L2
8678	21646		0.6	1.4E+00	P07893	SWISSPROT	GLUCOAMYLASE PRECURSOR (GLUCAN 1,4-ALPHA-GLUCOSIDASE) (1,4-ALPHA-D-GLUCAN GLUCOHYDROLASE)
9148	22112		4.6	1.4E+00	AJ271735.1	NT	Homo sapiens Xq pseudautosomal region; segment 1/2
9449	22413	35849	1.56	1.4E+00	R20459.1	EST_HUMAN	Y933712.1 Soares infant brain T1N1B Homo sapiens cDNA clone IMAGE:34345 5'
9552	22514	35965	3.46	1.4E+00	BE084687.1	EST_HUMAN	RC1-BT0313-301299-012-05 BT0313 Homo sapiens cDNA
9587	22649	36000	0.45	1.4E+00	AF134844.1	NT	Sceloporus undulatus ornithine transcarbamylase (OTC) mRNA, complete cds
10568	23490	36982	0.89	1.4E+00	BF575545.1	EST_HUMAN	602133135F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4288137 5'
10613	23535	37032	0.69	1.4E+00	BE145374.1	EST_HUMAN	IL5-HT0198-291099-008-C04 HT0198 Homo sapiens cDNA
10613	23535	37033	0.69	1.4E+00	BE145374.1	EST_HUMAN	IL5-HT0198-291099-008-C04 HT0198 Homo sapiens cDNA
10892	23812	37319	0.92	1.4E+00	D63441.1	NT	Pandorina colemaniae chloroplast rbcL gene for ribulose biphosphate carboxylase, partial cds
10892	23812	37320	0.92	1.4E+00	D63441.1	NT	Pandorina colemaniae chloroplast rbcL gene for ribulose biphosphate carboxylase, partial cds
11559	24498	38055	4.43	1.4E+00	AB006882.1	NT	Homo sapiens APECED mRNA for AIRE-1, complete cds
11733	24619	38196	2.83	1.4E+00	BE962107.2	EST_HUMAN	601655184R1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3845805 3'
11733	24619	38197	2.83	1.4E+00	BE962107.2	EST_HUMAN	601655184R1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3845805 3'
11756	24684	38263	2.15	1.4E+00	U30790.1	NT	Pneumocystis carinii f. sp. ratti guanine nucleotide binding protein alpha subunit (pcg1) gene, complete cds
11756	24684	38264	2.15	1.4E+00	U30790.1	NT	Pneumocystis carinii f. sp. ratti guanine nucleotide binding protein alpha subunit (pcg1) gene, complete cds
12360	25827		1.7	1.4E+00	AL161500.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 12
13068	25602		1.4	1.4E+00	7657624	NT	Homo sapiens staufen (Drosophila, RNA-binding protein) homolog 2 (STAU2), mRNA
572	13641		1.56	1.3E+00	Z73640.1	NT	M.mucedo gene encoding 4-Dihydroxyethyl-trisporate dehydrogenase
903	13958	26915	3.12	1.3E+00	AJ271192.1	NT	Cantharellus sp. partial 25S rRNA gene, isolate Tibet
1131	14174		32.4	1.3E+00	Y19213.1	NT	Homo sapiens putative psinHbA pseudogene for hair keratin, exons 2 to 7
1300	14336	27299	19.22	1.3E+00	4507998	NT	Homo sapiens zinc finger protein 157 (HZF22) (ZNF157) mRNA
1300	14336	27300	19.22	1.3E+00	4507998	NT	Homo sapiens zinc finger protein 157 (HZF22) (ZNF157) mRNA
1358	14393		0.99	1.3E+00	U61730.2	NT	Cox lacryma-jobi dihydrodipicolinate synthase (dcpA) gene, complete cds
1614	14646		2.59	1.3E+00	AE002338.2	NT	Chlamydia muridarum, section 66 of 85 of the complete genome
2255	15289		1.22	1.3E+00	AB030447.1	NT	Cyprinus carpio MRPb and MASPb genes for mannose-binding lectin-associated serine protease (MASP)
2416	15422	28445	1.03	1.3E+00	P25391	SWISSPROT	and MASP-related protein, complete cds
2557	15559		2.6	1.3E+00	BE966735.2	EST_HUMAN	LAMININ ALPHA-1 CHAIN PRECURSOR (LAMININ A CHAIN)
2950	16007	28931	0.67	1.3E+00	6755621	NT	601661233R1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3916945 3'
							Mus musculus alpha-spectrin 1, erythroid (Spn1), mRNA

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Table 4
Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3611	16656	29574	1.02	1.3E+00	AF016494.1	NT	Fugu rubripes gamma-aminobutyric acid receptor beta subunit gene, partial cds; 55kd erythrocyte membrane protein (P55), synaptic vesicle-associated integral membrane protein (VAMP-1), procollagen C-proteinase enhancer protein (PCOLCE) genes, complete c>
5284	18290	31152	0.9	1.3E+00	AJ390500.1	NT	Candida albicans partial mRNA for ribonucleotide reductase large subunit (mr1 gene)
5592	18688	31657	1.08	1.3E+00	P19732	SWISSPROT	PHENOL HYDROXYLASE P3 PROTEIN (PHENOL 2-MONOXYGENASE P3 COMPONENT)
5794	18886	32087	0.52	1.3E+00	M27138.1	NT	Human estradiol 17 beta-dehydrogenase gene, complete cds
6063	19144	32355	0.54	1.3E+00	BF663825.1	EST_HUMAN	PMO-CT0289-291199-004-f08 CT0289 Homo sapiens cDNA
6134	19211	32437	8.25	1.3E+00	AW362834.1	EST_HUMAN	PMO-CT0289-291199-004-f08 CT0289 Homo sapiens cDNA
6134	19211	32438	8.25	1.3E+00	AW362834.1	EST_HUMAN	D melanogaster no-on-transient A gene product, complete cds
6557	19617	32882	1.14	1.3E+00	M33496.1	NT	HYPOTHEITICAL GENE 64 PROTEIN
6914	19966		0.69	1.3E+00	Q00155	SWISSPROT	SPORE GERMINATION PROTEIN KB
6956	20181		0.54	1.3E+00	P49840	SWISSPROT	Homo sapiens fibronectin receptor alpha-subunit precursor (ITGA5) mRNA, partial cds
7014	20140	33457	0.81	1.3E+00	M13918.2	NT	IL-2-ST0311-020200-040-G12 ST0311 Homo sapiens cDNA
7124	25673	33363	0.52	1.3E+00	AW821580.1	EST_HUMAN	601061420F1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3447965 5'
7141	20117	33430	1.04	1.3E+00	BE638819.1	EST_HUMAN	TCBAP1D0959 Pediatric pre-B cell acute lymphoblastic leukemia Baylor-HGSC project=TCBA Homo sapiens cDNA clone TCBAP0959
7307	20278	33616	0.8	1.3E+00	BE243571.1	EST_HUMAN	ACYLPHOSPHATASE, ORGAN-COMMON TYPE ISOZYMES A AND B (ACYLPHOSPHATE PHOSPHOHYDROLASE)
7691	20649	34013	0.72	1.3E+00	P24540	SWISSPROT	Sus scrofa plp gene
8641	21609	35032	1.09	1.3E+00	AJ009912.1	NT	601657145R1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:3866195 3'
8790	21757	35179	2.29	1.3E+00	BE963379.2	EST_HUMAN	601680250R2 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:3950532 3'
8907	21873	35299	0.87	1.3E+00	BE974280.1	EST_HUMAN	Homo sapiens GL004 protein (GL004), mRNA
9059	22025		1.68	1.3E+00	9910247	NT	601657145R1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:3866195 3'
9142	22108	35534	0.92	1.3E+00	AJ927629.1	EST_HUMAN	Homo sapiens heparan glucosaminyl N-deacetylase/sulfotransferase-2 gene, complete cds
9873	22826		4.86	1.3E+00	AF042084.1	NT	S. alba phi-1 mRNA for photolase
9882	22835	36288	2.2	1.3E+00	X72019.1	NT	S. alba phi-1 mRNA for photolase
9882	22835	36289	2.2	1.3E+00	X72019.1	NT	Homo sapiens lipoxigenase (ALOX12B) mRNA, complete cds
9882	22909	36374	1.02	1.3E+00	AF059250.1	NT	LYSOSOMAL ALPHA-MANNOSIDASE PRECURSOR (MANNOSIDASE, ALPHA B) (LYSOSOMAL ACID ALPHA-MANNOSIDASE) (LAMN)
10029	22956	36424	1.57	1.3E+00	Q00754	SWISSPROT	601657145R1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:3866195 3'
10108	23034	36511	1.32	1.3E+00	AJ927629.1	EST_HUMAN	Lactococcus lactis cremoris NCDO-invt1 chromosomal inversion junction DNA
10185	23110	36593	0.83	1.3E+00	AJ223962.1	NT	Lactococcus lactis cremoris NCDO-invt1 chromosomal inversion junction DNA
10185	23110	36594	0.83	1.3E+00	AJ223962.1	NT	Lactococcus lactis cremoris NCDO-invt1 chromosomal inversion junction DNA
10225	23150	36639	3.75	1.3E+00	BE963379.2	EST_HUMAN	601657145R1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:3866195 3'

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Table 4
Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10286	23211		0.64	1.3E+00	AI559944.1	EST_HUMAN	tg77a12.x1 NCI_CGAP_UH Homo sapiens cDNA clone IMAGE:2214814 3' similar to gb:U14723
10509	23431	36927	0.45	1.3E+00	AF061251.1	NT	GLUSTERIN PRECURSOR (HUMAN); Eschericia coli serotype O157:H7 O antigen gene cluster
10509	23431	36928	0.45	1.3E+00	AF061251.1	NT	Eschericia coli serotype O157:H7 O antigen gene cluster
10574	23496	36989	1.24	1.3E+00	AE004392.1	NT	Vibrio cholerae chromosome II, section 48 of 93 of the complete chromosome
10591	23513	37006	1.53	1.3E+00	MP29933.1	NT	Campylobacter jejuni kanamycin phosphotransferase (aphA-7) gene, complete cds
10948	23668		0.85	1.3E+00	AL163302.2	NT	Homo sapiens chromosome 21 segment HS21C102
10975	23895	37409	0.49	1.3E+00	AI950846.1	EST_HUMAN	ws32e10.x1 NCI_CGAP_G06 Homo sapiens cDNA clone IMAGE:2498922 3' similar to SW:TRXB_HUMAN
10987	23907		0.43	1.3E+00	8923637	NT	Q16881 THIOREDOXIN REDUCTASE ;
11052	24015		3.63	1.3E+00	Q14117	SWISSPROT	Homo sapiens hypothetical protein FLJ20707 (FLJ20707), mRNA
11252	24205	37727	2.35	1.3E+00	P25299	SWISSPROT	DIHYDROPYRIMIDINASE (DHPASE) (HYDANTOINASE) (DHP)
11273	24225	37751	1.71	1.3E+00	Z18892.2	NT	MRNA 3'-END PROCESSING PROTEIN RNA15
11867	24749	38331	2.61	1.3E+00	D42042.1	NT	Mus musculus desmin gene
11945	24825	38420	2.1	1.3E+00	Z88882.1	NT	Human mRNA for KIAA0085 gene, partial cds
12001	24878		1.55	1.3E+00	L31891.1	NT	Bacillus subtilis genomic DNA 23.9kB fragment
12498	25239		3.37	1.3E+00	AF187873.1	NT	Arabidopsis thaliana 3-ketoacyl-acyl carrier protein synthase III (KAS III) mRNA, complete cds
12669	25344	31762	6.47	1.3E+00	BF348043.1	EST_HUMAN	Cavia porcellus inwardly-rectifying potassium channel Kir2.2 (KCNJ12) gene, complete cds
12679	25724		3.24	1.3E+00	P33464	SWISSPROT	602023185F1 NCI_CGAP_Bin67 Homo sapiens cDNA clone IMAGE:4158452 5'
12785	25407		1.88	1.3E+00	AF187035.1	NT	E1 GLYCOPROTEIN PRECURSOR (MATRIX GLYCOPROTEIN) (MEMBRANE GLYCOPROTEIN)
651	13717	26639	13.29	1.2E+00	AA676246.1	EST_HUMAN	Stumira lillum cytochrome b gene, complete cds; mitochondrial gene for mitochondrial product
824	13882	26833	1.37	1.2E+00	P05228	SWISSPROT	z122d08.s1 Soares_fetal_liver_spleen_TNFSF_S1 Homo sapiens cDNA clone IMAGE:431535 3'
824	13882	26834	1.37	1.2E+00	P05228	SWISSPROT	HISTIDINE-RICH PROTEIN PRECURSOR (CLONE PFHRP-III)
824	13882	26835	1.37	1.2E+00	P05228	SWISSPROT	HISTIDINE-RICH PROTEIN PRECURSOR (CLONE PFHRP-III)
879	13934		0.95	1.2E+00	8924234	NT	HISTIDINE-RICH PROTEIN PRECURSOR (CLONE PFHRP-III)
1165	14206	27160	7.4	1.2E+00	AF080245.2	NT	HISTIDINE-RICH PROTEIN PRECURSOR (CLONE PFHRP-III)
1210	14248	27206	1.43	1.2E+00	AJ252242.1	NT	Elaeis oleifera sesquiterpene synthase mRNA, complete cds
1210	14248	27207	1.43	1.2E+00	AJ252242.1	NT	pea seed-borne mosaic virus complete genome
2025	15045	28058	1.08	1.2E+00	AF140631.1	NT	pea seed-borne mosaic virus complete genome
3127	16154	29033	0.99	1.2E+00	AB020681.1	NT	Homo sapiens G-protein coupled receptor 14 (GPR14) gene, complete cds
3179	16234	29151	6.14	1.2E+00	AL161563.2	NT	Homo sapiens mRNA for KIAA0874 protein, partial cds
3179	16234	29152	6.14	1.2E+00	AL161563.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 63
3299	16352		3.07	1.2E+00	P64910	SWISSPROT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 63
3367	16417	28343	0.78	1.2E+00	AF188740.1	NT	CONJUGAL TRANSFER PROTEIN TRBE PRECURSOR
							Homo sapiens LHX3 gene, intron 2

Table 4

Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3725	16767	29678	8.48	1.2E+00	U75602.1	NT	Mus musculus subtilisin-like serine protease LPC (PC7) gene, exons 1 to 9, partial cds
4012	17051	29957	1.76	1.2E+00	BF373570.1	EST_HUMAN	MR0-FT0175-050900-203-g06_1 FT0175 Homo sapiens cDNA
4327	16417	29343	1.09	1.2E+00	AF188740.1	NT	Homo sapiens LHX3 gene, intron 2
4498	17523	30464	2.12	1.2E+00	M87060.1	NT	Rattus rattus cardiac AE3 gene, exons 1-23
4551	17574	30464	1.33	1.2E+00	AL161509.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 21
4592	17613	30507	2.1	1.2E+00	AF156495.1	NT	Homo sapiens post-synaptic density 95 (DLG4) gene, complete cds
4618	17640		6.6	1.2E+00	Y09200.1	NT	T. pinnae chloroplast rbcL gene, partial
5052	18064	30942	2.36	1.2E+00	P06228	SWISSPROT	HISTIDINE-RICH PROTEIN PRECURSOR (CLONE PFHRP-III)
5052	18064	30943	2.36	1.2E+00	P06228	SWISSPROT	HISTIDINE-RICH PROTEIN PRECURSOR (CLONE PFHRP-III)
5052	18064	30944	2.36	1.2E+00	P06228	SWISSPROT	HISTIDINE-RICH PROTEIN PRECURSOR (CLONE PFHRP-III)
5612	18612	31544	1.06	1.2E+00	U20760.1	NT	Human extracellular calcium-sensing receptor mRNA, complete cds
5634	18730	31892	1.89	1.2E+00	AW813276.1	EST_HUMAN	MR3-ST0191-140200-013-c05 ST0191 Homo sapiens cDNA
5894	18882		0.57	1.2E+00	X81876.1	NT	Calicivirus cDNA for orf1, orf2 and orf3
5974	19059	32260	0.78	1.2E+00	AF016052.1	NT	Homo sapiens zinc finger protein ZNF191 (ZNF191) gene, complete cds
6275	19348	32580	2.39	1.2E+00	X74885.1	NT	D. hydei ey1 repeat cluster DNA, fragment D
6338	19407	32648	4.12	1.2E+00	BE003113.1	EST_HUMAN	QV4-BN0090-270400-190-a03 BN0090 Homo sapiens cDNA
6423	19490	32741	1.41	1.2E+00	X89084.1	NT	C. glutamicum pla gene and ackA gene
6423	19490	32742	1.41	1.2E+00	X89084.1	NT	C. glutamicum pla gene and ackA gene
6467	19532	32780	38.6	1.2E+00	AA759254.1	EST_HUMAN	ah84g12.s1 Scores_testis_NHT Homo sapiens cDNA clone 1322374 3'
6575	19635	32901					y93b12.s1 Scores_melanocyte 2NblHM Homo sapiens cDNA clone IMAGE:273599 3' similar to gb J87935 HUMAAU472 Human carcinoma cell-derived Alu RNA transcript (rRNA); gb J04970
6650	19708	32984	0.6	1.2E+00	N33295.1	EST_HUMAN	CARBOXYPEPTIDASE M PRECURSOR (HUMAN);
6654	19711	32988	0.71	1.2E+00	P17671	SWISSPROT	ECODYSONE-INDUCIBLE PROTEIN E75-A
7100	20034	33337	2.01	1.2E+00	AW813276.1	EST_HUMAN	MR3-ST0191-140200-013-c05 ST0191 Homo sapiens cDNA
7113	20047	33349	1.17	1.2E+00	AB026010.1	NT	Homo sapiens mRNA for KIAA1087 protein, partial cds
7113	20047	33349	2.68	1.2E+00	AJ002141.1	NT	Mus musculus DSPP gene
7465	20431		0.64	1.2E+00	AJ271735.1	NT	Homo sapiens Xq pseudautosomal region, segment 1/2
7610	20685	33934	1.64	1.2E+00	AV734585.1	EST_HUMAN	AV734585 cda Homo sapiens cDNA clone cdaAF103 5'
7912	20655	34243	2.6	1.2E+00	X74207.1	NT	L. lactis pyd and pyf genes
8122	21059	34457	0.63	1.2E+00	BE787846.1	EST_HUMAN	601481781F1 NIH_MGC_88 Homo sapiens cDNA clone IMAGE:3884270 5'
8915	21881	35307	3.24	1.2E+00	AB033030.1	NT	Homo sapiens mRNA for KIAA1204 protein, partial cds
9010	21976	35396	0.65	1.2E+00	P38427	SWISSPROT	ALPHA, ALPHA-TREHALOSE-PHOSPHATE SYNTHASE [UDP-FORMING] 123 KD SUBUNIT (TREHALOSE-6-PHOSPHATE SYNTHASE) (UDP-GLUCOSE-GLUCOSEPHOSPHATE GLUCOSYLTRANSFERASE)

Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9228	22194		0.58	1.2E+00	7706271	NT	Homo sapiens CGI-30 protein (LOC51611), mRNA
9380	22345	35777	1.88	1.2E+00	AW377210.1	EST_HUMAN	MR2-CT0222-201099-001-e07 CT0222 Homo sapiens cDNA
9584	22556	36006	0.47	1.2E+00	H48599.1	EST_HUMAN	yt80a06.r1 Soares fetal liver spleen 1NFSL Homo sapiens cDNA clone IMAGE:202066 5'
9763	22694	36150	3.63	1.2E+00	Z32850.1	NT	R.communis gene for pyrophosphate-dependent phosphofructokinase beta subunit
9864	22891	36353	1.71	1.2E+00	D11745.1	EST_HUMAN	HUMHMO1A01 Liver HepG2 cell line. Homo sapiens cDNA clone hm01a01
10281	23216	36700	3.52	1.2E+00	X56832.1	NT	H.sapiens ENO3 gene for muscle specific endase
10689	23611		0.73	1.2E+00	AB009666.1	NT	Homo sapiens klotho gene, exon 1
11674	24840	38219	1.89	1.2E+00	AW817817.1	EST_HUMAN	PMO-ST0264-161199-001-d01 ST0264 Homo sapiens cDNA
11713	24876		7.68	1.2E+00	BE160761.1	EST_HUMAN	PM1-HT0422-160200-007-g10 HT0422 Homo sapiens cDNA
11785	23940	37462	2.69	1.2E+00	U50147.1	NT	Rattus norvegicus synapse-associated protein 102 mRNA, complete cds
12466	25799	31524	18.09	1.2E+00	AL163203.2	NT	Homo sapiens chromosome 21 segment HS21C003
12487	25232		2.7	1.2E+00	AP001515.1	NT	Bacillus halodurans genomic DNA, section 9/14
464	13537	26463	1.43	1.1E+00	D88980.1	NT	Human mRNA for KIAA0227 gene, partial cds
1771	14806	27792	1.97	1.1E+00	AW955393.1	EST_HUMAN	QVO-BN0042-170300-163-g12 BN0042 Homo sapiens cDNA
1915	14939	27935	1.08	1.1E+00	AW575889.1	EST_HUMAN	U1HF-BR0p-ajk-f-02-Q-U1.st NIH_MGC_52 Homo sapiens cDNA clone IMAGE:3074834 3'
3341	16392	29313	7.34	1.1E+00	AL163213.2	NT	Homo sapiens chromosome 21 segment HS21C013
3341	16392	29314	7.34	1.1E+00	AL163213.2	NT	Homo sapiens chromosome 21 segment HS21C013
3498	16545	29471	0.79	1.1E+00	8922641	NT	Homo sapiens hypothetical protein FLJ10749 (FLJ10749), mRNA
							wf54h11.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2359461 3' similar to
3593	16638	29558	3.34	1.1E+00	AI808360.1	EST_HUMAN	SW-P531_HUMAN Q12888 P53-BINDING PROTEIN 53BP1 ;
3731	16773	29684	1.52	1.1E+00	AE003886.1	NT	Xylella fastidiosa, section 32 of 229 of the complete genome
3731	16773	29685	1.52	1.1E+00	AE003886.1	NT	Xylella fastidiosa, section 32 of 229 of the complete genome
3831	16871		0.86	1.1E+00	X85374.1	NT	H. parahaemolyticus hphIM(A), hphIM(C), hphIR and menB genes
3964	17004	29918	0.87	1.1E+00	8922641	NT	Homo sapiens hypothetical protein FLJ10749 (FLJ10749), mRNA
4050	17087	29983	1.02	1.1E+00	6755205	NT	Mus musculus proteasome (prosome, macropain) subunit, beta type 7 (Psmb7), mRNA
4243	17272		6.78	1.1E+00	5836331	NT	R.unicornis complete mitochondrial genome
5028	18042	30925	3.15	1.1E+00	U18466.1	NT	African swine fever virus, complete genome
5085	18095	30971	3.91	1.1E+00	U34740.1	NT	Emmericella nidulans sterigmatocystin biosynthetic gene cluster: (stcA), (stcB), (stcC), (stcE), (stcF), (stcI), (stcJ), (stcK), (stcL), (stcO), (stcQ), (stcS), (stcT), (stcU), (stcV) and (stcW) genes, complete cds
5109	18119	30993	1.04	1.1E+00	X78425.1	NT	E.faecalis pbp5 gene
5269	18276	31139	0.9	1.1E+00	6690080	NT	Homo sapiens putative GR6 protein (GR6), mRNA
5380	18484	31359	1.53	1.1E+00	6978530	NT	Rattus norvegicus Aquaporin 4 (Aqp4), mRNA
5695	18780	31981	13.39	1.1E+00	BE960184.1	EST_HUMAN	601652776R1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:3825835 3'

Table 4

Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5715	18809	31987	0.99	1.1E+00	AI138582.1	EST_HUMAN	q65c03.x1 Scores_NHT Homo sapiens cDNA clone IMAGE:1738260 3'
6211	19285	32517	1.93	1.1E+00	11419739	NT	Homo sapiens solute carrier family 6 (neurotransmitter transporter), member 14 (SLC6A14), mRNA
6405	19473	32721	0.94	1.1E+00	AF197861.1	NT	Macgregoria pulchra cytochrome b gene, complete cds; mitochondrial gene for mitochondrial product
6547	19808	32870	0.83	1.1E+00	R06037.1	EST_HUMAN	ye89d03.r1 Scores fetal liver spleen 1NLS Homo sapiens cDNA clone IMAGE:124924 5'
6876	19929	33226	1.21	1.1E+00	AJ404004.1	NT	Mus musculus mRNA for ER protein 58 (EP58 gene)
7468	20434		0.68	1.1E+00	AF101091.1	NT	Homo sapiens collagen type XI alpha-1 (COL11A1) gene, exons 25 through 28
7514	20479	33840	0.82	1.1E+00	X55981.1	NT	Maize mRNA for endase (2-phospho-D-glycerate hydrolase)
7732	20887	34050	1.83	1.1E+00	Z72338.1	NT	Herpes simplex virus type 1 (strain KOS) UL41 gene
7732	20887	34051	1.83	1.1E+00	Z72338.1	NT	Herpes simplex virus type 1 (strain KOS) UL41 gene
7754	20707	34076	8.13	1.1E+00	AL161888.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 84
7833	25691	34158	0.94	1.1E+00	11967960	NT	Mus musculus silent mating type Information regulation 2, (S.cerevisiae, homolog)-like (Sir2), mRNA
8470	21439	34857	2.95	1.1E+00	BF693996.1	EST_HUMAN	602082582F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4246828 5'
8563	21531	34951	0.73	1.1E+00	AI478339.1	EST_HUMAN	tm39h11.x1 NCJ_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2160549 3'
9089	22056	35479	0.63	1.1E+00	AB003088.1	NT	Acetabularia caliculus mitochondrial COX-like gene
9167	22133	35559	1.42	1.1E+00	S80750.1	NT	VH=anti-cytomegalovirus glycoprotein B antibody 4D4 heavy chain variable region [human, mRNA, Partial, 375 nt]
9278	22244	35673	0.45	1.1E+00	AJ079946.1	EST_HUMAN	cc34f05.x1 Scores_NHIMPu_S1 Homo sapiens cDNA clone IMAGE:1677249 3'
9792	21115		0.64	1.1E+00	BE394876.1	EST_HUMAN	601276278F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3617418 5'
9886	22913	36378	0.95	1.1E+00	AJ245772.1	NT	Mus musculus mRNA for stretch responsive muscle (X-chromosome) protein (Srmx gene)
10040	22867		0.69	1.1E+00	Y12227.1	NT	Arabidopsis thaliana DNA, 24 kb surrounding PFL locus
10130	23056	36534	0.95	1.1E+00	L76301.1	NT	Yersinia pseudotuberculosis psaeF, psaeF, adhesin (psaA), chaperone (psaB), and usher (psaC) genes, complete cds
10192	23117	36601	1.38	1.1E+00	AB020151.1	NT	Homo sapiens mRNA for KIAA0934 protein, partial cds
10297	23222	36706	5.65	1.1E+00	AL161515.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 27
10387	23281	36757	20.52	1.1E+00	6754021	NT	Mus musculus guanine nucleotide binding protein (G protein), gamma 3 subunit (Gng3), mRNA
10867	23787	37287	1.09	1.1E+00	P73769	SWISSPROT	DNA MISMATCH REPAIR PROTEIN MUTS
10989	23909	37422	0.63	1.1E+00	BF343844.1	EST_HUMAN	602014488F1 NCJ_CGAP_Bm64 Homo sapiens cDNA clone IMAGE:4150508 5'
10989	23909	37423	0.63	1.1E+00	BF343844.1	EST_HUMAN	602014489F1 NCJ_CGAP_Bm64 Homo sapiens cDNA clone IMAGE:4150508 5'
11012	23977	37502	2.03	1.1E+00	11067364	NT	Homo sapiens KIAA0626 gene product (KIAA0626), mRNA
11084	24027		3.83	1.1E+00	AF068942.1	NT	Klebsiella fluitans cytochrome c oxidase subunit 2 (cox2) gene, mitochondrial gene encoding mitochondrial protein, partial cds

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Table 4
Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
11435	18340		4.65	1.1E+00	8922973	NT	Homo sapiens hypothetical protein FLJ11280 (FLJ11280), mRNA
11439	24382	37921	3.12	1.1E+00	AF012862.1	NT	Petroselinum crispum cytosolic glucose-6-phosphate dehydrogenase 1 (cG6PDH1) mRNA, complete cds
11439	24382	37922	3.12	1.1E+00	AF012862.1	NT	Petroselinum crispum cytosolic glucose-6-phosphate dehydrogenase 1 (cG6PDH1) mRNA, complete cds
11883	24649	38227	3.44	1.1E+00	AB009698.1	EST_HUMAN	wf76e11.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2361548 3'
12439	25202	31807	3.12	1.1E+00	P07886	SWISSPROT	LOW TEMPERATURE ESSENTIAL PROTEIN
12539	25263	31807	1.55	1.1E+00	AF216696.1	NT	Taenia solium immunogenic protein Ts76 mRNA, partial cds
12661	25796		2.26	1.1E+00	AF234189.1	NT	Dicystidium discoidale isopentenyl pyrophosphate isomerase (DipI) mRNA, complete cds
99	13215		1.55	1.0E+00	U23808.1	NT	Xenopus laevis rhodopsin gene, complete cds
113	13224	26148	1.66	1.0E+00	D88425.1	NT	Cavia cobaya mRNA for serine/threonine kinase, complete cds
418	13491		3.03	1.0E+00	AB021684.1	NT	Marchantia polymorpha genes for 26S rRNA, 5S rRNA, 18S rRNA, 5.8S rRNA and 26S rRNA
578	13647	26580	2.22	1.0E+00	AJ251680.1	NT	Giardia tigrina mRNA for homeodomain transcription factor (so gene)
678	13741	26668	6.74	1.0E+00	AL163218.2	NT	Homo sapiens chromosome 21 segment HS21C018
679	13742		1.35	1.0E+00	AF125984.1	NT	Aedes aegypti mucin-like protein MUC7 mRNA, complete cds
1386	15866		3.53	1.0E+00	X80416.1	NT	V. carteri Algal-CAM mRNA
1771	14800	27786	0.97	1.0E+00	AB006531.1	NT	Plautia stali intestine virus RNA for nonstructural polyprotein, capsid protein precursor, complete cds
2493	15496	28521	1.42	1.0E+00	P48355	SWISSPROT	DNA GYRASE SUBUNIT B
2493	15496	28522	1.42	1.0E+00	P48355	SWISSPROT	DNA GYRASE SUBUNIT B
2887	15946	28861	4.42	1.0E+00	P24008	SWISSPROT	3-OXO-5-ALPHA-STEROID 4-DEHYDROGENASE 1 (STEROID 5-ALPHA-REDUCTASE 1) (SR TYPE 1)
2887	15946	28862	4.42	1.0E+00	P24008	SWISSPROT	3-OXO-5-ALPHA-STEROID 4-DEHYDROGENASE 1 (STEROID 5-ALPHA-REDUCTASE 1) (SR TYPE 1)
2978	16036		0.81	1.0E+00	O14226	SWISSPROT	HYPOTHETICAL 67.8 KD PROTEIN C6F12.08C IN CHROMOSOME I
3212	16267	29190	1.08	1.0E+00	AA828453.1	EST_HUMAN	af26g08.s1 Soares_total_fetus_NB2HF8_gw Homo sapiens cDNA clone IMAGE:1032830 3' similar to
3613	13215		0.93	1.0E+00	U23808.1	NT	WP-C42D8.3 CE04204; contains element MER22 MER22 repetitive element;
3693	16736	29649	1.33	1.0E+00	AJ223816.1	NT	Xenopus laevis rhodopsin gene, complete cds
4097	17131	30024	1.18	1.0E+00	AF223391.1	NT	Agaricus bisporus mRNA for tyrosinase
4304	17333		0.73	1.0E+00	8922245	NT	Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced
4843	17860	30755	1.54	1.0E+00	AL163247.2	NT	Homo sapiens hypothetical protein FLJ10139 (FLJ10139), mRNA
5053	18065		0.9	1.0E+00	D10852.1	NT	Homo sapiens chromosome 21 segment HS21C047
							Rattus norvegicus mRNA for N-acetylglucosaminyltransferase III, complete cds

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5354	18459	31328	3.23	1.0E+00	Z97022.1	NT	Hordeum vulgare gene encoding cysteine proteinase
5949	19035	32228	5.05	1.0E+00	AF248054.1	NT	Bos taurus micromolar calcium activated neutral protease 1 (CAPN1) gene, exons 11-20, and partial cds
5949	19035	32229	5.05	1.0E+00	AF248054.1	NT	Bos taurus micromolar calcium activated neutral protease 1 (CAPN1) gene, exons 11-20, and partial cds
6087	19148	32360	1.44	1.0E+00	Z97341.2	NT	Arabidopsis thaliana DNA chromosome 4, ESSA FCA contig fragment No. 6
6236	19309	32541	4.52	1.0E+00	P04501	SWISSPROT	FIBER PROTEIN
6243	19316	32546	1.77	1.0E+00	AW452782.1	EST_HUMAN	UIH-B18-alk-d-09-0-UI.s1 NC1_CGAP_Sub5 Homo sapiens cDNA clone IMAGE:3088969 3'
6837	19695	32972	2.12	1.0E+00	U75902.1	NT	Mus musculus subtilisin-like serine protease LPC (PC7) gene, exons 1 to 9, partial cds
6891	19748	33025	0.68	1.0E+00	AF104669.1	NT	Homo sapiens cell cycle protein (PA2G4) gene, exons 2 through 5
6786	19841		0.98	1.0E+00	P46506	SWISSPROT	SRB-11 PROTEIN
6813	19867	33155	0.71	1.0E+00	BE797716.1	EST_HUMAN	601581891F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3936382 5'
6813	19867	33158	0.71	1.0E+00	BE797716.1	EST_HUMAN	601581891F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3936382 5'
6944	20168	33491	1.17	1.0E+00	Y11204.1	NT	V. carteri gene encoding Yolkapopsin
7033	18365	31252	0.64	1.0E+00	U63721.1	NT	Human elastin (ELN) gene, partial cds, and LIM-kinase (LIMK1) gene, complete cds
7345	20316	33661	1	1.0E+00	S52770.1	NT	Insulin-like growth factor-binding protein 4 [cattle, pulmonary artery endothelial cells, mRNA, 2028 nt]
7719	20876		8.7	1.0E+00	P20273	SWISSPROT	B-CELL RECEPTOR CD22 PRECURSOR (LEU-14) (B-LYMPHOCYTE CELL ADHESION MOLECULE)
7979	20918	34309	1.52	1.0E+00	AF102531.1	NT	Homo sapiens endothelin-converting enzyme 2 (ECE2) mRNA, complete cds
7997	20936	34330	6.07	1.0E+00	AA775191.1	EST_HUMAN	ac79b08.s1 Stratiene lung (#937210) Homo sapiens cDNA clone IMAGE:868791 3'
8165	21103		0.57	1.0E+00	BF679213.1	EST_HUMAN	602153782F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4294727 5'
8294	21263	34673	1.49	1.0E+00	BE868287.1	EST_HUMAN	601443950F1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3848005 5'
8294	21263	34674	1.49	1.0E+00	BE868287.1	EST_HUMAN	601443950F1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3848005 5'
8481	18065		1.22	1.0E+00	D10852.1	NT	Rattus norvegicus mRNA for N-acetylglucosaminyltransferase III, complete cds
8693	21661	35084	2.31	1.0E+00	Q02207	SWISSPROT	PEROXISOMAL HYDRATASE-DEHYDROGENASE-EPIMERASE (HDE) (MULTIFUNCTIONAL BETA-OXIDATION PROTEIN) (MFP) [INCLUDES: 2-ENOYL-COA HYDRATASE; D-3-HYDROXYACYL COA DEHYDROGENASE]
8693	21661	35085	2.31	1.0E+00	Q02207	SWISSPROT	PEROXISOMAL HYDRATASE-DEHYDROGENASE-EPIMERASE (HDE) (MULTIFUNCTIONAL BETA-OXIDATION PROTEIN) (MFP) [INCLUDES: 2-ENOYL-COA HYDRATASE; D-3-HYDROXYACYL COA DEHYDROGENASE]
8821	21788		0.83	1.0E+00	P51784	SWISSPROT	UBIQUITIN CARBOXYL-TERMINAL HYDROLASE 11 (UBIQUITIN THIOLESTERASE 11) (UBIQUITIN-SPECIFIC PROCESSING PROTEASE 11) (DEUBIQUITINATING ENZYME 11)

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8855	21822	35242	0.44	1.0E+00	Q9Y5T5	SWISSPROT	UBIQUITIN CARBOXYL-TERMINAL HYDROLASE 16 (UBIQUITIN THIOLESTERASE 16) (UBIQUITIN-SPECIFIC PROCESSING PROTEASE 16) (DEUBIQUITINATING ENZYME 16) (UBIQUITIN PROCESSING PROTEASE UBP-M)
8855	21822	35243	0.44	1.0E+00	Q9Y5T5	SWISSPROT	UBIQUITIN CARBOXYL-TERMINAL HYDROLASE 16 (UBIQUITIN THIOLESTERASE 16) (UBIQUITIN-SPECIFIC PROCESSING PROTEASE 16) (DEUBIQUITINATING ENZYME 16) (UBIQUITIN PROCESSING PROTEASE UBP-M)
8883	25696		2.37	1.0E+00	BE147331.1	EST_HUMAN	RC1-PT0229-181099-011-e08 HT0229 Homo sapiens cDNA
8923	21889	35316	0.89	1.0E+00	U42720.2	NT	Simian immunodeficiency virus Gag protein (gag) gene, complete cds; Pol protein (pol) gene, partial cds; and Vif protein (vif), Vpr protein (vpr), Tat protein (tat), Rev protein (rev), Vpu protein (vpu), Env protein (env), and Nef protein (nef) genes, >
9075	22041	35464	1.55	1.0E+00	M38427.1	NT	Human immunodeficiency virus type 1 (HIV-1), isolate SF33,
9826	22570	36019	2.14	1.0E+00	BE907592.1	EST_HUMAN	601497581F1 NIH_MGC_70 Homo sapiens cDNA clone IMAGE:3889421 5'
9836	22772	36227	1.25	1.0E+00	6753429	NT	Mus musculus chloride channel calcium activated 1 (Ciccat1), mRNA
9836	22772	36228	1.25	1.0E+00	6753429	NT	Mus musculus chloride channel calcium activated 1 (Ciccat1), mRNA
9869	22896	36359	1.94	1.0E+00	AV689554.1	EST_HUMAN	AV688554 GKGC Homo sapiens cDNA clone GKCCYA11 5'
9974	22901	36364	1.23	1.0E+00	U44952.1	NT	Xenopus laevis zona pellucida C glycoprotein precursor (MZPC) mRNA, complete cds
9974	22901	36365	1.23	1.0E+00	U44952.1	NT	Xenopus laevis zona pellucida C glycoprotein precursor (MZPC) mRNA, complete cds
10212	23137	36624	0.56	1.0E+00	X15498.1	NT	Human Coronavirus gene for membrane protein
10212	23137	36625	0.56	1.0E+00	X15498.1	NT	Human Coronavirus gene for membrane protein
10471	23383	36889	0.72	1.0E+00	X15498.1	NT	Human Coronavirus gene for membrane protein
10471	23383	36890	0.72	1.0E+00	X15498.1	NT	Human Coronavirus gene for membrane protein
10564	23488	36980	0.68	1.0E+00	A1077920.1	EST_HUMAN	Human sapiens MHC binding factor, beta (MHCBBF) mRNA
10564	23488	36980	0.68	1.0E+00	A1077920.1	EST_HUMAN	Human sapiens MHC binding factor, beta (MHCBBF) mRNA
10690	23612	37106	3.7	1.0E+00	AV758825.1	EST_HUMAN	oy15d07.s1 Soares_senescent_fibroblasts NBHSF Homo sapiens cDNA clone IMAGE:1665901 3'
10842	23762	37262	20.08	1.0E+00	AA004982.1	EST_HUMAN	AV758825 BM Homo sapiens cDNA clone BMFAW04 5'
10842	23762	37263	20.08	1.0E+00	AA004982.1	EST_HUMAN	AV758825 BM Homo sapiens cDNA clone BMFAW04 5'
10876	23796	37297	1.18	1.0E+00	L11910.1	NT	zh94a02.r1 Soares_fetal_liver_spleen_TNFRSF11B Homo sapiens cDNA clone IMAGE:428906 5'
12048	18489	31328	1.66	1.0E+00	Z97022.1	NT	zh94a02.r1 Soares_fetal_liver_spleen_TNFRSF11B Homo sapiens cDNA clone IMAGE:428906 5'
12327	25129		3.26	1.0E+00	P15306	SWISSPROT	Human retinoblastoma susceptibility gene exon 1-27, complete cds
12650	25333		2.48	1.0E+00	AW976184.1	EST_HUMAN	Hordeum vulgare gene encoding cysteine proteinase
1575	14608	27580	3.22	9.9E-01	AF245455.1	NT	THROMBOMODULIN PRECURSOR (FETOMODULIN) (TM)
1575	14608	27581	3.22	9.9E-01	AF245455.1	NT	EST388283 MAGE resequences, MAGE Homo sapiens cDNA
2645	15642	28666	1	9.9E-01	AL163302.2	NT	Drosophila melanogaster regulator of G-protein signalling LOCO III mRNA, complete cds
3619	16663		1.1	9.9E-01	AF174585.1	NT	Drosophila melanogaster regulator of G-protein signalling LOCO III mRNA, complete cds
5717	18811	31980	8.62	9.9E-01	P49657	SWISSPROT	Homo sapiens chromosome 21 segment HS21C102
							Apple mosaic virus RNA 2 putative polymerase gene, complete cds
							SERINE/THREONINE PROTEIN KINASE MINIBRAIN

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5969	19054	32254	0.79	9.8E-01	Q09632	SWISSPROT	PROBABLE OXIDOREDUCTASE ZK1290.5 IN CHROMOSOME II
9616	22560		1.4	9.8E-01	U69687.1	NT	Lycopodium esculentum putative Mit copy 1 nematode-resistance gene
8913	22734		3.02	9.8E-01	Q28642	SWISSPROT	B2 BRADYKININ RECEPTOR (BK-2 RECEPTOR)
11069	24032	37556	1.48	9.8E-01	AJ005029.1	NT	Danio rerio mRNA for Eph-like receptor tyrosine kinase rtk8
524	13595	26513	1.12	9.8E-01	P22567	SWISSPROT	AMINO-ACID ACETYLTRANSFERASE (N-ACETYLGLUTAMATE SYNTHASE) (AGS) (NAGS)
2305	15317		1.28	9.8E-01	AJ003108.1	NT	Callitrix jacchus UBE1 gene derived retroposon on the Y chromosome
2813	15805		1.29	9.8E-01	AF174844.1	NT	Xenopus laevis rac GTPase mRNA, complete cds
7406	20374	33725	4.12	9.8E-01	AJ302158.1	NT	Enterobacteriaceae sp. JM983 partial groES gene for GroES-like protein and partial groEL gene for GroEL-like protein, isolate JM983
7406	20374	33726	4.12	9.8E-01	AJ302158.1	NT	Enterobacteriaceae sp. JM983 partial groES gene for GroES-like protein and partial groEL gene for GroEL-like protein, isolate JM983
7907	20850	34236	0.99	9.8E-01	BF034016.1	EST_HUMAN	601456337F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3860049 5'
7907	20850	34237	0.99	9.8E-01	BF034016.1	EST_HUMAN	601456337F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3860049 5'
9069	22035	35458	0.88	9.8E-01	P38652	SWISSPROT	PHOSPHOGLUCOMUTASE (GLUCOSE PHOSPHOMUTASE) (PGM)
10804	23725		0.53	9.8E-01	AA825865.1	EST_HUMAN	cd55804.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1371847 3'
11339	24289	37813	2.06	9.8E-01	BE258705.1	EST_HUMAN	601110258F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3350750 5'
11339	24289	37814	2.06	9.8E-01	BE258705.1	EST_HUMAN	601110258F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3350750 5'
12545	25268		1.41	9.8E-01	U52111.2	NT	Homo sapiens X28 region near ALD locus containing dual specificity phosphatase 9 (DUSP9), ribosomal protein L18a (RPL18a), Ca2+/Calmodulin-dependent protein kinase I (CAMK1), creatine transporter (CRTR), CDM protein (CDM), adrenoleukodystrophy protein > and e, partial cds
7366	20336	33686	2.3	9.7E-01	U26716.1	NT	Drosophila melanogaster sodium channel protein (para) gene, exons 9,10,11,12 and optional segments b, c, d and e, partial cds
8948	21815	35235	1.81	9.7E-01	AF149112.1	NT	Triticum aestivum stripe rust resistance protein Yr10 (Yr10) gene, complete cds
8954	21821	35241	1.33	9.7E-01	M90544.1	NT	Salmonella typhimurium adenine-methyltransferase (moe) and restriction endonuclease (res)
11505	24447		3.87	9.7E-01	BF511209.1	EST_HUMAN	U1-H-B14-act-e-07-q-UJ.s1 NCI_CGAP_Sub8 Homo sapiens cDNA clone IMAGE:3085140 3'
12117	24987	38589	2.29	9.7E-01	U87514.1	NT	Dicotyledon discolorum CAR3 gene, promoter region
4486	17511	30399	1.68	9.6E-01	AW799874.1	EST_HUMAN	PM2-UM0053-240300-005-f12 UM0053 Homo sapiens cDNA
5179	18188	31065	0.9	9.6E-01	7682375	NT	Homo sapiens KIAA0914 gene product (KIAA0914), mRNA
5847	18937	32121	3.85	9.6E-01	Z70556.1	NT	Parvovirus B19 DNA, patient C, genome position 2448-2894
5847	18937	32122	3.85	9.6E-01	Z70556.1	NT	Parvovirus B19 DNA, patient C, genome position 2448-2894
6910	19962	33258	0.57	9.6E-01	Z97341.2	NT	Arabidopsis thaliana DNA chromosome 4, ESSA 1 FCA contig fragment No. 6
8735	21703		1.21	9.6E-01	X95275.1	NT	P. taicai parum complete gene map of plastid-like DNA (IR-A)
9203	22169	35599	0.51	9.6E-01	U81138.1	NT	Rattus norvegicus (strain R21) Rps2r gene, complete cds

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9446	22410	35847	0.44	9.6E-01	AF228843.1	NT	Mus musculus WNT-2 gene, partial cds; putative ankyrin-related protein and cystic fibrosis transmembrane conductance regulator (CFTR) genes, section 1 of 2 of the complete cds; and unknown gene
11848	24731	38317	3.04	9.6E-01	AV752605.1	EST_HUMAN	AV752605 NP2 Homo sapiens cDNA clone NPOBAG06 5'
11848	24731	38318	3.04	9.6E-01	AV752605.1	EST_HUMAN	AV752605 NP2 Homo sapiens cDNA clone NPOBAG06 5'
12223	25060		2.19	9.6E-01	11421722	NT	Homo sapiens centrosomal protein 2 (CEP2), mRNA
12839	25874	31416	3.03	9.6E-01	U91423.1	NT	Sphyrna tiburo NADH dehydrogenase subunit 2 (NADH2) gene, mitochondrial gene encoding mitochondrial protein, partial cds
2484	15488	28512	1.03	9.5E-01	7705591	NT	Homo sapiens CGI-125 protein (LOC51003), mRNA
3796	16836	29741	2.39	9.5E-01	BE902340.1	EST_HUMAN	601675639F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3958473 5'
3796	16836	29742	2.39	9.5E-01	BE902340.1	EST_HUMAN	601675639F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3958473 5'
9354	22319	35745	0.68	9.5E-01	AI190162.1	EST_HUMAN	q657407.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1733581 3'
9461	22425	35863	1.1	9.5E-01	AW661102.1	EST_HUMAN	RC1-GT0285-241199-011-b02 CT0285 Homo sapiens cDNA
11574	24512	38069	1.5	9.5E-01	BE218771.1	EST_HUMAN	601885163F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4103830 5'
11780	23935	37456	1.52	9.5E-01	AF283799.1	EST_HUMAN	UI-H-B12-ahp-f-03-0-UJ.s1 NCI_CGAP_Sub4 Homo sapiens cDNA clone IMAGE:2727677 3'
3214	16269		3.77	9.4E-01	AF165990.1	NT	Bartonella clarridgeiae RNA polymerase beta subunit (rpoB) gene, partial cds
3231	16286		1.93	9.4E-01	AF080595.1	NT	Human Fc-gamma-receptor IIA (FCGR2A) gene, exon 4
9217	22183	35616	0.69	9.4E-01	M80724.1	NT	Pimpinella brachycarpa zinc finger protein (ZFP1) mRNA, complete cds
12490	25235		2.09	9.4E-01	BE781261.1	EST_HUMAN	Human Fc-gamma-receptor IIA (FCGR2A) gene, exon 4
12838	25790		1.93	9.4E-01	11419857	NT	Homo sapiens epidermal growth factor receptor (avian erythroblastic leukemia viral (v-erb-b) oncogene homolog) (EGFR), mRNA
1745	14774		1.34	9.3E-01	AF242382.1	NT	Homo sapiens phytoacyl-CoA hydroxylase (PHYH) gene, exon 5
2641	15639	28663	1.01	9.3E-01	BE071172.1	EST_HUMAN	RC5-BT0503-271199-011-B01 BT0503 Homo sapiens cDNA
4066	17102	29993	0.82	9.3E-01	M20219.1	NT	Bovine papillomavirus type 2, complete genome
4066	17102	29994	0.82	9.3E-01	M20219.1	NT	Bovine papillomavirus type 2, complete genome
5673	18768	31940	1.47	9.3E-01	AF213884.1	NT	Homo sapiens nuclear factor of kappa light polypeptide gene enhancer in B-cells 1 (NFKB1) gene, complete cds
5761	18854	32034	3.92	9.3E-01	L36189.1	NT	Spodoptera frugiperda methylerythritolololate dehydrogenase mRNA, complete cds
7554	20517		0.76	9.3E-01	AF270648.1	NT	Plasmodium falciparum mature parasite-infected erythrocyte surface antigen (MESA) gene, complete cds
8402	21371	34779	1.75	9.3E-01	AA847040.1	EST_HUMAN	oe09b03.s1 NCI_CGAP_Ov2 Homo sapiens cDNA clone IMAGE:1385357
9165	22131		0.95	9.3E-01	AF061981.1	NT	Xenopus laevis CCGH zinc finger protein C3H-2 (C3H-2) mRNA, complete cds
9289	22255	35685	0.91	9.3E-01	AL161534.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 34
12953	25528	31713	1.34	9.3E-01	11440298	NT	Homo sapiens inositol 1,4,5-trisphosphate receptor, type 2 (ITPR2), mRNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
12965	25534		3.29	9.3E-01	AF271207.1	NT	Aedes triseriatus putative large subunit ribosomal protein rpl34 mRNA, complete cds
3253	16307	29231	3.14	9.2E-01	BE822702.1	EST_HUMAN	801441338T1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3916184 3'
5808	18896		1.73	9.2E-01	7106410	NT	Mus musculus sdcute carrier family 30 (zinc transporter), member 4 (Slc30a4), mRNA
6101	19180	32399	4.04	9.2E-01	BF037586.1	EST_HUMAN	801461153F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3864661 5'
6789	19843	33127	0.61	9.2E-01	M64703.1	NT	N crassa val4-RNA synthetase (cyl-20/un-3) gene
10018	22945	36412	0.77	9.2E-01	AL161565.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 65
10105	23031	36509	1.21	9.2E-01	6671677	NT	Mus musculus carbonic anhydrase 4 (Car4), mRNA
10628	23550	37050	3.42	9.2E-01	11430963	NT	Homo sapiens lysosomal apyrase-like protein 1 (LALP1), mRNA
10780	23701	37199	1.84	9.2E-01	BF693251.1	EST_HUMAN	7658e06x1 NCI_CGAP_K1111 Homo sapiens cDNA clone IMAGE:3578219 3' similar to SW.NUSM_TRYBB
12031	24907	38501	1.54	9.2E-01	BF132402.1	EST_HUMAN	P04540 NADH-UBIQUINONE OXIDOREDUCTASE CHAIN 5;
1629	14682	27638	2.31	9.1E-01	T98675.1	EST_HUMAN	801820312F1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:4052018 5'
2134	15151		2.06	9.1E-01	8923056	NT	ye52701.s1 Soares fetal liver spleen INFLS Homo sapiens cDNA clone IMAGE:121369 3' similar to contains
2582	15583	28602	1.12	9.1E-01	AF082919.1	NT	Alu repetitive element;
							Homo sapiens hypothetical protein FLJ20048 (FLJ20048), mRNA
3218	16273	29195	1.11	9.1E-01	T26418.1	EST_HUMAN	Pseudomonas fluorescens DNA polymerase III (dnaE) gene, complete cds
3218	16273	29195	1.11	9.1E-01	T26418.1	EST_HUMAN	AB200G8R Infant brain, LLNL array of Dr. M. Soares 1N1B Homo sapiens cDNA clone LLAB200G8 5'
6201	19363	32602	1.68	9.1E-01	L38033.1	NT	AB200G8R Infant brain, LLNL array of Dr. M. Soares 1N1B Homo sapiens cDNA clone LLAB200G8 5'
6655	19712	32989	2.94	9.1E-01	Q61704	SWISSPROT	Human pre-B cell stimulating factor homologue (SDF1b) mRNA, complete cds
7627	20775	34152	18.4	9.1E-01	AA806623.1	EST_HUMAN	INTER-ALPHA-TRYPsin INHIBITOR HEAVY CHAIN H3 PRECURSOR (ITI HEAVY CHAIN H3)
8011	20949	34342	2.58	9.1E-01	U72995.1	NT	ob71g08.st NCI_CGAP_GC51 Homo sapiens cDNA clone IMAGE:1336862 3'
10538	23458	36955	0.45	9.1E-01	P38432	SWISSPROT	Rattus norvegicus Rab3 GDP/GTP exchange protein mRNA, complete cds
12580	25867		10.31	9.1E-01	AF050113.1	NT	P80-COLLIN
4406	17434	30319	1.77	9.0E-01	AF099810.1	NT	Homo sapiens uncoupling protein-3 (UCP3) gene, complete cds
7622	20582	33946	0.85	9.0E-01	L42547.1	NT	Homo sapiens neurexin III-alpha gene, partial cds
7652	20612		1.32	9.0E-01	D38621.1	NT	Danio rerio LIM class homeodomain protein (lim5) mRNA, complete cds
9704	22657	36112	0.55	9.0E-01	AF086761.1	NT	Xenopus laevis gene for aldolase, complete cds
10189	23114	36598	0.44	9.0E-01	U39702.1	NT	Danio rerio semaphorin 21a mRNA, complete cds
							Mycoplasma genitalium section 24 of 51 of the complete genome
5781	18873	32054	2.37	8.9E-01	AF026198.1	NT	Fugu rubripes neural cell adhesion molecule L1 homolog (L1-CAM) gene, complete cds; putative protein 1 (PUT1) gene, partial cds; mitosis-specific chromosome segregation protein SMC1 homolog (SMC1) gene, complete cds; and calcium channel alpha-1 subunit
6377	19445		1.28	8.9E-01	X60996.1	NT	Rabbit MHC fragment RLA-DF DNA

Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6605	25663	32937	0.69	8.9E-01	BF217939.1	EST_HUMAN	601882708F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4095216 5'
6605	25663	32938	0.69	8.9E-01	BF217939.1	EST_HUMAN	601882708F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4095216 5'
7408	20375		0.54	8.9E-01	AB042297.1	NT	Homo sapiens PIS gene for 6-pyruvoyl-tetrahydropterin synthase, complete cds
8553	21621		0.43	8.9E-01	AF260225.1	NT	Homo sapiens TESTIN 2 and TESTIN 3 genes, complete cds, alternatively spliced
8769	21736	35157	1.09	8.9E-01	AF259667.1	NT	Orithona nana cytochrome-c oxidase subunit I (cox) gene, partial cds; mitochondrial gene for mitochondrial product
12074	24946	38541	2.99	8.9E-01	AE003944.1	NT	Xylella fastidiosa, section 90 of 228 of the complete genome
12420	25190		5.46	8.9E-01	AE002186.2	NT	Chlamydia pneumoniae AR39, section 21 of 94 of the complete genome
4573	17695	30489	1.58	8.8E-01	O26350	SWISSPROT	PUTATIVE F420-DEPENDENT NADP REDUCTASE
5238	18246	31118	0.9	8.8E-01	L41854.1	NT	Trypanosoma brucei microtubule-associated protein (MAPP15) mRNA, 3' end of cds
5447	18549	31462	0.7	8.8E-01	AF310617.1	NT	Pseudorabies virus Ea glycoprotein M gene, complete cds
11418	24362	37897	2.31	8.8E-01	Z28337.1	NT	M. aeruginosa (HUB 5-2.4) DNA from plasmid PM41
12082	24954	38549	6.51	8.8E-01	AA808055.1	EST_HUMAN	cc38h11.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1352037 3' similar to contains Alu repetitive element; contains element MER22 repetitive element
12237	25952		2.3	8.8E-01	D90911.1	NT	Synochocystis sp. PCC6803 complete genome, 13/27, 1576593-1719643
465	13538	26464	1.78	8.7E-01	AF106993.2	NT	Homo sapiens SOS1 (SOS1) gene, partial cds
2411	15418	26442	0.91	8.7E-01	5901893	NT	Homo sapiens AT-binding transcription factor 1 (ATBF1), mRNA
2885	15944	28859	5.42	8.7E-01	AA595863.1	EST_HUMAN	nn05f11.s1 NCI_CGAP_P4.1 Homo sapiens cDNA clone IMAGE:1076877
5043	18056		2.78	8.7E-01	AF121970.1	NT	Pseudomonas aeruginosa (top), putative transcriptional regulatory protein OhbR (ohbR), ortho-halobenzoate 1,2-dioxygenase beta-ISP protein OhbA (ohbA), OhbC (ohbC), ortho-halobenzoate 1,2-dioxygenase alpha-ISP protein OhbB (ohbB), and put-
5247	18255	31125	0.97	8.7E-01	BF218306.1	EST_HUMAN	601883175F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4095378 5'
8374	21343	34754	0.65	8.7E-01	AW897335.1	EST_HUMAN	RC4-NN0057-120500-073-c07 NN0057 Homo sapiens cDNA
9282	22248	35677	0.71	8.7E-01	A1239458.1	EST_HUMAN	q136e06.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1846786 3'
9282	22248	35678	0.71	8.7E-01	A1239458.1	EST_HUMAN	q136e06.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1846786 3'
10095	23021	36496	1.32	8.7E-01	AE004963.1	NT	Pseudomonas aeruginosa PAO1, section 524 of 529 of the complete genome
11181	24137	37869	4.56	8.7E-01	BF363970.1	EST_HUMAN	QVQ-NN1021-100800-337-c03 NN1021 Homo sapiens cDNA
12042	24917	38512	3.97	8.7E-01	BF107694.1	EST_HUMAN	601823684R1 NIH_MGC_79 Homo sapiens cDNA clone IMAGE:4043564 3'
12042	24917	38513	3.97	8.7E-01	BF107694.1	EST_HUMAN	601823684R1 NIH_MGC_79 Homo sapiens cDNA clone IMAGE:4043564 3'
475	13547		2.65	8.6E-01	X17012.1	NT	Rat IGFI gene for insulin-like growth factor II
859	13915	26874	4.32	8.6E-01	W69089.1	EST_HUMAN	z444e03.r1 Soares_fetal_heart_NBHHT9W Homo sapiens cDNA clone IMAGE:343516 5'
2278	15291	28316	1	8.6E-01	4503210	NT	Homo sapiens cytochrome P450, subfamily XXVIIA (steroid 27-hydroxylase, cerebrotendinous xanthomatosis), polypeptide 1 (CYP27A1b) mRNA
3635	16678	25592	0.87	8.6E-01	AL161665.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 65

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Table 4
Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3813	18653	28760	1.38	8.6E-01	U49724.1	NT	Drosophila melanogaster merlin (Dmerlin) mRNA, complete cds
5207	18216	31091	2.6	8.6E-01	BE147609.1	EST_HUMAN	RC1-HT0228-160300-019-c05 HT0229 Homo sapiens cDNA
6001	19084	32283	7.79	8.6E-01	X60547.1	NT	Chicken lipoprotein lipase gene
6001	19084	32284	7.79	8.6E-01	X60547.1	NT	Chicken lipoprotein lipase gene
6515	25661	32835	0.54	8.6E-01	S76772.1	NT	polyprotein [Coxsackie B4 virus CB4, host-mice, E2, originally derived from Edwards CB4 human strain, Genomic RNA Complete, 7397 nt]
6867	19920	33215	1.7	8.6E-01	AF143732.1	NT	Grus canadensis recombination activating protein 1 (RAG-1) gene, partial cds
6867	19920	33216	1.7	8.6E-01	AF143732.1	NT	Grus canadensis recombination activating protein 1 (RAG-1) gene, partial cds
7770	20723		0.81	8.6E-01	AE000591.1	NT	Helicobacter pylori 26695 section 69 of 134 of the complete genome
8260	21229		1.29	8.6E-01	AP001518.1	NT	Bacillus halodurans genomic DNA, section 12/14
8377	21346	34757	0.51	8.6E-01	AF077837.1	NT	Drosophila melanogaster collapsin response mediator protein (CRMP) mRNA, complete cds
10044	22971		0.46	8.6E-01	AE000979.1	NT	Archaeoglobus fulgidus section 128 of 172 of the complete genome
12798	25717		1.44	8.6E-01	AL112162.1	NT	Botrytis cinerea strain T4 cDNA library under conditions of nitrogen deprivation
6888	19940	33235	1.5	8.5E-01	AF165214.1	NT	Bacteriophage D3, complete genome
7768	20721	34093	2.49	8.5E-01	BE542612.1	EST_HUMAN	601067107F1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3453505 5'
8323	21292	34706	0.42	8.5E-01	AL161572.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 68
8761	21728	35150	0.93	8.5E-01	P06601	SWISSPROT	SEGMENTATION PROTEIN PAIRED
8761	21728	35151	0.93	8.5E-01	P06601	SWISSPROT	SEGMENTATION PROTEIN PAIRED
8849	21816	35236	0.57	8.5E-01	AJ243213.1	NT	Homo sapiens partial 5-HT4 receptor gene, exons 2 to 5
10715	23637	37129	1.35	8.5E-01	AB006799.1	NT	Cyanidium caldarium gene for SigC, complete cds
10715	23637	37130	1.35	8.5E-01	AB006799.1	NT	Cyanidium caldarium gene for SigC, complete cds
12565	25869		2.25	8.5E-01	11418543	NT	Homo sapiens human immunodeficiency virus type 1 enhancer-binding protein 1 (HIVEP1), mRNA
12572	26283		1.37	8.5E-01	9507008	NT	Rattus norvegicus protein tyrosine phosphatase, non-receptor type 5 (Ptpn5), mRNA
4782	17802	30603	0.85	8.4E-01	AF083975.2	NT	Fowl adenovirus 8, complete genome
5571	25641	31627	2.68	8.4E-01	L78726.1	NT	Human fibroblast growth factor receptor 3 (FGFR3) gene, intron 7
5571	25641	31628	2.68	8.4E-01	L78726.1	NT	Human fibroblast growth factor receptor 3 (FGFR3) gene, intron 7
8707	21044	34443	0.51	8.4E-01	AF051142.1	NT	Mamestra brassicae pheromone binding protein 2 precursor (PBP2) mRNA, complete cds
10317	23241		3.25	8.4E-01	AJ248287.1	NT	Pyrococcus abyssi complete genome, segment 5/6
12005	24882	38478	1.54	8.4E-01	M55584.1	NT	Human collagenase type IV (CLG4) gene, exon 4
743	13804	26743	3.01	8.3E-01	M69437.1	NT	Thermus thermophilus cytochrome c-552 (cycA) and CycB (cycB) genes, complete cds
3111	16168	29078	3.15	8.3E-01	AL161506.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 18
3823	18683	29787	0.83	8.3E-01	AB010879.1	NT	Nicotiana tabacum mRNA for chloroplast ribosomal protein L10, complete cds
4040	17078	29978	3.15	8.3E-01	Y19177.1	NT	Streptomyces antibioticus polyketide biosynthetic gene cluster
5341	18446	31199	2.42	8.3E-01	AL161540.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 40

Table 4

Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10028	22955		4.53	8.3E-01	AI791952.1	EST_HUMAN	nr01112.y5 NCJ_CGAP_C09 Homo sapiens cDNA clone IMAGE:1076495 5' similar to contains THR11 THR repetitive element;
10469	23391	36886	1.1	8.3E-01	AF08070.1	NT	Drosophila melanogaster Lis1 homolog mRNA, complete cds
10579	23501	36993	3.97	8.3E-01	AF108133.1	NT	Mus musculus neuro-d4 gene, exons 3 through 12 and partial cds
							Methanobacterium thermoautotrophicum from bases 1270510 to 1283409 (section 109 of 148) of the complete genome
11033	23997	37524	2.97	8.3E-01	AE000903.1	NT	complete genome
11050	24013		1.92	8.3E-01	7212472	NT	Phytophthora infestans mitochondrion, complete genome
11634	24571	38135	2.22	8.3E-01	AF020503.1	NT	Homo sapiens FRA3B common fragile region, diadenosine triphosphate hydrolase (FHIT) gene, exon 5
2088	15085	28103	2.24	8.2E-01	AB000489.1	NT	Rattus norvegicus mRNA for RPHO-1, complete cds
2101	15118		1.08	8.2E-01	AF145889.1	NT	Mus musculus trophinin (Tnn) gene, complete cds
2688	15684		1.06	8.2E-01	AW376890.1	EST_HUMAN	IL3-CT0219-161199-031-C08 CT0219 Homo sapiens cDNA
3918	16958	29871	0.75	8.2E-01	AB014574.1	NT	Homo sapiens mRNA for KIAA0674 protein, partial cds
3940	16980	29895	0.92	8.2E-01	AF063417.1	NT	Taristylum orbicularis elongation factor 1-alpha mRNA, partial cds
6800	19854	33139	0.57	8.2E-01	X95283.1	NT	G.gallus mRNA for C-Serrate-1 protein
6800	19854	33140	0.57	8.2E-01	X95283.1	NT	G.gallus mRNA for C-Serrate-1 protein
6941	20165	33488	0.85	8.2E-01	AJ010142.1	NT	Amanita muscaria mRNA for SCII25 protein
7082	20103	33414	3.69	8.2E-01	AW379433.1	EST_HUMAN	GM4-HT0243-081199-037-e01 HT0243 Homo sapiens cDNA
							S.cerevisiae MET, LEU4, and POL1 genes encoding MET4 protein, alpha-isopropylmalate (alpha-IPM) synthetase (partial), and DNA polymerase alpha (partial)
7484	25682	33807	4.38	8.2E-01	Z12126.1	NT	60114-885F2 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:3160412 5'
8787	21754	35176	0.58	8.2E-01	BE263145.1	EST_HUMAN	Homo sapiens mRNA for KIAA0630 protein, partial cds
10385	23307	36785	0.86	8.2E-01	AB014530.1	NT	Homo sapiens thiodoxin-related protein mRNA, complete cds
10419	23341	36827	1.59	8.2E-01	AF052659.1	NT	Oncorhynchus tshawytscha isolate T-20 somatolactin precursor gene, exon 1
10583	23505	36998	0.59	8.2E-01	AF223888.1	NT	Oncorhynchus tshawytscha isolate T-20 somatolactin precursor gene, exon 1
10583	23505	36999	0.59	8.2E-01	AF223888.1	NT	Oncorhynchus tshawytscha isolate T-20 somatolactin precursor gene, exon 1
10751	23673	37169	3.84	8.2E-01	Q9J170	SWISSPROT	MCKUSICK-KAUFMAN/BARDET-BIEDL SYNDROMES PUTATIVE CHAPERONIN
10751	23673	37170	3.84	8.2E-01	Q9J170	SWISSPROT	MCKUSICK-KAUFMAN/BARDET-BIEDL SYNDROMES PUTATIVE CHAPERONIN
11957	24836	38432	2.97	8.2E-01	L10127.1	NT	Mollusca conglaculum virus type 1 ORF1 and ORF2 DNA
12038	24913	38507	4.82	8.2E-01	P10383	SWISSPROT	OVARIAN TUMOR LOCUS PROTEIN
12043	24918	38514	6.1	8.2E-01	H87398.1	EST_HUMAN	yw14d02.r1 Soares_placenta_8h9weeks_2Nblp8c9w Homo sapiens cDNA clone IMAGE:252195 5' similar to gblv36072 60S RIBOSOMAL PROTEIN L7A (HUMAN);
12586	26290	31781	2.98	8.2E-01	AJ001261.1	NT	Mus musculus mRNA for NIPSNAP2 protein
2769	15761		1.48	8.1E-01	AF191839.1	NT	Mus musculus TANK binding kinase TBK1 (Tbk1) mRNA, complete cds
3472	16518	29439	3.67	8.1E-01	AF05066.1	NT	Homo sapiens MHC class 1 region

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Table 4

Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3472	16518	29440	3.67	8.1E-01	AF05066.1	NT	Homo sapiens MHC class 1 region
5792	18884	32066	0.51	8.1E-01	Q01727	SWISSPROT	MELANOCYTE STIMULATING HORMONE RECEPTOR (MSH-R) (MELANOTROPIN RECEPTOR)
6448	19513	32763	0.84	8.1E-01	U18780.1	NT	(MELANOCORTIN-1 RECEPTOR) (MC1-R)
6777	19832	33114	2.47	8.1E-01	Q13491	SWISSPROT	Mus musculus putative collagen alpha-2 (X1) chain (COL11A2) gene, partial cds
6777	19832	33115	2.47	8.1E-01	Q13491	SWISSPROT	NEURONAL MEMBRANE GLYCOPROTEIN M6-B
7755	20708	34077	0.55	8.1E-01	Q47477	SWISSPROT	NEURONAL MEMBRANE GLYCOPROTEIN M6-B
							CYTOSCHROME B
8243	21212	34618	1.12	8.1E-01	AF022713.2	NT	Drosophila melanogaster putative inorganic phosphate cotransporter (Pi cot) gene, partial cds; putative sodium channel (Nach) and putative amylase-related protein (Amyrel) genes, complete cds; and putative serine-enriched protein (gprs) gene, partial cd>
8243	21212	34619	1.12	8.1E-01	AF022713.2	NT	Drosophila melanogaster putative inorganic phosphate cotransporter (Pi cot) gene, partial cds; putative sodium channel (Nach) and putative amylase-related protein (Amyrel) genes, complete cds; and putative serine-enriched protein (gprs) gene, partial cd>
8958	21922	35349	0.91	8.1E-01	AP001517.1	NT	Bacillus halodurans genomic DNA, section 11/14
8958	21922	35350	0.91	8.1E-01	AP001517.1	NT	Bacillus halodurans genomic DNA, section 11/14
9122	22088	35516	1.13	8.1E-01	AW242647.1	EST_HUMAN	xd01h03.x1 NC1 CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2892469 3' similar to SW:LYAR_MOUSE
10484	23406	36902	0.84	8.1E-01	P06425	SWISSPROT	Q08288 CELL GROWTH REGULATING NUCLEOLAR PROTEIN ; contains MER22.b1 PTR5 repetitive element ;
10776	23697	37195	0.42	8.1E-01	N84541.1	EST_HUMAN	PROBABLE E4 PROTEIN
11812	24697	38277	4.05	8.1E-01	BE838558.1	EST_HUMAN	KK8872F Human fetal heart, Lambda ZAP Express Homo sapiens cDNA clone KK8872 5' similar to
11812	24697	38278	4.05	8.1E-01	BE838558.1	EST_HUMAN	EST (CLONE C-0PE11)
12298	25109	31839	1.73	8.1E-01	AE001711.1	NT	RCD-TN0080-220800-025-d10 TN0080 Homo sapiens cDNA
178	13279		3.32	8.0E-01	AJ271510.1	NT	RCD-TN0080-220800-025-d10 TN0080 Homo sapiens cDNA
288	13383	26310	5.97	8.0E-01	AJ132772.1	NT	Thermotoga maritima section 23 of 136 of the complete genome
2051	15070		1.72	8.0E-01	BF530982.1	EST_HUMAN	Staphylococcus aureus partial pla gene for phosphate acetyltransferase allele 15
3093	16151	29065	1.41	8.0E-01	AF127897.1	NT	Bos taurus full and rtf genes
3324	16375	29296	1.3	8.0E-01	AB009183.1	NT	602072473F1 NC1 CGAP_Brn67 Homo sapiens cDNA clone IMAGE:4215081 5'
3717	16780		2.36	8.0E-01	AL162788.2	NT	Saimiri boliviensis olfactory receptor (SBO27) gene, partial cds
4563	17588	30478	6.45	8.0E-01	X83739.2	NT	Mus musculus gene for oviductal glycoprotein, complete cds
8322	21291		2.31	8.0E-01	AW901489.1	EST_HUMAN	Neisseria meningitidis serogroup A strain Z2491 complete genome; segment 717
8870	21837	35259	1.05	8.0E-01	Y11095.1	NT	G gallus mRNA for nicotinic acetylcholine receptor (nAChR) beta 3 subunit
11303	24283	37779	1.58	8.0E-01	Q92793	SWISSPROT	RCD-NN1012-270300-021-h06 NN1012 Homo sapiens cDNA
							Rice stripe virus RNA 3
							CREB-BINDING PROTEIN

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Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
454	13527	26457	0.78	7.9E-01	D11476.1	NT	Lymantia dispar nuclear polyhedrosis virus gene for DNA polymerase, complete cds
716	13778		0.78	7.9E-01	AE002130.1	NT	Ureaplasma urealyticum section 31 of 59 of the complete genome
1609	14841		23.05	7.9E-01	AB040865.1	NT	Homo sapiens mRNA for KIAA1452 protein, partial cds
1663	14895		1.28	7.9E-01	U32739.1	NT	Haemophilus influenzae Rd section 54 of 163 of the complete genome
2272	15285	28311	7.38	7.9E-01	AB004816.1	NT	Oryctolagus cuniculus mRNA for mitsugumin29, complete cds
2273	15286	28312	2.36	7.9E-01	AF130459.1	NT	Danio rerio Trp4-associated protein Tap1A (tap1A) mRNA, complete cds
3528	16574	29497	3	7.9E-01	AF228664.1	NT	Gallus gallus SOX8 transcription factor (SOX8) mRNA, complete cds
4330	17358		0.88	7.9E-01	BE263612.1	EST_HUMAN	601192033F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3535785 5'
4642	17663	30551	1.15	7.9E-01	6753745	NT	Mus musculus embigin (Emb), mRNA
4642	17663	30552	1.15	7.9E-01	6753745	NT	Mus musculus embigin (Emb), mRNA
5244	18252	31123	1.03	7.9E-01	AF229843.1	NT	Mus musculus WNT-2 gene, partial cds; putative ankyrin-related protein and cystic fibrosis transmembrane
6479	19544	32792	0.78	7.9E-01	D38145.1	NT	conductance regulator (CFTR) genes, section 1 of 2 of the complete cds; and unknown gene
8446	21415	34828	3.37	7.9E-01	X90966.1	NT	Human mRNA for prostacyclin synthase, complete cds
9905	22857	36319	4.3	7.9E-01	U01912.1	NT	P. sativum GR gene
10409	23331	36816	4.3	7.9E-01	P19719	SWISSPROT	Giardia lamblia variant-specific surface protein G3M-B (vspG3M-B) mRNA, partial cds
10451	23373	36864	0.82	7.9E-01	AV700880.1	EST_HUMAN	SMALL HYDROPHOBIC PROTEIN
10877	23797	37298	0.82	7.9E-01	AB000631.1	NT	AV700860 GKC Homo sapiens cDNA clone GKCDRE12 3'
11350	24300		2.81	7.9E-01	7662471	NT	Streptococcus mutans DNA for sigma 42 protein, dTDP-4-keto-L-thiamnose reductase, complete cds
11546	24487	38041	2.22	7.9E-01	P19022	SWISSPROT	Homo sapiens KIAA1072 protein (KIAA1072), mRNA
877	13932		1.96	7.8E-01	Z43785.1	EST_HUMAN	NEURAL-CADHERIN PRECURSOR (N-CADHERIN)
2283	15296	28320	6.12	7.8E-01	AW99567.1	EST_HUMAN	HSC1KH041 normalized infant brain cDNA Homo sapiens cDNA clone c-1kh04
4730	17750	30642	1.33	7.8E-01	U87305.1	NT	EST1371637 MAGE resequences, MAGF Homo sapiens cDNA
5075	18085		0.8	7.8E-01	AW753353.1	EST_HUMAN	Rattus norvegicus transmembrane receptor Unc5H1 mRNA, complete cds
6187	19262	32498	2.5	7.8E-01	AF115856.1	NT	RC3-CT0264-130100-023-c02 CT0264 Homo sapiens cDNA
6344	19413	32855	1.04	7.8E-01	P05231	SWISSPROT	Sphenodon punctatus alpha enolase mRNA, partial cds
6606	19564	32939	0.72	7.8E-01	AL445066.1	NT	INTERLEUKIN-6 PRECURSOR (IL-6) (B-CELL STIMULATORY FACTOR 2) (BSF-2) (INTERFERON
8836	21803	35221	1.29	7.8E-01	BF108927.1	EST_HUMAN	BETA-2 (HYBRIDOMA GROWTH FACTOR)
9589	22551	36002	1.34	7.8E-01	Y10159.1	NT	Thermoplasma acidophilum complete genome; segment 4/5
9687	22640	36097	0.52	7.8E-01	4826873	NT	7154405.x1 Soares NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:3525176 3'
10483	23405		1.01	7.8E-01	Q25452	SWISSPROT	D. discoideum racGAP gene
							Homo sapiens nucleoporin 214kD (CAN) (NUP214), mRNA
							MUSCLE CALCIUM CHANNEL ALPHA-1 SUBUNIT (MDL-ALPHA1)

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
12558	25848		2.32	7.8E-01	L29260.1	NT	Arabidopsis thaliana 1-amino-1-cyclopropanecarboxylate synthase (ACS5) gene, complete cds
145	13248	26177	6.69	7.7E-01	AF184345.1	NT	Lycopodium obscurum ADP-glucose pyrophosphorylase large subunit (AGP-L1) mRNA, complete cds
727	13788		3.26	7.7E-01	AF050157.1	NT	Mus musculus major histocompatibility locus class II region: major histocompatibility protein class II alpha chain (IAalpha) and major histocompatibility protein class II beta chain (IEbeta) genes, complete cds;
2724	15718	28736	2	7.7E-01	O33915	SWISSPROT	butyrophilin-like (NG9), butyrophilin-1p
3368	16418		0.76	7.7E-01	8393408	NT	CITRATE SYNTHASE
3614	16658	29576	3.83	7.7E-01	AF118085.1	NT	Homo sapiens UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylglucosaminyltransferase 7 (GALNAc-T7) (GALNAc-T7), mRNA
4425	17452	30343	3.04	7.7E-01	AF199488.1	NT	Homo sapiens PRO1975 mRNA, complete cds
4425	17452	30344	3.04	7.7E-01	AF199488.1	NT	Coturnix coturnix japonica sub-species japonica beta-actin mRNA, partial cds
5640	18736	31899	1.25	7.7E-01	P16583	SWISSPROT	Coturnix coturnix japonica sub-species japonica beta-actin mRNA, partial cds
5640	18736	31900	1.25	7.7E-01	P16583	SWISSPROT	RAFFINOSE INVERTASE (INVERTASE)
6066	19147	32359	0.53	7.7E-01	R08600.1	EST_HUMAN	RAFFINOSE INVERTASE (INVERTASE)
10204	23129	36616	0.72	7.7E-01	AB021134.1	NT	Y24802.s1 Scores fetal liver spleen INFLS Homo sapiens cDNA clone IMAGE:127755 3'
12447	25207		5.53	7.7E-01	11497621	NT	Daphnia magna hemoglobin gene cluster (dhb3, dhb1 and dhb2 genes), complete cds
6218	19292	32525	4.49	7.6E-01	AF050510.1	NT	Archaeoglobus fulgidus, complete genome
6218	19292	32526	4.49	7.6E-01	AF050510.1	NT	Arabidopsis thaliana 3-methylcrotonyl-CoA carboxylase non-biotinylated subunit (MCCB) mRNA, complete cds
6967	19724	32999	0.55	7.6E-01	P37938	SWISSPROT	Arabidopsis thaliana 3-methylcrotonyl-CoA carboxylase non-biotinylated subunit (MCCB) mRNA, complete cds
7029	18361	31248	0.98	7.6E-01	A1253399.1	EST_HUMAN	MATING-TYPE PROTEIN A-ALPHA Z4
7029	18361	31282	0.98	7.6E-01	A1253399.1	EST_HUMAN	eq14b12.x1 Stanley Frontal NS pool 2 Homo sapiens cDNA clone IMAGE:2030878
7252	19987	33255	0.89	7.6E-01	U72487.1	NT	eq14b12.x1 Stanley Frontal NS pool 2 Homo sapiens cDNA clone IMAGE:2030879
						NT	Rattus norvegicus calcium-independent alpha-latrotoxin receptor mRNA, complete cds
8400	21369	34778	1.33	7.6E-01	AF146793.2	NT	Mus musculus neuromedin U precursor (Nmu) gene, partial cds; tPhLP (Tphlp) gene, partial cds; CLOCK (Clock) gene, complete cds; PFT27 (PFT27) gene, complete cds; and H5AR (H5ar) gene, complete cds
8464	21433	34849	1.92	7.6E-01	6857752	NT	Mus musculus advillin (Advil-pending), mRNA
8464	21433	34850	1.92	7.6E-01	6857752	NT	Mus musculus advillin (Advil-pending), mRNA
8668	21636	35058	0.43	7.6E-01	Q01098	SWISSPROT	GLUTAMATE (NMDA) RECEPTOR SUBUNIT EPSILON 3 PRECURSOR (N-METHYL D-ASPARTATE RECEPTOR SUBTYPE 2C) (NR2C) (NMDAR2C)
8668	21636	35059	0.43	7.6E-01	Q01098	SWISSPROT	GLUTAMATE (NMDA) RECEPTOR SUBUNIT EPSILON 3 PRECURSOR (N-METHYL D-ASPARTATE RECEPTOR SUBTYPE 2C) (NR2C) (NMDAR2C)

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9318	22283	35714	1.01	7.6E-01	6763577	NT	Mus musculus cytochrome P450, 2b9, phenobarbital inducible, type a (Cyp2b9), mRNA
9634	22578	36028	5.25	7.6E-01	P30372	SWISSPROT	MUSCARINIC ACETYLCHOLINE RECEPTOR M2
9634	22578	36029	5.25	7.6E-01	P30372	SWISSPROT	MUSCARINIC ACETYLCHOLINE RECEPTOR M2
11685	24651	38223	2.09	7.6E-01	X86347.1	NT	H. aspersa mRNA for neurofilament NF70
11685	24651	38230	2.09	7.6E-01	X86347.1	NT	H. aspersa mRNA for neurofilament NF70
12020	24897		3.05	7.6E-01	AL161592.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 88
12203	25045		3.8	7.6E-01	AB020702.1	NT	Homo sapiens mRNA for KIAA0895 protein, partial cds
514	13586		1.67	7.5E-01	AL163301.2	NT	Homo sapiens chromosome 21 segment HS21C101
586	13654	26568	1.01	7.5E-01	AF020503.1	NT	Homo sapiens FRA3B common fragile region, diadenosine triphosphate hydrolase (FHIT) gene, exon 5
7764	20717	34090	0.78	7.5E-01	AF052730.1	NT	Drosophila melanogaster tyrosine kinase receptor protein (eph) mRNA, complete cds
12516	25247		4.53	7.5E-01	AF163151.2	NT	Homo sapiens dentin sialophosphoprotein precursor (DSPP) gene, complete cds
13027	25575	31697	1.57	7.5E-01	AE000823.1	NT	Methanobacterium thermoautotrophicum from bases 317350 to 328792 (section 29 of 148) of the complete genome
1132	14175	27124	1.35	7.4E-01	AI598146.1	EST_HUMAN	In14B09.x1 NCI_CGAP_Bim25 Homo sapiens cDNA clone IMAGE:2167577 3' similar to contains Alu repetitive element; contains element MIR repetitive element ;
2350	15359	28381	0.93	7.4E-01	AB011106.1	NT	Homo sapiens mRNA for KIAA0834 protein, partial cds
3739	16781	29693	18.81	7.4E-01	AF112638.1	NT	Maiva pusilla actin (Act1) mRNA, complete cds
3919	16959	29872	2.01	7.4E-01	AF133310.1	NT	Vibrio cholerae phage CTXphi Calcutta-rsR-a (rsR-a) and Calcutta-rsR-b (rsR-b) genes, complete cds
4340	17367	30250	6.99	7.4E-01	AL163248.2	NT	Homo sapiens chromosome 21 segment HS21C046
8176	21146	34553	1.04	7.4E-01	AL161551.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 51
8176	21146	34554	1.04	7.4E-01	AL161551.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 51
8980	21946	35370	0.78	7.4E-01	BF343266.1	EST_HUMAN	602018456FT NCI_CGAP_Bim67 Homo sapiens cDNA clone IMAGE:4154340 5'
9063	22029		0.64	7.4E-01	U87960.1	NT	Rattus norvegicus leukocyte common antigen receptor (LAR) gene, trans-spliced alternative untranslated exon
9452	22416	35854	7.09	7.4E-01	BE747503.1	EST_HUMAN	601573026F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3834174 5'
9511	22474	35918	1.14	7.4E-01	AA187986.1	EST_HUMAN	zp67n01.s1 Stratagene endothelial cell 937223 Homo sapiens cDNA clone IMAGE:625297 3' similar to SW:TCPO_MOUSE_P42932 T-COMPLEX PROTEIN 1, THETA SUBUNIT ;
10767	23688	37165	0.74	7.4E-01	11424933	NT	Homo sapiens NY-REN-45 antigen (LOC61133), mRNA
12171	25021		4.46	7.4E-01	6753217	NT	Homo sapiens complement component 1 inhibitor (C1inh), mRNA
12284	25101		1.54	7.4E-01	AI472641.1	EST_HUMAN	la13n01.x1 NCI_CGAP_Lym5 Homo sapiens cDNA clone IMAGE:2043985 3'
3999	17038		0.64	7.3E-01	AP000062.1	NT	Aeropyrum pernix genomic DNA, section 5/7
4647	17668	30555	0.97	7.3E-01	AE001166.1	NT	Borrelia burgdorferi (section 52 of 70) of the complete genome

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4728	17749	30641	4.57	7.3E-01	AF225421.1	NT	Homo sapiens HT017 mRNA, complete cds
5135	18144	31024	1.18	7.3E-01	O43103	SWISSPROT	FERRICHRONE SIDEROPHORE PEPTIDE SYNTHETASE
6761	19815	33094	6.03	7.3E-01	L35772.1	NT	Mus musculus antigen (CD72) gene
6761	19815	33095	6.03	7.3E-01	L35772.1	NT	Mus musculus antigen (CD72) gene
7301	25679	33608	0.92	7.3E-01	AJ011418.1	NT	Lycopodium esculentum mRNA for ubiquitin activating enzyme
7692	20650	34014	0.53	7.3E-01	Z14133.1	NT	D.melanogaster Orc mRNA for clathrin heavy chain
7794	20748	34119	7.46	7.3E-01	M26511.1	NT	V.alginolyticus sucrose (scrB) gene, complete cds
7794	20748	34120	7.46	7.3E-01	M26511.1	NT	V.alginolyticus sucrose (scrB) gene, complete cds
8115	21052	34450	0.51	7.3E-01	U34631.1	NT	Mus musculus alpha-4 integrin gene, exon 7
11759	24687	38267	3.11	7.3E-01	AA878019.1	EST_HUMAN	225608.s1 Soares_fetal_liver_spleen_1NPLS_S1 Homo sapiens cDNA clone IMAGE:431799 3'
11759	24687	38268	3.11	7.3E-01	AA878019.1	EST_HUMAN	225608.s1 Soares_fetal_liver_spleen_1NPLS_S1 Homo sapiens cDNA clone IMAGE:431799 3'
832	13889		2.03	7.2E-01	L29281.1	NT	Rattus norvegicus initiation factor-2 kinase (eIF-2a) mRNA, complete cds
1974	14995	27997	3.23	7.2E-01	X79140.1	NT	N.tabacum Nelf-4A13 mRNA
2468	15472	28495	1.91	7.2E-01	AB009805.1	NT	Gallus gallus gene for melanocortin 2-receptor, complete cds
3080	16137	29048	1.47	7.2E-01	AF198100.1	NT	Fowlpox virus, complete genome
3487	16513	29434	2.44	7.2E-01	AF065806.1	NT	Giardia intestinalis variant-specific surface protein (vsp417-6) gene, vsp417-6(A-1) allele, complete cds
4803	17820	30714	2.99	7.2E-01	D90314.1	NT	L.mesenteroides gene for sucrose phosphorylase (EC 2.4.1.7)
5159	18168	31046	1.57	7.2E-01	AF198779.1	NT	Homo sapiens transcription factor (GHM enhancer 3, JM11 protein, JM4 protein, JM5 protein, T54 protein, JM10 protein, A4 differentiation-dependent protein, triple LIM domain protein 6, and synaptophysin genes, complete cds; and L-type calcium channel a2)
5159	18168	31047	1.57	7.2E-01	AF198779.1	NT	Homo sapiens transcription factor (GHM enhancer 3, JM11 protein, JM4 protein, JM5 protein, T54 protein, JM10 protein, A4 differentiation-dependent protein, triple LIM domain protein 6, and synaptophysin genes, complete cds; and L-type calcium channel a2)
7421	20388	33739	0.78	7.2E-01	U69633.1	NT	Solanum tuberosum cold-stress inducible protein (C17) gene, complete cds
8797	21784	35186	1.24	7.2E-01	AF236061.1	NT	Oryctolagus cuniculus RING-finger binding protein mRNA, partial cds
9314	22279		0.52	7.2E-01	AV743773.1	EST_HUMAN	AV743773 CB Homo sapiens cDNA clone CBNAFD06 5'
10705	23627	37123	2.59	7.2E-01	BF670061.1	EST_HUMAN	602118381.F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4275381 5'
11091	24051	37574	3.38	7.2E-01	U82623.1	NT	Rattus norvegicus cytochrome mRNA, complete cds
12823	18343	31291	1.43	7.2E-01	U02568.1	NT	Dictyocaulus viviparus nematode polyprotein antigen precursor (DvA) mRNA, complete cds
12700	25360		5.56	7.2E-01	AP000063.1	NT	Aeropyrum pumilus genomic DNA, section 617
693	13755	26685	13.3	7.1E-01	D21070.1	NT	Rana catesbeiana mRNA for bullfrog skeletal muscle calcium release channel (ryanodine receptor) alpha isoform (RyR1), complete cds
3075	16132	29045	13.21	7.1E-01	AJ270777.1	NT	Homo sapiens partial TCF-4 gene for T-cell transcription factor-4, exons 15-16

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4236	17265	30151	3.29	7.1E-01	7305360	NT	Mus musculus obogelin (Olog), mRNA
4236	17265	30152	3.29	7.1E-01	7305360	NT	Mus musculus obogelin (Olog), mRNA
6058	19139	32350	1.55	7.1E-01	BF681034.1	EST_HUMAN	602155438F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4296344 5'
6058	19139	32351	1.55	7.1E-01	BF681034.1	EST_HUMAN	602155438F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4296344 5'
7137	20113	33428	6.92	7.1E-01	U36232.1	NT	Drosophila melanogaster 6-pyruvyltetrahydropterin synthase (pr) gene, complete cds
8533	21501	34918	0.48	7.1E-01	H5424.1	EST_HUMAN	y48409.s1 Soares fetal liver spleen 1NFSL Homo sapiens cDNA clone IMAGE:202961 3'
9088	22054	35477	0.85	7.1E-01	BE074185.1	EST_HUMAN	RC1-BT0567-301299-011-409 BT0567 Homo sapiens cDNA
9088	22054	35478	0.85	7.1E-01	BE074185.1	EST_HUMAN	RC1-BT0567-301299-011-409 BT0567 Homo sapiens cDNA
10214	23139	36628	1.28	7.1E-01	BE04405.1	EST_HUMAN	601496330F1 NIH_MGC_70 Homo sapiens cDNA clone IMAGE:3898495 5'
10774	23695	37193	1.13	7.1E-01	M12991.1	NT	Human T-cell receptor gamma-chain J2 gene
12499	25773	27229	2.34	7.1E-01	AA21492.1	EST_HUMAN	zu06h11.s1 Soares testis NHT Homo sapiens cDNA clone IMAGE:731109 3'
1233	14270	27229	1.13	7.0E-01	AB014514.1	NT	Homo sapiens mRNA for KIAA0614 protein, partial cds
1233	14270	27230	1.13	7.0E-01	AB014514.1	NT	Homo sapiens mRNA for KIAA0614 protein, partial cds
2455	15480	28482	1.09	7.0E-01	N62412.1	EST_HUMAN	yzf3e07.s1 Soares multiple sclerosis_2Nbf-HMSP Homo sapiens cDNA clone IMAGE:288708 3' similar to contains Alu repetitive element;
2455	15480	28483	1.09	7.0E-01	N62412.1	EST_HUMAN	yzf3e07.s1 Soares multiple sclerosis_2Nbf-HMSP Homo sapiens cDNA clone IMAGE:288708 3' similar to contains Alu repetitive element
5096	18108		2.11	7.0E-01	AL163301.2	NT	Homo sapiens chromosome 21 segment HS21C101
6062	19143		0.95	7.0E-01	AB021316.1	NT	Arabidopsis thaliana mRNA for chlorophyll b synthase, complete cds
8721	21689		8.51	7.0E-01	AE000258.1	NT	Escherichia coli K-12 MG1655 section 143 of 400 of the complete genome
9671	22624	35077	0.52	7.0E-01	U53888.1	NT	Clostridium acetabutylicum mannitol-specific phosphotransferase system (PTS) system, mltA, mltR, mltF, and mltD genes, complete cds
9671	22624	36078	0.52	7.0E-01	U53888.1	NT	Clostridium acetabutylicum mannitol-specific phosphotransferase system (PTS) system, mltA, mltR, mltF, and mltD genes, complete cds
11454	24397	37943	1.71	7.0E-01	AV763842.1	EST_HUMAN	AV763842 MDS Homo sapiens cDNA clone MDSCH04 5'
11454	24397	37944	1.71	7.0E-01	AV763842.1	EST_HUMAN	AV763842 MDS Homo sapiens cDNA clone MDSCH04 5'
13035	25811	31528	1.35	7.0E-01	9630464	NT	Bacteriophage N15 virion, complete genome
971	14023	26976	12.59	6.9E-01	U69674.1	NT	Candida albicans squalene epoxidase (CAERG1) gene, complete cds and translational regulator gene, partial cds
971	14023	26977	12.59	6.9E-01	U69674.1	NT	Candida albicans squalene epoxidase (CAERG1) gene, complete cds and translational regulator gene, partial cds
1313	14349	27315	2.22	6.9E-01	AA593630.1	EST_HUMAN	mt28a09.s1 NCI_CGAP_Gas1 Homo sapiens cDNA clone IMAGE:1085178 3'
3233	16288	29210	1.8	6.9E-01	AE002271.2	NT	Chlamydia muridarum, section 3 of 85 of the complete genome
5249	18257	31126	0.92	6.9E-01	AV714502.1	EST_HUMAN	AV714502 DCB Homo sapiens cDNA clone DCBATD12 5'

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5878	18987	32158	0.8	6.9E-01	AB035882.1	NT	Branchiostoma belcheri BbNA3 mRNA for notchord actin, complete cds
6104	19183	32402	0.55	6.9E-01	Y18278.1	NT	Drosophila melanogaster mRNA for A-kinase anchor protein DAKAP550, partial
6906	19570	32822	1.5	6.9E-01	BE298188.1	EST_HUMAN	601177333F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3532328 5'
8312	21281	34692	3.39	6.9E-01	AL161573.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 69
8312	21281	34693	3.39	6.9E-01	AL161573.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 69
9526	22489	36447	0.73	6.9E-01	AF118046.1	NT	Entamoeba dispar cation transporting ATPase (atpase) gene, partial cds
10053	22980	36448	0.55	6.9E-01	AF206319.1	NT	Musa acuminata pectate lyase 1 (PL1) mRNA, complete cds
10053	22980	36448	0.55	6.9E-01	AF206319.1	NT	Musa acuminata pectate lyase 1 (PL1) mRNA, complete cds
11587	24525	38081	2.03	6.9E-01	D89013.1	NT	Homo sapiens DAN gene, complete cds
11587	24525	38082	2.03	6.9E-01	D89013.1	NT	Homo sapiens DAN gene, complete cds
12145	25766		3.91	6.9E-01	Q99958	SWISSPROT	FORKHEAD BOX PROTEIN C2 (FORKHEAD-RELATED PROTEIN FKHL14) (MESENCHYME FORK HEAD PROTEIN 1) (MFH-1 PROTEIN) (TRANSCRIPTION FACTOR FKHL14)
958	14011	26964	1.52	6.8E-01	AF017784.1	NT	Giardia intestinalis carbamate kinase gene, complete cds
2682	15678		1.26	6.8E-01	D90917.1	NT	Synechocystis sp. PCC6803 complete genome, 27/27, 3418852-3573470
2840	14651	27627	1.5	6.8E-01	AA854475.1	EST_HUMAN	aj75a05.81 Soares_parathyroid_tumor_NbHPA Homo sapiens cDNA clone IMAGE:1402256 3' similar to gb:X56411_ma1 ALCOHOL DEHYDROGENASE CLASS II PI CHAIN (HUMAN);
4602	17623	30516	1.75	6.8E-01	J00782.1	NT	Rat(hooded) prolactin gene: exon iii and flanks
9996	22923	36388	1.67	6.8E-01	AB037766.1	NT	Homo sapiens mRNA for KIAA1345 protein, partial cds
11424	24368	37903	1.77	6.8E-01	AJ276675.1	NT	Siagonospora avenae bgII gene for beta-glucosidase, exons 1-4
11424	24368	37904	1.77	6.8E-01	AJ276675.1	NT	Siagonospora avenae bgII gene for beta-glucosidase, exons 1-4
11450	24393	37938	1.82	6.8E-01	AF038939.1	NT	Mus musculus zinc finger protein (Peg3) mRNA, complete cds
11450	24393	37939	1.82	6.8E-01	AF038939.1	NT	Mus musculus zinc finger protein (Peg3) mRNA, complete cds
							Mus musculus major histocompatibility complex region NG27, NG28, RPS28, NADH oxidoreductase, NG29, KIFC1, Fas-binding protein, BING1, lapasin, RalGDS-like, KE2, BING4, beta 1,3-galactosyl transferase, and RPS18 genes, complete cds; Sacm21 gene, partial>
11931	24812	38407	1.49	6.8E-01	AF110520.1	NT	Mus musculus major histocompatibility complex region NG27, NG28, RPS28, NADH oxidoreductase, NG29, KIFC1, Fas-binding protein, BING1, lapasin, RalGDS-like, KE2, BING4, beta 1,3-galactosyl transferase, and RPS18 genes, complete cds; Sacm21 gene, partial>
11931	24812	38408	1.49	6.8E-01	AF110520.1	NT	Mus musculus major histocompatibility complex region NG27, NG28, RPS28, NADH oxidoreductase, NG29, KIFC1, Fas-binding protein, BING1, lapasin, RalGDS-like, KE2, BING4, beta 1,3-galactosyl transferase, and RPS18 genes, complete cds; Sacm21 gene, partial>
298	13392	26320	25.45	6.7E-01	AF213884.1	NT	Homo sapiens nuclear factor of kappa light polypeptide gene enhancer in B-cells 1 (NFKB1) gene, complete cds
339	13428	26350	28.03	6.7E-01	AF213884.1	NT	Homo sapiens nuclear factor of kappa light polypeptide gene enhancer in B-cells 1 (NFKB1) gene, complete cds
1927	14951		1.07	6.7E-01	M12132.1	NT	Quail fast skeletal muscle troponin I gene, complete cds

Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2157	15173	28192	1.79	6.7E-01	AA451864.1	EST_HUMAN	zx12g12.s1 Soares_total_fetus_Nb2HF8_9w Homo sapiens cDNA clone IMAGE:786310 3' similar to contains element TAR1 repetitive element:
2176	15886	28213	2.65	6.7E-01	AF186073.1	NT	Drosophila melanogaster Ms85C gene, complete cds; NMDMC isoform (Nmdmc) gene, complete cds, alternatively spliced; and transcription factor (Relish) gene, complete cds, alternatively spliced
3009	16067	28987	3.96	6.7E-01	6878580	NT	Mus musculus Wiskott-Aldrich syndrome protein (Wasp), mRNA
4481	17506	30395	0.78	6.7E-01	X74421.1	NT	S. tuberosum mRNA for glucose-6-phosphate dehydrogenase
5002	18016	30903	0.97	6.7E-01	AW079110.1	EST_HUMAN	xa95g12.x1 NCLCGAP_Co17 Homo sapiens cDNA clone IMAGE:2574598 3'
5587	18883	31651	0.7	6.7E-01	J04836.1	NT	M. barteri ATPase alpha and beta subunit (atpA and atpB) genes, complete cds
5587	18883	31652	0.7	6.7E-01	J04836.1	NT	M. barteri ATPase alpha and beta subunit (atpA and atpB) genes, complete cds
6073	19154	32366	0.93	6.7E-01	AE001486.1	NT	Helicobacter pylori, strain J99 section 47 of 132 of the complete genome
6456	19521	32771	1.26	6.7E-01	9635035	NT	Gallid herpesvirus 2, complete genome
6456	19521	32772	1.26	6.7E-01	9635035	NT	Gallid herpesvirus 2, complete genome
7537	20500	33884	4.57	6.7E-01	AE004606.1	NT	Pseudomonas aeruginosa PA01, section 167 of 529 of the complete genome
7563	20526	33884	0.98	6.7E-01	AE001486.1	NT	Helicobacter pylori, strain J99 section 47 of 132 of the complete genome
10503	23425	37776	2.62	6.7E-01	M34046.1	NT	Human placental protein 14 (PP14) gene, complete cds
11300	24250	37776	2.62	6.7E-01	BF364649.1	EST_HUMAN	OM3-HT0769-010600-197-c03 HT0769 Homo sapiens cDNA
11787	23942	37464	3.23	6.7E-01	O14367	SWISSPROT	N-ACETYLGLUCOSAMINYL-PHOSPHATIDYLOSITOL BIOSYNTHETIC PROTEIN GPI1
11969	24847	38444	1.62	6.7E-01	AA342521.1	EST_HUMAN	EST48065 Fetal spleen Homo sapiens cDNA 3' end
2509	15512	28538	1.92	6.8E-01	AF075240.1	NT	Homo sapiens SLIT1 protein (SLIT2) mRNA, partial cds
2711	15705	28721	1.4	6.8E-01	AF198339.1	NT	Homo sapiens lens epithelium-derived growth factor gene, alternatively spliced, complete cds
3501	16548	29474	1.41	6.8E-01	4506880	NT	Homo sapiens sema domain, seven thrombospondin repeats (type 1 and type 1-like), transmembrane domain (TM) and short cytoplasmic domain, (semaphorin) 5A (SEMA5A) mRNA
3670	16713	29628	4.37	6.8E-01	Y07669.1	NT	C. albicans random DNA marker, 282bp
4136	17168					NT	Human hereditary haemochromatosis region, histone 2A-like protein gene, hereditary haemochromatosis (HLA-H) gene, RoRet gene, and sodium phosphate transporter (NP-T3) gene, complete cds
5258	18286	31134	0.86	6.8E-01	U91328.1	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 68
5282	18288	31150	1.13	6.8E-01	AL161572.2	NT	S. pneumoniae popB and popC genes
5282	18288	31151	0.95	6.8E-01	Z82002.1	NT	S. pneumoniae popB and popC genes
5282	18288	31151	0.95	6.8E-01	Z82002.1	NT	S. pneumoniae popB and popC genes
6468	19531	32779	3.83	6.8E-01	6680577	NT	Mus musculus Kinesin light chain 2 (Klc2), mRNA
7949	20890	34281	3.57	6.8E-01	AV660508.1	EST_HUMAN	AV660508 GLC Homo sapiens cDNA clone GLCGID04 3'
8912	21878	35304	0.58	6.8E-01	AV704700.1	EST_HUMAN	AV704700 ADB Homo sapiens cDNA clone ADBCAF11 5'
10023	22950		1.56	6.8E-01	AL163278.2	NT	Homo sapiens chromosome 21 segment HS21C078

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Table 4
Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
12746	25395	31758	1.76	6.8E-01	AE004382.1	NT	Vibrio cholerae chromosome II, section 39 of 93 of the complete chromosome
624	13689	26608	0.96	8.5E-01	M75140.1	NT	H. vulgaris Na,K-ATPase alpha subunit mRNA, complete cds
624	13689	26607	0.96	8.5E-01	M75140.1	NT	H. vulgaris Na,K-ATPase alpha subunit mRNA, complete cds
3448	16493	29412	4.63	8.5E-01	AB041228.1	NT	Mus musculus gene for Tob2, complete cds
4311	17340	30220	4.28	8.5E-01	AJ272265.1	NT	Homo sapiens SPP2 gene for secreted phosphoprotein 24 precursor, exons 1-8
5102	18112	30984	3.71	8.5E-01	U28921.1	NT	Phaseolus vulgaris ATPase gamma subunit mRNA, nuclear gene encoding mitochondrial protein, partial cds
5204	18213	31088	1.13	8.5E-01	Z70628.1	NT	H. sapiens mRNA for immunoglobulin heavy chain variable region (9D4-A6, VH4, 4-59/DP-71)
5518	25640	31551	2.13	8.5E-01	P18480	SWISSPROT	TRANSCRIPTION REGULATORY PROTEIN SNF5 (SWI/SNF COMPLEX COMPONENT SNF5) (TRANSCRIPTION FACTOR TFE4)
5802	18894	32077	0.58	8.5E-01	AL163249.2	NT	Homo sapiens chromosome 21 segment HS21C049
6887	19939	33234	1.24	8.5E-01	D88348.1	NT	Chicken mRNA for 115-kDa melanosomal matrix protein, complete cds
7841	20788	34163	0.84	8.5E-01	X04768.1	NT	Murine Ig-related lambda(50) gene (exon 1) transcribed selectively in pre-B lymphocytes
7930	20873	34262	0.89	8.5E-01	AI799882.1	EST_HUMAN	wc46a2.ct NCI_CGAP_Pr28 Homo sapiens cDNA clone IMAGE:2321642 3'
10197	23122	37117	1.03	8.5E-01	T78904.1	EST_HUMAN	y221b04.s1 Soares fetal liver spleen 1NLS Homo sapiens cDNA clone IMAGE:108847 3'
10699	23621	37117	2.2	8.5E-01	AF119676.1	NT	Mus musculus small GTP-binding protein RAB25 (Rab25) gene, complete cds
10997	23963	37487	2.19	8.5E-01	H87583.1	EST_HUMAN	wv17f06.r1 Soares, placenta_8to9weeks_2NbHP8to9w Homo sapiens cDNA clone IMAGE:252515 5'
11045	24009	37535	2.88	8.5E-01	AA601287.1	EST_HUMAN	no15c07.s1 NCI_CGAP_Phet Homo sapiens cDNA clone IMAGE:1100748 3'
11143	24103		3.43	8.5E-01	AU138076.1	EST_HUMAN	AU138078 PLACE1 Homo sapiens cDNA clone PLACE1007810 5'
11925	24806	38399	2.3	8.5E-01	AF014115.1	NT	Plasmodium berghei cytochrome c oxidase subunit III, cytochrome c oxidase subunit I, and cytochrome b genes, mitochondrial genes encoding mitochondrial proteins, complete cds
11970	24848	38445	1.47	8.5E-01	AF146687.1	NT	Fugu rubripes U2 small nuclear ribonucleoprotein auxiliary factor subunit-related protein (U2AF1-RS2), 19 kDa Gdgi adaptor protein adaptin (AP19), and phosphorylase kinase alpha 2 subunit (PHKA2) genes, complete cds; kelch protein (KELCH1) and kelch p2
12130	24999	38604	1.61	8.5E-01	AL161580.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 76'
12554	25278		2.55	8.5E-01	BE465050.1	EST_HUMAN	hw74a10.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3179130 3'
252	13349	26275	10.51	8.4E-01	U48848.1	NT	Drosophila melanogaster 8kd dynein light chain mRNA, complete cds
3470	16516	29437	3.26	8.4E-01	U48854.2	NT	Mus musculus dystroglycan 1 (DAG1) gene, exons 1 and 2 and complete cds
3875	16914	29823	1.34	8.4E-01	AB046827.1	NT	Homo sapiens mRNA for KIAA1607 protein, partial cds
4519	17544	30430	0.89	8.4E-01	Y12488.1	NT	M. musculus whn gene
4519	17544	30431	0.89	8.4E-01	Y12488.1	NT	M. musculus whn gene
5192	18201	31073	1	8.4E-01	H85337.1	EST_HUMAN	ye90c08.r1 Soares retina N265HR Homo sapiens cDNA clone IMAGE:222086 5'
8950	21926	35353	1.57	8.4E-01	AE001247.1	NT	Treponema pallidum section 63 of 67 of the complete genome

Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10449	23371	36863	6.94	6.4E-01	U82828.1	NT	Homo sapiens ataxia telangiectasia (ATM) gene, complete cds
10454	23386	36879	1.18	6.4E-01	BF670405.1	EST_HUMAN	802150289F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4291126 5'
12666	25342		5.76	6.4E-01	AV759212.1	EST_HUMAN	AV759212 MDS Homo sapiens cDNA clone MDSCGC09 5'
494	13508	26442	3.27	6.3E-01	P05228	SWISSPROT	HISTIDINE-RICH PROTEIN PRECURSOR (CLONE PFHRP-III)
536	13607	26525	2.19	6.3E-01	U32889.1	NT	Haemophilus influenzae Rd section 4 of 163 of the complete genome
2171	15187	28208	3.4	6.3E-01	U81136.1	NT	Shigella flexneri multi-antigen resistance locus
2583	15584	28603	2.72	6.3E-01	U75331.1	NT	Gallus gallus bone morphogenetic protein 1 (BMP1) mRNA, partial cds
2583	15584	28604	2.72	6.3E-01	U75331.1	NT	Gallus gallus bone morphogenetic protein 1 (BMP1) mRNA, partial cds
3029	16087		0.8	6.3E-01	Y17275.1	NT	Lycopodium obscurum p69a gene, complete CDS
6182	19257	32490	0.87	6.3E-01	BE093906.1	EST_HUMAN	PMO-BT0757-010500-002-a05 B10757 Homo sapiens cDNA
6753	19807	33088	1.07	6.3E-01	L27798.1	NT	Streptococcus dysgalactiae (mag) gene, complete cds
6753	19807	33089	1.07	6.3E-01	L27798.1	NT	Streptococcus dysgalactiae (mag) gene, complete cds
8896	21833		3.17	6.3E-01	BE02044.1	EST_HUMAN	601676889F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3959351 5'
9238	22204	35636	0.8	6.3E-01	S62927.1	NT	glycoprotein IIIa (Alu 1 and 3 fusion junction) [human, Genomic Mutant, 300 nt]
9575	22537	35989	0.74	6.3E-01	BF216984.1	EST_HUMAN	601884050F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4102596 5'
9775	22716	36171	2.86	6.3E-01	9827521	NT	Varicella virus, complete genome
9775	22716	36172	2.86	6.3E-01	9827521	NT	Varicella virus, complete genome
10298	23223		0.63	6.3E-01	AE002329.2	NT	Chlamydia muridarum, section 69 of 95 of the complete genome
10792	23713	37215	1.55	6.3E-01	Z73003.1	NT	S.cerevisiae chromosome VII reading frame ORF YGR218w
10895	23815	37322	0.96	6.3E-01	AE000313.1	NT	Escherichia coli K-12 MG1665 section 203 of 400 of the complete genome
11400	24345	37878	1.52	6.3E-01	AA877745.1	EST_HUMAN	nr09h06.s1 NCL_CGAP_Co10 Homo sapiens cDNA clone IMAGE:1161371 3' similar to TR:002916 002916
11663	24589	38173	6.95	6.3E-01	AI904160.1	EST_HUMAN	HLARK :
11754	24682	38261	1.79	6.3E-01	P47003	SWISSPROT	GM-BT043-090289-046 B1043 Homo sapiens cDNA
11915	24795	38387	2.09	6.3E-01	P36073	SWISSPROT	HYPOTHETICAL 13.7 KD PROTEIN IN INO1-IDS2 INTERGENIC REGION
12258	25926	31306	5.44	6.3E-01	9910293	NT	HYPOTHETICAL 15.3 KD PROTEIN IN VMA12-APN1 INTERGENIC REGION
12359	25149		1.81	6.3E-01	AF105227.1	NT	Mus musculus keratin complex 2, gene 6g (K12-6g), mRNA
12570	25845		3.19	6.3E-01	X83528.1	NT	Homo sapiens 3'-phosphoadenosine 5'-phosphosulfate synthetase (PAPS) mRNA, complete cds
5970	19055	32255	2.37	6.2E-01	Q10135	SWISSPROT	C.limicola pscD gene
7737	20692		2.75	6.2E-01	AF022553.1	NT	HYPOTHETICAL 142.5 KD PROTEIN C2E2.02 IN CHROMOSOME I
7791	25690	34117	1.12	6.2E-01	AL021127.2	NT	Mus musculus calcium-sensing receptor related protein 4 (Casr-rs4) mRNA, partial cds
8644	21612	35034	5.41	6.2E-01	H72255.1	EST_HUMAN	Mus musculus chromosome X contig; putative Magee9 gene, Caltractin, NAD(P) steroid dehydrogenase and Zinc finger protein 185
							ys01e08.s1 Soares fetal liver spleen rNFLS Homo sapiens cDNA clone IMAGE:213542 3'

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Table 4
Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9208	22174	35605	0.54	6.2E-01	AF034411.1	NT	Lycopodium esculentum cytosolic Cu,Zn superoxide dismutase (Sod) gene, partial cds; and dehydroquinase
9804	21127	34531	1.87	6.2E-01	BE562987.1	EST_HUMAN	dehydratase/shikimate:NADP oxidoreductase gene, complete cds
9888	22804		2.17	6.2E-01	M24481.1	NT	601338146F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3690010 5'
10438	23360	39849	7.04	6.2E-01	AL161611.2	NT	Human pulmonary surfactant-associated protein SP-B (SFTPB) mRNA, complete cds
10902	23822	37332	5.32	6.2E-01	P27410	SWISSPROT	Arabidopsis thaliana DNA chromosome 4, contig. fragment No. 23
10902	23822	37333	5.32	6.2E-01	P27410	SWISSPROT	NON-STRUCTURAL POLYPEPTIDE [CONTAINS: RNA-DIRECTED RNA POLYMERASE ; THIOL PROTEASE P3C ; HELICASE (2C LIKE PROTEIN); COAT PROTEIN]
2404	15411		5.9	6.1E-01	6678076	NT	NON-STRUCTURAL POLYPEPTIDE [CONTAINS: RNA-DIRECTED RNA POLYMERASE ; THIOL PROTEASE P3C ; HELICASE (2C LIKE PROTEIN); COAT PROTEIN]
5614	18710	31888	1.3	6.1E-01	M59940.1	NT	Mus musculus secreted acidic cytosine rich glycoprotein (Spero), mRNA
7053	20076	33382	3.54	6.1E-01	M84733.1	NT	Caenorhabditis elegans N2 CcMyoD (hlt-1) alternatively spliced genes, complete cds
7053	20075	33383	3.54	6.1E-01	M84733.1	NT	Rat TRPM-2 gene, complete cds
7216	20238	33572	0.7	6.1E-01	AW105653.1	EST_HUMAN	Rat TRPM-2 gene, complete cds
7312	20283	33624	0.84	6.1E-01	Q63769	SWISSPROT	xd50h03.x1 NC1 CGAP_Ov23 Homo sapiens cDNA clone IMAGE:2597237 3' similar to gb:X12871_ma1
8575	21543	34963	3.66	6.1E-01	AF033533.1	NT	HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN A1 (HUMAN); SUSHI REPEAT-CONTAINING PROTEIN SRPX PRECURSOR (DRS PROTEIN) (DOWN-REGULATED BY V-SRC)
9147	22113	35537	1.17	6.1E-01	11431065	NT	Arabidopsis thaliana putative zinc transporter (ZIP1) mRNA, complete cds
9147	22113	35538	1.17	6.1E-01	11431065	NT	Homo sapiens mitogen-activated protein kinase kinase kinase 4 (MAP4K4), mRNA
9770	22711	36165	23.08	6.1E-01	AF236117.1	NT	Homo sapiens mitogen-activated protein kinase kinase kinase 4 (MAP4K4), mRNA
9770	22711	36166	23.08	6.1E-01	AF236117.1	NT	Homo sapiens G-protein coupled receptor EDG-7 mRNA, complete cds
10202	23127	36613	0.99	6.1E-01	AE004452.1	NT	Homo sapiens G-protein coupled receptor EDG-7 mRNA, complete cds
10406	23328	36812	1.53	6.1E-01	AF119117.1	NT	Pseudomonas aeruginosa PA01, section 13 of 629 of the complete genome
11306	24256		1.91	6.1E-01	X74507.1	NT	Homo sapiens dopamine transporter (SLC6A3) gene, complete cds
12041	24916	38510	1.63	6.1E-01	S83182.1	NT	P. sativum mdh mRNA for chloroplast malate dehydrogenase (NADP+)
12041	24916	38511	1.63	6.1E-01	S83182.1	NT	hyaluronan-binding protein=hepatocyte growth factor activator homolog [human, plasma, mRNA, 2408 nt]
12555	25731	31615	2.77	6.1E-01	AB041350.1	NT	hyaluronan-binding protein=hepatocyte growth factor activator homolog [human, plasma, mRNA, 2408 nt]
495	13567	26490	1.41	6.0E-01	D87675.1	NT	Mus musculus Col4a5 mRNA for type IV collagen alpha 5 chain, complete cds
563	13633		2.75	6.0E-01	5802999	NT	Homo sapiens DNA for amyloid precursor protein, complete cds
1364	14398	27369	1.92	6.0E-01	AF065253.1	NT	Homo sapiens adaptor-related protein complex 3, mu 2 subunit (CLA20), mRNA
3828	18688	28770	0.9	6.0E-01	AJ233961.1	NT	Human respiratory syncytial virus strain CH63-53b attachment protein (S) gene, complete cds
							Viral hemorrhagic septicemia virus N1, P, M, G, Nv, L genes, French strain 07-71

Table 4

Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4217	17246		1.61	6.0E-01	AF058895.1	NT	Homo sapiens Notch3 (NOTCH3) gene, exons 26, 27, and 28
4279	17308	30187	0.99	6.0E-01	AB025319.1	NT	Yaba monkey tumor virus DNA, BamH1 restriction fragment E, M and partial C, partial and complete cds
5353	18458	31327	2.14	6.0E-01	P20288	SWISSPROT	D(2) DOPAMINE RECEPTOR
5514	18614	31547	2.22	6.0E-01	AW139713.1	EST_HUMAN	UH-B11-aab-a-10-0-UI.s1 NCL CGAP_Sub3 Homo sapiens cDNA clone IMAGE:2718619 3'
6689	19746	33022	2.66	6.0E-01	U38813.1	NT	Musca domestica insecticide-susceptible strain voltage-sensitive sodium channel mRNA, complete cds
6818	19872	33181	0.67	6.0E-01	Q04912	SWISSPROT	MACROPHAGE-STIMULATING PROTEIN RECEPTOR PRECURSOR (MSP RECEPTOR) (P185-RON)
6988	20211	33539	0.78	6.0E-01	L10234.1	NT	Strongylocentrotus purpuratus kinesin light chain isoform 2 mRNA, complete cds
6988	20211	33540	0.78	6.0E-01	L10234.1	NT	Strongylocentrotus purpuratus kinesin light chain isoform 2 mRNA, complete cds
7577	20539	33898	5.51	6.0E-01	AJ277661.1	NT	Homo sapiens partial LMO1 gene for LIM domain only 1 protein, exon 1
8461	21430	34847	4.55	6.0E-01	P02835	SWISSPROT	SEGMENTATION PROTEIN FUSHI TARAZU
8461	21430	34848	4.55	6.0E-01	P02835	SWISSPROT	SEGMENTATION PROTEIN FUSHI TARAZU
10182	23107	36589	1.84	6.0E-01	AB008193.1	NT	Homo sapiens genes for leukotriene B4 receptor BLT2, leukotriene B4 receptor BLT1, complete cds
10636	23558		1.66	6.0E-01	Q01497	SWISSPROT	PEROXISOMAL MEMBRANE PROTEIN PER9 (PEROXIN-3)
10749	23671		0.46	6.0E-01	BE837779.1	EST_HUMAN	RC2-FN0094-190700-017-d08 FN0094 Homo sapiens cDNA
11878	24760	38345	2.79	6.0E-01	AI420623.1	EST_HUMAN	ff08f07.x1 NCL CGAP_P28 Homo sapiens cDNA clone IMAGE:2085621 3'
12638	25322	31788	1.87	6.0E-01	11421663	NT	Homo sapiens nuclear factor (erythroid-derived 2)-like 3 (NFE2L3), mRNA
12731	25384		2.78	6.0E-01	AA706087.1	EST_HUMAN	z98g05.s1 Scarses fetal_liver_spleen_INFLS_S1 Homo sapiens cDNA clone IMAGE:462776 3'
12918	25777	31522	4.71	6.0E-01	9055303	NT	Mus musculus cGMP-inhibited phosphodiesterase (Pde3a), mRNA
12947	25715		3.4	6.0E-01	BE157617.1	EST_HUMAN	RC1-HT0375-030500-015-033 HT0375 Homo sapiens cDNA
1002	14053	27005	0.97	5.9E-01	U32701.1	NT	Haemophilus influenzae Rd section 16 of 163 of the complete genome
3283	16337	29256	4.95	5.9E-01	AL163267.2	NT	Homo sapiens chromosome 21 segment HS21C067
3283	16337	29257	4.95	5.9E-01	AL163267.2	NT	Homo sapiens chromosome 21 segment HS21C067
4250	17279		4.09	5.9E-01	AF162756.1	NT	Rattus norvegicus cenexin 2 mRNA, partial cds
6609	19667	32943	1.45	5.9E-01	AF065440.2	NT	Homo sapiens low density lipoprotein receptor-related protein II (LRP2) gene, exon 1 and partial cds
7481	20447	33803	2.44	5.9E-01	AB023486.1	NT	Homo sapiens gene for histamine H2 receptor, promoter region and complete cds
8332	21301	34718	0.46	5.9E-01	D90911.1	NT	Synechocystis sp. PCC6803 complete genome, 13/27, 1576593-1719643
8985	21951	35375	0.48	5.9E-01	D12922.1	NT	Legionella pneumophila gene for iron superoxide dismutase, complete cds
9901	22853	36314	0.89	5.9E-01	AF063204.2	NT	Chlamydia trachomatis strain K/UW31/Cx major outer membrane protein (omp1) gene, complete cds

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10273	23198		0.66	5.9E-01	P06463	SWISSPROT	E6 PROTEIN
10548	23470	36965	1.19	5.9E-01	P55284	SWISSPROT	VASCULAR ENDOTHELIAL-CADHERIN PRECURSOR (VE-CADHERIN) (CADHERIN-5)
11031	23995	37523	2.46	5.9E-01	Q8X013	SWISSPROT	THYMIDYLATE KINASE (DTMP KINASE)
11037	24001	37526	49.8	5.9E-01	AF197944.1	NT	Xenopus laevis receptor protein tyrosine phosphatase delta (XPTP-D) mRNA, complete cds
11309	24259	37785	2.49	5.9E-01	AW937175.1	EST_HUMAN	PM1-DT0041-190700-002-h03 DT0041 Homo sapiens cDNA
11528	24467	38021	1.53	5.9E-01	AF064626.1	NT	Mus spretus strain SPRET/El CD48 antigen (Cd48) gene, partial cds
12297	25108	31838	2.43	5.9E-01	L42320.1	NT	Oryctolagus cuniculus alpha 1 anti-trypsin (alpha 1 AT) gene, promoter region
12541	25264		2.86	5.9E-01	AB017705.1	NT	Aspergillus oryzae pyrG gene for orotidine-5-phosphate decarboxylase, complete cds
12740	25390		6.24	5.9E-01	P34926	SWISSPROT	MICROTUBULE-ASSOCIATED PROTEIN 1A [CONTAINS: MAP1 LIGHT CHAIN LC2]
1924	14948	27944	1.28	5.8E-01	P40472	SWISSPROT	SIM1 PROTEIN
2571	15572	28592	1	5.8E-01	7305230	NT	Mus musculus low density lipoprotein B (Ldlb), mRNA
4009	17048	29854	1	5.8E-01	BF695738.1	EST_HUMAN	601852474F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4076131 5'
4542	17565	30452	4.23	5.8E-01	AB090977.1	NT	Vigna radiata mRNA for protein tyrosine phosphatase, complete cds
5448	18550		0.84	5.8E-01	AE002152.1	NT	Ureaplasma urealyticum section 53 of 59 of the complete genome
5609	18705	31862	0.75	5.8E-01	Q10699	SWISSPROT	POTENTIAL 5'-3' EXONUCLEASE
6308	19379	32618	1.82	5.8E-01	D78659.1	EST_HUMAN	HUM500E068 Human placenta polyA+ (TFujiwara) Homo sapiens cDNA clone GEN-500E06 5'
6445	19510	32760	0.73	5.8E-01	D50601.1	NT	Shigella sonnei DNA for 26 ORFs, complete cds
6985	20208		2.55	5.8E-01	S65091.1	NT	cyclic AMP-regulated phosphoprotein [rats, mRNA, 1030 nt]
8219	21188		2.63	5.8E-01	H41571.1	EST_HUMAN	yn91b03.s1 Scores adult brain N2B5HB55Y Homo sapiens cDNA clone IMAGE:175757 3' similar to gb:S78187 M-PHASE INDUCER PHOSPHATASE 2 (HUMAN);
8423	21392	34802	0.59	5.8E-01	A1280051.1	EST_HUMAN	qh85d10.x1 Scores_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1853779 3'
8423	21392	34803	0.59	5.8E-01	A1280051.1	EST_HUMAN	qh85d10.x1 Scores_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1853779 3'
8532	21500	34916	2.57	5.8E-01	P14328	SWISSPROT	SPORE COAT PROTEIN SP96
8532	21500	34917	2.57	5.8E-01	P14328	SWISSPROT	SPORE COAT PROTEIN SP96
9243	22209	35640	9.77	5.8E-01	AJ270774.1	NT	Homo sapiens partial TCF-4 gene for T-cell transcription factor-4, exons 6-11
9323	22288	35718	1.02	5.8E-01	Q27368	SWISSPROT	TRANSCRIPTION FACTOR E2F
9324	22289	35719	0.46	5.8E-01	Q20471	SWISSPROT	PUTATIVE CASEIN KINASE I F46F2.2 IN CHROMOSOME X
9854	22881		0.81	5.8E-01	BF031608.1	EST_HUMAN	601557774F1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:3827298 5'
11334	24284	37808	6.9	5.8E-01	AJ243213.1	NT	Homo sapiens partial 5-HT4 receptor gene, exons 2 to 5
11373	24320		2.89	5.8E-01	BF700092.1	EST_HUMAN	602127577F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4284403 5'
11476	24419		1.61	5.8E-01	BF700092.1	EST_HUMAN	602127577F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4284403 5'
1492	14525	27496	1.11	5.7E-01	P08727	SWISSPROT	APOLIPOPROTEIN A-IV PRECURSOR (APO-AIV)
1492	14525	27497	1.11	5.7E-01	P08727	SWISSPROT	APOLIPOPROTEIN A-IV PRECURSOR (APO-AIV)
3056	16113		0.77	5.7E-01	6756253	NT	Mus musculus plasmacytoma variant translocation 1 (Pvt1), mRNA

Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3237	16292	29214	1.38	5.7E-01	Q9WTJ2	SWISSPROT	PUTATIVE TRANSCRIPTION FACTOR OVO-LIKE 1 (MOV01) (MOV01A)
3515	16561		2.79	5.7E-01	AB033503.1	NT	Populus euramericana peacs-2 mRNA for 1-aminocyclopropane-1-carboxylate synthase, complete cds
3922	16962	29875	1.05	5.7E-01	AF011581.1	NT	Homo sapiens T cell receptor beta chain (BV6S72-BJ1S1) mRNA, partial cds
5213	18222	31097	11.22	5.7E-01	4505050	EST	Homo sapiens lymphocyte antigen 6 complex, locus H (LY6H) mRNA
6490	19555	32805	4.36	5.7E-01	BF035413.1	EST_HUMAN	601454962F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:365674 5'
6869	19922	33218	0.82	5.7E-01	AA194201.1	EST_HUMAN	z38c06.r1 Soares_NIHMPu_S1 Homo sapiens cDNA clone IMAGE:365674 5'
7042	18374	31262	1.3	5.7E-01	AL111440.1	NT	Bovine cilia/retina strain T4 cDNA library under conditions of nitrogen deprivation
8041	20978	34374	2.13	5.7E-01	P00373	SWISSPROT	PYRROLINE-5-CARBOXYLATE REDUCTASE (P50R) (P50 REDUCTASE)
8303	21272		0.51	5.7E-01	AJ251835.1	NT	Mus musculus Kngq1, Lrp5, Mash2, Tapa-1, Tsc4 and Tsc6 genes, alternative transcripts
8723	21691		0.52	5.7E-01	AJ065081.1	EST_HUMAN	HA0895 Human fetal liver cDNA library Homo sapiens cDNA
10159	23084	36580	1.22	5.7E-01	AL161532.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 32
10159	23084	36581	1.22	5.7E-01	AL161532.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 32
10940	23860	37376	0.75	5.7E-01	BF540982.1	EST_HUMAN	602067712F1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:4066610 5'
12252	25078		1.49	5.7E-01	BE175051.1	EST_HUMAN	MR3-HT0736-180700-003-a02 HT0736 Homo sapiens cDNA
1889	14914	27907	1.6	5.6E-01	AF097732.1	NT	Homo sapiens caspase recruitment domain-containing protein (BCL10) gene, complete cds
1889	14914	27908	1.6	5.6E-01	AF097732.1	NT	Homo sapiens caspase recruitment domain-containing protein (BCL10) gene, complete cds
3376	16426	29351	1.53	5.6E-01	AB018283.2	NT	Homo sapiens mRNA for KIAA0740 protein, partial cds
3376	16426	29352	1.53	5.6E-01	AB018283.2	NT	Homo sapiens mRNA for KIAA0740 protein, partial cds
4268	17297	30174	0.77	5.6E-01	D83135.1	NT	Chicken TBP gene, exon8, complete cds
5205	18214	31089	0.93	5.6E-01	BF032377.1	EST_HUMAN	601452855F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3856717 5'
9155	22121	35550	14.66	5.6E-01	AV684703.1	EST_HUMAN	AV684703 GK Hom sapiens cDNA clone GKCF5F05 5'
9155	22121	35551	14.66	5.6E-01	AV684703.1	EST_HUMAN	AV684703 GK Hom sapiens cDNA clone GKCF5F05 5'
9730	22758	36211	1.23	5.6E-01	AB038782.1	NT	Homo sapiens MUC3A gene for intestinal mucin, partial cds
12153	25011		3.4	5.6E-01	BE988280.1	EST_HUMAN	601514007F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3916457 5'
12270	25092	36178	1.73	5.6E-01	AA493535.1	EST_HUMAN	ng75g10 s1 NCL_CGAP_Pr6 Homo sapiens cDNA clone IMAGE:940874 similar to contains element PTR7
12638	18341	31290	1.51	5.6E-01	AL161501.2	NT	repetitive element 1
12662	26340		3.05	5.6E-01	P50505	SWISSPROT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 13
13060	25596		4.96	5.6E-01	BF573829.1	EST_HUMAN	HIGH AFFINITY POTASSIUM TRANSPORTER
13110	25630		1.33	5.6E-01	AA663881.1	EST_HUMAN	602132020F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4271334 5'
1216	14254	27212	0.82	5.6E-01	83939312	NT	ae74b04.s1 Stratiotes alopecuroides brain S11 Homo sapiens cDNA clone IMAGE:969871 3'
2742	15706	28722	5.31	5.5E-01	P03341	SWISSPROT	GAG POLYPROTEIN [CONTAINS: INNER COAT PROTEIN P12; CORE PROTEIN P16; CORE SHELL PROTEIN P30; NUCLEOPROTEIN P10]

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2712	15706	28723	5.31	5.5E-01	P03341	SWISSPROT	GAG POLYPROTEIN [CONTAINS: INNER COAT PROTEIN P12; CORE PROTEIN P16; CORE SHELL PROTEIN P30; NUCLEOPROTEIN P10]
2929	15987	28908	0.78	5.5E-01	5902085	NT	Homo sapiens superkiller viralicidic activity 2 (S. cerevisiae homolog)-like (SKIV2L), mRNA
3079	16136		1.48	5.5E-01	H48219.1	EST_HUMAN	yo16a10.s1 Soares adult brain N2b5HB55Y Homo sapiens cDNA clone IMAGE:178266 3'
3248	16303	29227	4.75	5.5E-01	AF227240.1	NT	Rabbit oral papillomavirus, complete genome
3704	16747	29661	2.24	5.5E-01	P48765	SWISSPROT	FOS-RELATED ANTIGEN-1
5209	18218	31094	1.06	5.5E-01	U69097.1	NT	Bos taurus MHC class II beta-chain BoLA-DIB1 gene, partial cds
7467	20433	33789	0.58	5.5E-01	AF030001.1	NT	Mus musculus major histocompatibility locus class III region:butyrophilin-like protein gene, partial cds; Noich4, PBX2, RAGE, lysophosphatidic acid acyl transferase-alpha, palmitoyl-protein thioesterase 2 (PPT2), CREB-RP, and tenascin X (TNX) genes, complex
7467	20433	33790	0.59	5.5E-01	AF030001.1	NT	Mus musculus major histocompatibility locus class III region:butyrophilin-like protein gene, partial cds; Noich4, PBX2, RAGE, lysophosphatidic acid acyl transferase-alpha, palmitoyl-protein thioesterase 2 (PPT2), CREB-RP, and tenascin X (TNX) genes, complex
7504	20469		0.67	5.5E-01	AB015896.1	NT	Carassius auratus gene for gonadotropin II beta subunit, complete cds
8792	21759	35181	0.86	5.5E-01	A1781766.1	EST_HUMAN	orf62c01.y5 NCI_CGAP_Lu5 Homo sapiens cDNA clone IMAGE:1602336 5'
10125	23051		0.69	5.5E-01	U88415.1	NT	Crimean-Congo hemorrhagic fever virus strain SPV 415/85 nucleoprotein gene, complete cds
10743	23665	37160	0.87	5.5E-01	T05047.1	EST_HUMAN	EST029355 Fetal brain, Stratagene (cat#936206) Homo sapiens cDNA clone HFBQCQ35
146	13249	26178	9.02	5.4E-01	7657266	NT	Homo sapiens KIAA0929 protein Mx2 interacting nuclear target (MINT) homolog (KIAA0929), mRNA
146	13249	26179	9.02	5.4E-01	7657266	NT	Homo sapiens KIAA0929 protein Mx2 interacting nuclear target (MINT) homolog (KIAA0929), mRNA
587	13655	26569	1.34	5.4E-01	AF232006.1	NT	Pseudomonas syringae pv. tomato strain DC3000 AvrE (avrE), HrpW (hrpW), and GsaA (gsaA) genes, complete cds; and unknown genes
587	13655	26570	1.34	5.4E-01	AF232006.1	NT	Pseudomonas syringae pv. tomato strain DC3000 AvrE (avrE), HrpW (hrpW), and GsaA (gsaA) genes, complete cds; and unknown genes
1276	14311	27272	2.99	5.4E-01	AW86087.1	EST_HUMAN	QV4-NN0040-070400-160-c04 NN0040 Homo sapiens cDNA
2116	15133		2.81	5.4E-01	AE002247.2	NT	Chlamydia pneumoniae AF39, section 74 of 84 of the complete genome
2265	15279	28304	2.26	5.4E-01	AJ276682.1	NT	Drosophila melanogaster mRNA for 15.15 beta carotene dioxygenase (beta-diox gene)
5740	18834	32014	0.91	5.4E-01	AW842327.1	EST_HUMAN	PM2-CN0030-030200-003-c10 CN0030 Homo sapiens cDNA
6315	18386	32628	0.8	5.4E-01	AB025017.1	NT	Rattus norvegicus gene for TIS11, complete cds
7226	20248	33582	0.77	5.4E-01	BE868592.2	EST_HUMAN	601660276R1 NIH_MGC 71 Homo sapiens cDNA clone IMAGE:3906090 3'
7558	20521	33877	0.76	5.4E-01	Z21619.1	NT	S. cerevisiae RIB3 gene encoding DBP synthase
7558	20521	33878	0.76	5.4E-01	Z21619.1	NT	S. cerevisiae RIB3 gene encoding DBP synthase

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Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7560	20523	33881	1.78	5.4E-01	Q64428	SWISSPROT	MITOCHONDRIAL TRIFUNCTIONAL ENZYME ALPHA SUBUNIT PRECURSOR (TP-ALPHA) (INCLUDES: LONG-CHAIN ENOYL-COA HYDRATASE ; LONG CHAIN 3-HYDROXYACYL-COA DEHYDROGENASE]
10348	23273		1.93	5.4E-01	BF572536.1	EST_HUMAN	602076548F1 NIH_MGC_62 Homo sapiens cDNA clone IMAGE:4243690 5'
11414	24358	37893	2.19	5.4E-01	P36858	SWISSPROT	NITRATE REDUCTASE [NADPH](NR)
11632	24589	38159	1.82	5.4E-01	AW373694.1	EST_HUMAN	QV4-BT0538-271299-059-104 BT0536 Homo sapiens cDNA
11941	24821	38416	3.29	5.4E-01	Q60675	SWISSPROT	LAMININ ALPHA-2 CHAIN PRECURSOR [LAMININ M CHAIN] (MEROSIN HEAVY CHAIN)
11941	24821	38417	3.29	5.4E-01	Q60675	SWISSPROT	LAMININ ALPHA-2 CHAIN PRECURSOR [LAMININ M CHAIN] (MEROSIN HEAVY CHAIN)
12215	25054		3.88	5.4E-01	AI858398.1	EST_HUMAN	w37g04.x1 NCL_CGAP_Lu11 Homo sapiens cDNA clone IMAGE:2427126 3' similar to gb:M13452 LAMIN A (HUMAN);
517	13588	26508	1.86	5.3E-01	AF019413.1	NT	Homo sapiens HLA class III region containing tenascin X (tenascin-X) gene, partial cds; cytochrome P450 21- hydroxylase (CYP21B), complement component C4 (C4B) G11, helicase (SKI2W), RD, complement factor B (Bf), and complement component C2 (C2) genes.>
2150	15166	28182	0.97	5.3E-01	AF113919.1	NT	Brassica oleracea var. capitata phospholipase D2 (PLD2) gene, complete cds
2150	15166	28183	0.97	5.3E-01	AF113919.1	NT	Brassica oleracea var. capitata phospholipase D2 (PLD2) gene, complete cds
2794	15786	28803	8.62	5.3E-01	4506328	NT	Homo sapiens protein tyrosine phosphatase, receptor-type, zeta polypeptide 1 (PTPRZ1) mRNA
2794	15786	28804	8.62	5.3E-01	4506328	NT	Homo sapiens protein tyrosine phosphatase, receptor-type, zeta polypeptide 1 (PTPRZ1) mRNA
3257	16311	29232	3.25	5.3E-01	AF087658.1	NT	Homo sapiens secreted C-type lectin precursor (LSLCL) gene, complete cds
4239	17268		1.33	5.3E-01	U39687.1	NT	Mycoplasma genitalium section 9 of 51 of the complete genome
5533	18631	31569	2.06	5.3E-01	AI820921.1	EST_HUMAN	zu42h12.j5 Soares ovary tumor NbHOT Homo sapiens cDNA clone IMAGE:740711 5'
5533	18631	31570	2.06	5.3E-01	AI820921.1	EST_HUMAN	zu42h12.j5 Soares ovary tumor NbHOT Homo sapiens cDNA clone IMAGE:740711 5'
5633	18729	31880	0.76	5.3E-01	AA193672.1	EST_HUMAN	zr42g09.r1 Soares_NHMPu_S1 Homo sapiens cDNA clone IMAGE:666112 5'
5633	18729	31891	0.76	5.3E-01	AA193672.1	EST_HUMAN	zr42g09.r1 Soares_NHMPu_S1 Homo sapiens cDNA clone IMAGE:666112 5'
5729	18823	32003	2	5.3E-01	BE645620.1	EST_HUMAN	7e73c12.x1 NCL_CGAP_Pt28 Homo sapiens cDNA clone IMAGE:3288118 3' similar to gb:J02783
5729	18823	32004	2	5.3E-01	BE645620.1	EST_HUMAN	PROTEIN DISULFIDE ISOMERASE PRECURSOR (HUMAN);
9255	22221		1.94	5.3E-01	L01950.2	NT	PROTEIN DISULFIDE ISOMERASE PRECURSOR (HUMAN);
9307	22272	35703	0.76	5.3E-01	BF433956.1	EST_HUMAN	Retidula gorgonias ribulose 1,5-bisphosphate carboxylase (rbcl) gene, partial cds; chloroplast gene for chloroplast product
9307	22272	35704	0.76	5.3E-01	BF433956.1	EST_HUMAN	7q71c12.x1 NCL_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3' similar to contains element MER29 repetitive element ;
9307	22272	35704	0.76	5.3E-01	BF433956.1	EST_HUMAN	7q71c12.x1 NCL_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3' similar to contains element MER29 repetitive element ;

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Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10572	23494	36986	0.74	5.3E-01	A1954210.1	EST_HUMAN	w394b02.x1 NCI CGAP_Mat15 Homo sapiens cDNA clone IMAGE:2551275 3' similar to SW:COXA_HUMAN P20674 CYTOCHROME C OXIDASE POLYPEPTIDE VA PRECURSOR ;
10977	23897	37410	0.7	5.3E-01	11428833	NT	Homo sapiens nucleoporin 214kD (CAIN) (NUP214), mRNA
11886	24767	38354	5.19	5.3E-01	BE688291.1	EST_HUMAN	601339867F1 NIH_MGC_53 Homo sapiens cDNA clone IMAGE:3682168 5'
12144	25775		4.97	5.3E-01	AA916053.1	EST_HUMAN	cg30e05.s1 NCI CGAP_Br7 Homo sapiens cDNA clone IMAGE:1441376 3' similar to gb:J02611
817	13875	26823	16.24	5.2E-01	L20770.1	NT	APOLIPROTEIN D PRECURSOR (HUMAN);
1168	14209	27163	7.88	5.2E-01	Q9WV30	SWISSPROT	Drosophila melanogaster helix-loop-helix mRNA, complete cds
1195	14235	27190	3.01	5.2E-01	AF224492.1	NT	NUCLEAR FACTOR OF ACTIVATED T CELLS 5 (T CELL TRANSCRIPTION FACTOR NFAT5) (NF-AT5)
1903	14927	28191	3.19	5.2E-01	AL163285.2	NT	(REL DOMAIN-CONTAINING TRANSCRIPTION FACTOR NFAT5)
2156	15172	28191	2.36	5.2E-01	AB018263.2	NT	Homo sapiens phospholipid scramblase 1 gene, complete cds
3136	16163	29102	1.57	5.2E-01	U65942.1	NT	Homo sapiens chromosome 21 segment HS21C085
3251	16306		1.14	5.2E-01	D73443.1	NT	Homo sapiens mRNA for KIAA0740 protein, partial cds
3416	16464		1.39	5.2E-01	AL116780.1	NT	Chlamydomonas reinhardtii strain S2838 POMP91A and POMP90A precursor, genes, complete cds
3458	16504	29424	2.72	5.2E-01	AA984165.1	EST_HUMAN	Azotobacter vinelandii lcd gene for isocitrate dehydrogenase, complete cds
3648	16691		1	5.2E-01	AF020269.1	NT	Botrytis cinerea strain T4 cDNA library under conditions of nitrogen deprivation
5180	18189		1.04	5.2E-01	AL163281.2	NT	am77g05.s1 Stragene schizo strain S11 Homo sapiens cDNA clone IMAGE:1616504 3'
5736	18830	32008	1.02	5.2E-01	AA284261.1	EST_HUMAN	Medicago sativa chloroplast malate dehydrogenase precursor (p1mdh) mRNA, nuclear gene encoding chloroplast protein, complete cds
10088	23700	36489	0.84	5.2E-01	X02218.1	NT	Homo sapiens chromosome 21 segment HS21C081
10088	25700	36490	0.84	5.2E-01	X02218.1	NT	zc44d09.T7 Soares_senescent_fibroblasts_NbHSF Homo sapiens cDNA clone IMAGE:325169 3'
10292	23217	36701	0.52	5.2E-01	AA194518.1	EST_HUMAN	Chicken duplicated genes for histone H2A, H4 and a histone H3 gene
10387	23309	36787	1.76	5.2E-01	AF143952.2	NT	Chicken duplicated genes for histone H2A, H4 and a histone H3 gene
13031	25578		6.82	5.2E-01	P18516	SWISSPROT	zq05b09.r1 Stragene muscle 937209 Homo sapiens cDNA clone IMAGE:628793 5'
619	13684	26602	2.34	5.1E-01	M58509.1	NT	Homo sapiens PELOTA (PELOTA) gene, complete cds
649	13715	26636	3.53	5.1E-01	AJ233944.1	NT	RETINOIC ACID RECEPTOR GAMMA (RAR-GAMMA) (RETINOIC ACID RECEPTOR DELTA) (RAR-DELTA)
649	13715	26637	3.53	5.1E-01	AJ233944.1	NT	Human adrenodoxin reductase gene, exons 3 to 12
1660	14692		1.28	5.1E-01	X87885.1	NT	Polyangium vitellinum (strain P1 vt1) 16S rRNA gene
4103	17137	30032	4.81	5.1E-01	A1859495.1	EST_HUMAN	Polyangium vitellinum (strain P1 vt1) 16S rRNA gene
4216	17245	30130	2.99	5.1E-01	P96380	SWISSPROT	R.norvegicus mRNA for mammalian fusca protein
6348	19417	32658	0.57	5.1E-01	BE541068.1	EST_HUMAN	w39b12.x1 NCI CGAP_U11 Homo sapiens cDNA clone IMAGE:2427263 3'
6407	19475		0.83	5.1E-01	AV712326.1	EST_HUMAN	TRANSCRIPTION-REPAIR COUPLING FACTOR (TRCF)
							601063606F1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3460000 5'
							AV712326 DCA Homo sapiens cDNA clone DCAAUF07 5'

Table 4

Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7102	20036	33339	1.52	5.1E-01	R80873.1	EST_HUMAN	y94a09.s1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:146872 3'
8918	21884	35309	0.62	5.1E-01	AW808881.1	EST_HUMAN	QV4-ST0023-160400-172-a01 ST0023 Homo sapiens cDNA
8918	21884	35310	0.62	5.1E-01	AW808881.1	EST_HUMAN	QV4-ST0023-160400-172-a01 ST0023 Homo sapiens cDNA
10043	22970	36437	4.3	5.1E-01	J05412.1	NT	Human regenerating protein (reg) gene, complete cds
10046	22973	36440	3.2	5.1E-01	W22302.1	EST_HUMAN	65B1 Human retina cDNA Tsp509I-cleaved sublibrary Homo sapiens cDNA not directional
10521	23443	36941	0.89	5.1E-01	M94579.1	NT	Human carboxyl ester lipase (CEL) gene, complete cds
12284	25088	38174	2.09	5.1E-01	BF540777.1	EST_HUMAN	602067471F1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:4066744 5'
12368	25709		2.47	5.1E-01	BF030207.1	EST_HUMAN	601556863F1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:3828787 5'
12611	25310		3.62	5.1E-01	BF439982.1	EST_HUMAN	nac51110.x1 NCI_CGAP_Bm23 Homo sapiens cDNA clone IMAGE:3406218 3' similar to contains element TAR1 repetitive element
2144	15161	28176	0.97	5.0E-01	4885552	NT	Homo sapiens postmeiotic segregation increased 2-like 9 (PMS2L9), mRNA
2144	15161	28177	0.97	5.0E-01	4885552	NT	Homo sapiens postmeiotic segregation increased 2-like 9 (PMS2L9), mRNA
2154	15170	28187	2.39	5.0E-01	AF008210.1	NT	Buchnera aphidicola genomic fragment containing (chaperone Hsp60) groEL, DNA biosynthesis initiating protein (dnaA), ATP operon (atpCDGAHFEB), and putative chromosome replication protein (gidA) genes, complete cds; and termination factor Rho (rho) gene>
2154	15170	28188	2.39	5.0E-01	AF008210.1	NT	Buchnera aphidicola genomic fragment containing (chaperone Hsp60) groEL, DNA biosynthesis initiating protein (dnaA), ATP operon (atpCDGAHFEB), and putative chromosome replication protein (gidA) genes, complete cds; and termination factor Rho (rho) gene>
2172	15188		0.91	5.0E-01	AL181533.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 33
3761	16802	29714	0.8	5.0E-01	U55574.1	NT	Mus musculus anti-DNA immunoglobulin light chain IgM mRNA, antibody 363p.138, partial cds
3842	16882	29786	1	5.0E-01	L38483.1	NT	Rattus norvegicus jagged protein mRNA, complete cds
3887	16927	29835	2.74	5.0E-01	AB030101.1	NT	Homo sapiens mRNA for KIAA1184 protein, partial cds
6801	19855		0.64	5.0E-01	BF576199.1	EST_HUMAN	602132642F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4271939 5'
7926	20869	34256	0.66	5.0E-01	AL181549.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 49
7926	20869	34257	0.66	5.0E-01	AL181549.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 49
8875	21842		1.87	5.0E-01	M92304.1	NT	Xenopus laevis smooth muscle beta-tropomyosin mRNA, complete cds
9018	21984	35404	0.59	5.0E-01	BF107848.1	EST_HUMAN	601823950R1 NIH_MGC_79 Homo sapiens cDNA clone IMAGE:4043485 3'
9813	21136	34538	3.16	5.0E-01	BF317212.1	EST_HUMAN	601903871F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4136832 5'
9983	22910	36375	1.31	5.0E-01	P35573	SWISSPROT	GLYCOTEN DEBRANCHING ENZYME (GLYCOGEN DEBRANCHER) [INCLUDES: 4-ALPHA-GLUCANOTRANSFERASE (OLIGO-1,4-1,4-GLUCANTRANSFERASE); AMYLO-1,6-GLUCOSIDASE (DEXTRIN 6-ALPHA-D-GLUCOSIDASE)]
9983	22910	36376	1.31	5.0E-01	P35573	SWISSPROT	GLYCOTEN DEBRANCHING ENZYME (GLYCOGEN DEBRANCHER) [INCLUDES: 4-ALPHA-GLUCANOTRANSFERASE (OLIGO-1,4-1,4-GLUCANTRANSFERASE); AMYLO-1,6-GLUCOSIDASE (DEXTRIN 6-ALPHA-D-GLUCOSIDASE)]

Table 4

Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10756	23678		1.38	5.0E-01	BE689218.1	EST_HUMAN	801445024F1 NIH_MGC. 65 Homo sapiens cDNA clone IMAGE:3849436 5'
12302	25113		6.28	5.0E-01	AF029215.1	NT	Mus musculus MRC OX-2 antigen homolog gene, exons 2-5, and complete cds
13004	25558		2.21	5.0E-01	AL163302.2	NT	Homo sapiens chromosome 21 segment HS21C102
13011	25563		5.6	5.0E-01	O13981	SWISSPROT	NUCLEAR ENVELOPE PROTEIN CUT11
790	13849	26796	2.03	4.9E-01	BF571482.1	EST_HUMAN	602076649F1 NIH_MGC. 62 Homo sapiens cDNA clone IMAGE:4243860 5'
1668	14700	27675	2.37	4.9E-01	AJ243955.1	NT	Xenopus laevis mRNA for c-Jun protein, 1978 BP
1921	14945	27941	0.99	4.9E-01	U40889.1	NT	Cavia porcellus pulmonary surfactant protein A (SP-a) mRNA, complete cds
5480	18580	31491	1.43	4.9E-01	Q61564	SWISSPROT	FIBRILLIN 1 PRECURSOR
6153	19228	32457	2.67	4.9E-01	AF020931.1	NT	Homo sapiens diacylglycerol kinase 3 (DAGK3) gene, exon 10
6153	19228	32458	2.67	4.9E-01	AF020931.1	NT	Homo sapiens diacylglycerol kinase 3 (DAGK3) gene, exon 10
7685	20643	34007	1.69	4.9E-01	AB040051.1	NT	Oryza sativa subsp. japonica mEF-G mRNA for mitochondrial elongation factor G, complete cds
7972	20911	34301	0.7	4.9E-01	Q10808	SWISSPROT	PUTATIVE UNDECAPRENYL-PHOSPHATE ALPHA-N-ACETYLGLUCOSAMINYLTRANSFERASE
7972	20911	34302	0.7	4.9E-01	Q10606	SWISSPROT	PUTATIVE UNDECAPRENYL-PHOSPHATE ALPHA-N-ACETYLGLUCOSAMINYLTRANSFERASE
9341	22306		1.77	4.9E-01	BF209791.1	EST_HUMAN	601874984F1 NIH_MGC. 54 Homo sapiens cDNA clone IMAGE:4102503 5'
9542	22505	35954	0.99	4.9E-01	AW339905.1	EST_HUMAN	hcd90c02.x1 Soares_NFL_I_GBC_S1 Homo sapiens cDNA clone IMAGE:2907266 3' similar to TR:095714
9651	26009		2.64	4.9E-01	10946863	NT	O95714 HERC2 ;
10681	23603	37097	0.86	4.9E-01	AF053980.1	NT	Mus musculus unc13 homolog (C. elegans) 1 (Unc13h1), mRNA
10888	23808	37314	0.57	4.9E-01	X90000.1	NT	Mus musculus adenyl cyclase 1 (Adcy1) cDNA, partial cds
12196	25041		1.41	4.9E-01	AF176912.1	NT	H. sapiens DNA for BCL7A gene and BCL7A/IGH locus fusion
12997	25963		6.43	4.9E-01	AA613562.1	EST_HUMAN	Homo sapiens neurotrophin-1/ β -cell stimulating factor-3 gene, complete cds
5585	18681	31649	8.83	4.8E-01	J02987.1	NT	mq22ef1.s1 NCL_CGAP_Co10 Homo sapiens cDNA clone IMAGE:1144852 3'
5636	19889	33184	0.69	4.8E-01	U92882.1	NT	Saccharomyces cerevisiae sporulation protein (SPO11) gene required for meiotic recombination, complete cds
5846	19899		3.82	4.8E-01	AA659878.1	EST_HUMAN	Mus musculus slow skeletal muscle troponin T (Tnni1) gene, complete cds
7538	20501		1.96	4.8E-01	5031650	NT	nu85f09.e1 NCL_CGAP_Alt1 Homo sapiens cDNA clone IMAGE:1217513
7929	20872	34261	0.78	4.8E-01	AL163209.2	NT	Homo sapiens chromosome 21 segment HS21C009
8037	20974	34369	3.56	4.8E-01	AL161492.2	NT	Homo sapiens chromosome 21 segment HS21C009
8037	20974	34370	3.56	4.8E-01	AL161492.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 4
8237	21208	34611	0.98	4.8E-01	A1820744.1	EST_HUMAN	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 4
9600	22604		0.97	4.8E-01	BE155148.1	EST_HUMAN	y177f10.y5 Soares breast 2NhbBst Homo sapiens cDNA clone IMAGE:154795 5' similar to contains element MER6 repetitive element ;
10368	23291		0.56	4.8E-01	BF558633.1	EST_HUMAN	PM1-HT0350-201299-004-b04 HT0350 Homo sapiens cDNA
11081	24043		1.75	4.8E-01	X83502.1	NT	602184267F1 NIH_MGC. 42 Homo sapiens cDNA clone IMAGE:4300048 5'
							S. cerevisiae ORFs from chromosome X

Table 4

Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
12277	25096		1.65	4.8E-01	AL183227.2	NT	Homo sapiens chromosome 21 segment HS21C027
12503	25737		3.32	4.8E-01	AF227565.1	NT	Trypanosoma cruzi transposon VIP II SIRE repeat region
13098	25786		1.49	4.8E-01	AJ132984.1	NT	Chlamydomonas reinhardtii cop gene, exons 1-8
6684	19721	32996	8.88	4.7E-01	BF217173.1	EST_HUMAN	601883880F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:406387 5'
7241	19976	33273	0.92	4.7E-01	AI204374.1	EST_HUMAN	q772a09.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1755544 3'
8197	21167	34577	0.59	4.7E-01	T11414.1	EST_HUMAN	hbc811 Human pancreatic islet Homo sapiens cDNA clone hbc811 5'end
8197	21167	34578	0.59	4.7E-01	T11414.1	EST_HUMAN	hbc811 Human pancreatic islet Homo sapiens cDNA clone hbc811 5'end
9430	22394	35834	0.57	4.7E-01	6881501	NT	Rattus norvegicus Spermine binding protein (Sbp), mRNA
11193	24148		4.76	4.7E-01	AF102673.1	NT	Influenza A virus isolate h51697 hemagglutinin (HA) gene, partial cds
11422	24366	37901	1.78	4.7E-01	U41069.1	NT	Human collagen alpha2(X) (COL11A2) gene, exons 6 through 16, and partial cds
11613	24551	38111	1.74	4.7E-01	BF529658.1	EST_HUMAN	602043889F1 NCI_OGAP_Brr67 Homo sapiens cDNA clone IMAGE:4181303 5'
11704	24669	38246	1.49	4.7E-01	AW889448.1	EST_HUMAN	RC8-NT0029-240400-011.E08 NT0029 Homo sapiens cDNA
12399	25173		1.53	4.7E-01	BE887763.1	EST_HUMAN	601511333F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3912488 5'
12929	25513		1.38	4.7E-01	BF679515.1	EST_HUMAN	602153926F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4294974 5'
3756	16798	29709	1.53	4.6E-01	BF693300.1	EST_HUMAN	602081103F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4245481 5'
3756	16798	29710	1.53	4.6E-01	BF693300.1	EST_HUMAN	602081103F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4245481 5'
5190	18199		0.93	4.6E-01	M11267.1	NT	Bovine steroid 21-hydroxylase gene (P-450-c21) gene, complete cds
5493	18593	31503	1	4.6E-01	BF313593.1	EST_HUMAN	601900234F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4129472 5'
5493	18593	31504	1	4.6E-01	BF313593.1	EST_HUMAN	601900234F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4129472 5'
5548	18645	31586	3.33	4.6E-01	Q90643	SWISSPROT	INTERFERON REGULATORY FACTOR 3 (IRF-3)
5548	18645	31587	3.33	4.6E-01	Q90643	SWISSPROT	INTERFERON REGULATORY FACTOR 3 (IRF-3)
5625	18721	31880	1.95	4.6E-01	BE734781.1	EST_HUMAN	601568755F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3843637 5'
5639	18735	31897	3.12	4.6E-01	AI247679.1	EST_HUMAN	q159h02.x1 Soares_fetal_liver_spleen_INFLS_S1 Homo sapiens cDNA clone IMAGE:1849011 3' similar to
5639	18735	31898	3.12	4.6E-01	AI247679.1	EST_HUMAN	q159h02.x1 Soares_fetal_liver_spleen_INFLS_S1 Homo sapiens cDNA clone IMAGE:1849011 3' similar to
5647	18743	31909	1.46	4.6E-01	P20050	SWISSPROT	MEIOSIS SPECIFIC PROTEIN HOP1
5730	18824		0.85	4.6E-01	AF212124.1	EST_HUMAN	Andalis schwartz cytochrome b gene, partial cds; mitochondrial gene for mitochondrial product
5821	18911		0.78	4.6E-01	BE817247.1	EST_HUMAN	PMO-BN0260-120600-001-F07 BN0260 Homo sapiens cDNA
6002	19086	32285	0.51	4.6E-01	D26215.1	NT	Unidentified soil bacteria 16S rRNA gene encoding 16S ribosomal RNA
6386	19454	32899	0.92	4.6E-01	AE000894.1	NT	Methanobacterium thermoautotrophicum from bases 1165751 to 1176238 (section 100 of 148) of the complete genome
6881	19933	33231	0.52	4.6E-01	AF115340.1	NT	Bacillus subtilis Bbma (bbma) gene, complete cds

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Table 4
Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6832	20156	33474	1.43	4.6E-01	U62332.1	NT	Emmericella nidulans NEMPA (nempA) gene, mitochondrial gene encoding putative mitochondrial protein, complete cds
6832	20156	33475	1.43	4.6E-01	U62332.1	NT	Emmericella nidulans NEMPA (nempA) gene, mitochondrial gene encoding putative mitochondrial protein, complete cds
7441	25681	33759	0.53	4.6E-01	L07320.1	NT	Murine cytomegalovirus e1 protein gene, complete cds
8001	20940	34333	0.78	4.6E-01	AA483577.1	EST_HUMAN	h04h05.s1 NCI_CGAP_Thy1 Homo sapiens cDNA clone IMAGE:943353 similar to contains Alu repetitive element; contains element L1 repetitive element;
8093	21029		0.53	4.6E-01	AE004031.1	NT	Xylella fastidiosa, section 177 of 228 of the complete genome
8663	21631	35052	13.26	4.6E-01	BF697399.1	EST_HUMAN	602130653F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4287828 5'
9089	22065	35490	0.47	4.6E-01	AA832237.1	EST_HUMAN	co76b08.s1 NCI_CGAP_Kid5 Homo sapiens cDNA clone IMAGE:1572087 3' similar to gb:IM36341 ADP-RIBOSYLATION FACTOR 4 (HUMAN);
9099	22065	35491	0.47	4.6E-01	AA832237.1	EST_HUMAN	co76b08.s1 NCI_CGAP_Kid5 Homo sapiens cDNA clone IMAGE:1572087 3' similar to gb:IM36341 ADP-RIBOSYLATION FACTOR 4 (HUMAN);
9656	22599	36048	0.99	4.6E-01	P55202	SWISSPROT	ATRIAL NATRIURETIC PEPTIDE RECEPTOR B PRECURSOR (ANP-B) (ANPRB) (GC-B) (GUANYLATE CYCLASE)
9656	22599	36049	0.99	4.6E-01	P55202	SWISSPROT	ATRIAL NATRIURETIC PEPTIDE RECEPTOR B PRECURSOR (ANP-B) (ANPRB) (GC-B) (GUANYLATE CYCLASE)
10024	22951	36418	0.89	4.6E-01	AF162283.1	NT	Glycine max acetyl-CoA carboxylase (accB-1) gene, complete cds; nuclear gene for chloroplast product
10024	22951	36419	0.89	4.6E-01	AF162283.1	NT	Glycine max acetyl-CoA carboxylase (accB-1) gene, complete cds; nuclear gene for chloroplast product
10335	23259	36736	1.62	4.6E-01	A1915634.1	EST_HUMAN	wg73e12.x1 Soares_NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:2370768 3'
10335	23259	36737	1.62	4.6E-01	A1915634.1	EST_HUMAN	wg73e12.x1 Soares_NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:2370768 3'
11335	24285		2.29	4.6E-01	P98183	SWISSPROT	PUTATIVE VITELLOGENIN RECEPTOR PRECURSOR (VL)
11343	24293	37818	4.94	4.6E-01	BE185449.1	EST_HUMAN	IL5-HT0730-100500-075-g05 HT0730 Homo sapiens cDNA
11343	24293	37819	4.94	4.6E-01	BE185449.1	EST_HUMAN	IL5-HT0730-100500-075-g05 HT0730 Homo sapiens cDNA
11445	24398	37830	3.88	4.6E-01	BE272325.1	EST_HUMAN	601126088F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:2989865 5'
11789	23954	37476	4.41	4.6E-01	AF013369.1	NT	Human thiopurine methyltransferase (TPMT) gene, exon 10 and complete cds
11789	23954	37477	4.41	4.6E-01	AF013369.1	NT	Human thiopurine methyltransferase (TPMT) gene, exon 10 and complete cds
12449	25208		1.69	4.6E-01	D53316.1	EST_HUMAN	HUM105F03B Clontech human fetal brain polyA+ mRNA (#5635) Homo sapiens cDNA clone GEN-105F03 5'
1718	14748		0.92	4.9E-01	BE511420.1	EST_HUMAN	601142105F1 NIH_MGC_14 Homo sapiens cDNA clone IMAGE:3505993 5'
1926	14950	27946	1.34	4.9E-01	AE001931.1	NT	Deinococcus radiodurans R1 section 68 of 229 of the complete chromosome 1
1926	14950	27947	1.34	4.9E-01	AE001931.1	NT	Deinococcus radiodurans R1 section 68 of 229 of the complete chromosome 1

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Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2881	15940	28857	5.36	4.5E-01	AA877086.1	EST_HUMAN	zj55d02.s1 Soares fetal liver spleen _INFLS_S1 Homo sapiens cDNA clone IMAGE:454179 3'
3328	16379	29300	3.85	4.5E-01	Q05793	SWISSPROT	BASEMENT MEMBRANE-SPECIFIC HEPARAN SULFATE PROTEOGLYCAN CORE PROTEIN PRECURSOR (HSPG) (PERLECAN) (PLC)
3389	16438	29384	1.62	4.5E-01	AF126378.1	NT	Mus musculus DNA polymerase epsilon catalytic subunit (Pole) gene, exons 2 through 12
4060	17096		1.23	4.5E-01	Q28247	SWISSPROT	COLLAGEN ALPHA 5(IV) CHAIN
4101	17135	30030	1.12	4.5E-01	A1708908.1	EST_HUMAN	as96e09.x1 Barslead actin HPLRB6 Homo sapiens cDNA clone IMAGE:2353480 3'
4205	18325		4.08	4.5E-01	AW873495.1	EST_HUMAN	hs80g02.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:3041810 3'
4980	17995	30884	1.09	4.5E-01	BE963445.2	EST_HUMAN	601657225R1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:3866023 3'
5928	18724	31885	1.3	4.5E-01	AW608814.1	EST_HUMAN	QV2-PT0012-140100-031-c09 PT0012 Homo sapiens cDNA
6760	19814		1.74	4.5E-01	Q00956	SWISSPROT	COAT PROTEIN
7644	20604	33969	0.93	4.5E-01	M37036.1	NT	Rat nucleolar proteins B23.1 and B23.2
7867	20811	34188	2.64	4.5E-01	A1858849.1	EST_HUMAN	w32602.x1 NCL_CGAP_U11 Homo sapiens cDNA clone IMAGE:2426618 3' similar to TR:Q92923 Q92923
7991	20930	34325	0.81	4.5E-01	P50070	SWISSPROT	SW/ISNF COMPLEX 170 KDA SUBUNIT. ;
8650	21618		0.87	4.5E-01	M32861.1	NT	D.melanogaster Shaw2 protein mRNA, complete cds
8746	21714	35137	3.86	4.5E-01	A1648598.1	EST_HUMAN	ts58g11.x1 NCL_CGAP_Ov35 Homo sapiens cDNA clone IMAGE:2292644 3'
8905	21871	35297	0.74	4.5E-01	Q52728	SWISSPROT	POLY-BETA-HYDROXYBUTYRATE POLYMERASE (POLY(B-HYDROXYBUTYRATE) POLYMERASE) (PHB POLYMERASE) (PHB SYNTHASE) (POLY(B-HYDROXYALKANOATE) POLYMERASE) (PHA POLYMERASE) (PHA SYNTHASE) (POLYHYDROXYALKANOIC ACID SYNTHASE)
9133	22099		1.72	4.5E-01	11444786	NT	Homo sapiens hypothetical protein DKFZp547G183 (DKFZp547G183), mRNA
9351	22316	35742	0.78	4.5E-01	AE000218.1	NT	Escherichia coli K-12 MG1655 section 108 of 400 of the complete genome
10300	23225		0.89	4.5E-01	9830816	NT	Bombyx mori nuclear polyhedrosis virus, complete genome
10861	23781	37281	26.2	4.5E-01	M86006.1	EST_HUMAN	EST02531 Fetal brain, Striatum (cat8938206) Homo sapiens cDNA clone HFBCY17
10881	23781	37282	26.2	4.5E-01	M86006.1	EST_HUMAN	EST02531 Fetal brain, Striatum (cat8938206) Homo sapiens cDNA clone HFBCY17
11212	24165	37895	2.3	4.5E-01	AW591271.1	EST_HUMAN	xc14h01.x1 NCL_CGAP_U13 Homo sapiens cDNA clone IMAGE:2703985 3' similar to SW:INT6_MOUSE
12165	25955		5.3	4.5E-01	BE871461.1	EST_HUMAN	Q64252 VIRAL INTEGRATION SITE PROTEIN INT-6. [1];
12949	28144		1.48	4.5E-01	O18638	SWISSPROT	601449201F1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3852981 5'
12452	25211		1.54	4.5E-01	AJ132045.1	NT	OUT AT FIRST PROTEIN
12891	25478		8.22	4.5E-01	11422099	NT	Theileria annulata shAT2 gene
2052	15071		2.23	4.5E-01	6680503	NT	Homo sapiens testis-specific kinase 2 (TESK2), mRNA
2398	15405	28430	7.02	4.5E-01	P49765	SWISSPROT	Mus musculus integral membrane-associated protein 1 (Itmap1), mRNA VASCULAR ENDOTHELIAL GROWTH FACTOR B PRECURSOR (VEGF-B) (VEGF RELATED FACTOR)

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3326	16377	29298	1.36	4.4E-01	AF058790.1	NT	Rattus norvegicus SynGAP-b mRNA, complete cds
3326	16377	29299	1.36	4.4E-01	AF058790.1	NT	Rattus norvegicus SynGAP-b mRNA, complete cds
3330	16381	29302	1.9	4.4E-01	BF056726.1	EST_HUMAN	791d02.yt NCL_CGAP_Bn16 Homo sapiens cDNA clone IMAGE:3393795 5'
4282	17291		1.75	4.4E-01	BE378707.1	EST_HUMAN	601237139F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3609393 5'
5494	18594	31505	1.63	4.4E-01	P04929	SWISSPROT	HISTIDINE-RICH GLYCOPROTEIN PRECURSOR
5494	18594	31508	1.63	4.4E-01	P04929	SWISSPROT	HISTIDINE-RICH GLYCOPROTEIN PRECURSOR
5772	18864	32045	1.77	4.4E-01	S65019.1	NT	mucin [rats, Sprague-Dawley, sulfur-dioxide-treated tracheal epithelium, mRNA Partial, 390 nt]
5780	18882	32064	1.82	4.4E-01	AV720408.1	EST_HUMAN	AV720408 GLC Homo sapiens cDNA clone GLCSC12 5'
6064	19145	32356	1.42	4.4E-01	A198413.1	EST_HUMAN	q162h11.x1 NCL_CGAP_Bn25 Homo sapiens cDNA clone IMAGE:1861125 3' similar to TR:Q29168 Q29168
6064	19146	32357	1.42	4.4E-01	A198413.1	EST_HUMAN	q162h11.x1 NCL_CGAP_Bn25 Homo sapiens cDNA clone IMAGE:1861125 3' similar to TR:Q29168 Q29168
6368	19436	32880	1.9	4.4E-01	AW080795.1	EST_HUMAN	UNKNOWN PROTEIN ; x227e08.x1 NCL_CGAP_C018 Homo sapiens cDNA clone IMAGE:2585510 3' similar to TR:O95154 O95154 AFLATOXIN B1-ALDEHYDE REDUCTASE ; aa85d11.s1 Stratagene schizo brain S11 Homo sapiens cDNA clone IMAGE:970965 3' similar to gb:M16038
6462	19527		1.17	4.4E-01	AA776132.1	EST_HUMAN	TYROSINE-PROTEIN KINASE LYN (HUMAN); Helicobacter pylori 26695 section 49 of 134 of the complete genome
7627	20587	33950	0.95	4.4E-01	AE000571.1	NT	S. tuberosum mRNA for induced stolon tip protein (partial)
8173	21143		12.58	4.4E-01	Z11679.1	NT	Helicobacter pylori 26695 section 49 of 134 of the complete genome
9115	22081	35509	0.74	4.4E-01	AA056427.1	EST_HUMAN	269a03.s1 Stratagene cdon (#637204) Homo sapiens cDNA clone IMAGE:509838 3'
9506	22469	35913	0.72	4.4E-01	AF112540.1	NT	HIV-1 isolate 08107v8 from USA, envelope glycoprotein (env) gene, partial cds
9538	22501	35949	0.56	4.4E-01	AW812578.1	EST_HUMAN	h105c08.x1 NCL_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2954222 3' similar to SW:MSH6_HUMAN P52701 DNA MISMATCH REPAIR PROTEIN MSH6 ;
9645	22589	36038	1.21	4.4E-01	O62838	SWISSPROT	ZINC FINGER X-CHROMOSOMAL PROTEIN
10321	23245	36725	2.1	4.4E-01	A1268650.1	EST_HUMAN	q339f09.x1 NCL_CGAP_Lu5 Homo sapiens cDNA clone IMAGE:1910921 3'
10322	23248		3.91	4.4E-01	P28922	SWISSPROT	GLYCOPROTEIN B PRECURSOR (GLYCOPROTEIN 14)
10457	23378	36872	5.07	4.4E-01	P35590	SWISSPROT	TYROSINE-PROTEIN KINASE RECEPTOR TIE-1 PRECURSOR
10740	23662	37156	1.27	4.4E-01	S78404.1	NT	beta-HKA=H.K-ATPase beta-subunit [rats, Genomic, 8983 nt, segment 2 of 2]
10740	23662	37157	1.27	4.4E-01	S78404.1	NT	beta-HKA=H.K-ATPase beta-subunit [rats, Genomic, 8983 nt, segment 2 of 2]
12432	25198	31824	5.76	4.4E-01	S76404.1	NT	Mus musculus sodium channel, type X, alpha polypeptide (Scn10a), mRNA
12861	25485	31727	2.83	4.4E-01	9627742	NT	Autographa californica nucleopolydnavirus, complete genome
12867	25535		1.45	4.4E-01	P54725	SWISSPROT	UV EXCISION REPAIR PROTEIN RAD23 HOMOLOG A (HHR23A)
411	13484	28419	2.49	4.3E-01	AF155218.1	NT	Callithrix jacchus MW/LW opsin gene, upstream flanking region
411	13484	28420	2.49	4.3E-01	AF155218.1	NT	Callithrix jacchus MW/LW opsin gene, upstream flanking region
1607	14639	27616	0.98	4.3E-01	AW866550.1	EST_HUMAN	QV4-SN0024-200400-183-b01 SN0024 Homo sapiens cDNA

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2883	15942		1.83	4.3E-01	AW935289.1	EST_HUMAN	CM2-DT0003-010200-077-c01 DT0003 Homo sapiens cDNA
3073	19130	29042	0.94	4.3E-01	AW999477.1	EST_HUMAN	MRO-BN0070-270300-008-g04 BN0070 Homo sapiens cDNA
4178	17209	30095	1.32	4.3E-01	J00306.1	NT	Human somatostatin 1 gene and flanks
4435	13484	26419	1.63	4.3E-01	AF155218.1	NT	Callitrix jacchus MW/LW opsin gene, upstream flanking region
4435	13484	26420	1.63	4.3E-01	AF155218.1	NT	Callitrix jacchus MW/LW opsin gene, upstream flanking region
5154	18164		1.17	4.3E-01	9635250	NT	Xestia c-nigrum granulovirus, complete genome
5291	18296	31157	1.16	4.3E-01	BE780182.1	EST_HUMAN	601488030F1 NIH_MGC_87 Homo sapiens cDNA clone IMAGE:3871255 5'
5438	18540	31449	0.89	4.3E-01	P48634	SWISSPROT	LARGE PROLINE-RICH PROTEIN BAT2 (HLA-B-ASSOCIATED TRANSCRIPT 2)
5438	18540	31450	0.89	4.3E-01	P48634	SWISSPROT	LARGE PROLINE-RICH PROTEIN BAT2 (HLA-B-ASSOCIATED TRANSCRIPT 2)
5960	19075	32273	1.5	4.3E-01	BE181655.1	EST_HUMAN	QV1-HT0638-070500-191-d08 HT0638 Homo sapiens cDNA
6010	19063	32293	1.93	4.3E-01	AF179825.1	NT	Salmiit sclureus olfactory receptor (SSC186) gene, partial cds
6866	19919	33214	4	4.3E-01	AJ001678.1	NT	Ootumix columbix japonica fnG gene
7049	20071		0.86	4.3E-01	O33367	SWISSPROT	DNA GYRASE SUBUNIT B
7682	20622		1.83	4.3E-01	BF348001.1	EST_HUMAN	602023134F NCI_CGAP_Bm67 Homo sapiens cDNA clone IMAGE:4158286 5'
8116	21053		0.82	4.3E-01	M58643.1	NT	Human lipoprotein associated coagulation inhibitor (LACI) gene, exon 2
8770	21737		2.56	4.3E-01	U97040.1	NT	Methanococcus voltae flagella-related protein C-1 (flaC-flaI) genes, complete cds
9810	22614	36066	1.04	4.3E-01	Y14604.1	NT	Escherichia coli rcsV gene
10084	23011	36483	1.88	4.3E-01	AW630048.1	EST_HUMAN	hh74e10.y1 NCI_CGAP_GU1 Homo sapiens cDNA clone IMAGE:2968554 5'
10084	23011	36484	1.88	4.3E-01	AW630048.1	EST_HUMAN	hh74e10.y1 NCI_CGAP_GU1 Homo sapiens cDNA clone IMAGE:2968554 5'
10689	23511	37005	0.85	4.3E-01	AW170559.1	EST_HUMAN	xn63e05.x1 Soares_NHGC_cervical_tumor Homo sapiens cDNA clone IMAGE:2698400 3' similar to
10879	23799	37301	0.46	4.3E-01	H65292.1	EST_HUMAN	TR-000189 000189 MU-ADAPTIN-RELATED PROTEIN 2 ;
11277	20178	33603	1.55	4.3E-01	AF075629.1	NT	yr45b05.s1 Soares fetal liver spleen 1NLS Homo sapiens cDNA clone IMAGE:208209 3'
11539	24480	38031	1.77	4.3E-01	AW993658.1	EST_HUMAN	Equus caballus microsatellite LEX027
11539	24480	38032	1.77	4.3E-01	AW993658.1	EST_HUMAN	RC3-BN0034-290200-013-c12 BN0034 Homo sapiens cDNA
13055	25592		2.24	4.3E-01	AJ003022.1	NT	RC3-BN0034-290200-013-c12 BN0034 Homo sapiens cDNA
1360	15865	27365	1.77	4.2E-01	Q39102	SWISSPROT	Streptomyces coelicolor whiH gene
3623	16666	29580	4.43	4.2E-01	AE003947.1	NT	CELL DIVISION PROTEIN FTSH HOMOLOG PRECURSOR
3651	16594	29609	1.04	4.2E-01	AJ280338.1	EST_HUMAN	Xyella fastidiosa, section 93 of 229 of the complete genome
3724	18324		1.22	4.2E-01	N81203.1	EST_HUMAN	q194b01.x1 Soares_NHMPu_S1 Homo sapiens cDNA clone IMAGE:1879945 3'
3893	16933	29843	0.69	4.2E-01	AW835527.1	EST_HUMAN	788IE1 fetal brain cDNA Homo sapiens cDNA clone 788IE-1-K similar to R07879, Z40498
4007	17046	29953	1.72	4.2E-01	Q04886	SWISSPROT	QV0-L T0015-180200-127-h01 LT0015 Homo sapiens cDNA
							SOX-8 PROTEIN
							h189h01.s1 NCI_CGAP_P10 Homo sapiens cDNA clone IMAGE:987777 similar to gb:M33600 HLA CLASS II HISTOCOMPATIBILITY ANTIGEN, DR-1 BETA CHAIN (HUMAN);
4726	17746	30837	4.9	4.2E-01	AA534093.1	EST_HUMAN	

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4820	17837	30735	3.62	4.2E-01	R13467.1	EST_HUMAN	y77601.r1 Soares infant brain 1N1B Homo sapiens cDNA clone IMAGE:28278 5'
5801	18893	32076	1.38	4.2E-01	BF242055.1	EST_HUMAN	601879721F1 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:4108493 5'
5876	18965	32156	1.23	4.2E-01	AW654162.1	EST_HUMAN	RC3-CT0254-060-009-g04 CT0254 Homo sapiens cDNA
6329	19399	32841	0.91	4.2E-01	AL163247.2	NT	Homo sapiens chromosome 21 segment HS21C047
7139	20115	33428	9.39	4.2E-01	AU158472.1	EST_HUMAN	AU158472 PLACE2 Homo sapiens cDNA clone PLACE2000470 3'
7139	20115	33428	9.39	4.2E-01	AU158472.1	EST_HUMAN	AU158472 PLACE2 Homo sapiens cDNA clone PLACE2000470 3'
7207	25677	33563	5.51	4.2E-01	S82504.1	NT	Breast-breast cancer gene (rats, W.F. spleen, Genomic, 419 nt, segment 2 of 2)
7300	20272	33607	5.9	4.2E-01	AL161547.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 47
7822	20770	34146	0.52	4.2E-01	AL163252.2	NT	Homo sapiens chromosome 21 segment HS21C052
8325	21294	34708	2.56	4.2E-01	AW957448.1	EST_HUMAN	EST369413 MAGE resequences, MAGE Homo sapiens cDNA
8325	21294	34709	2.56	4.2E-01	AW957448.1	EST_HUMAN	EST369413 MAGE resequences, MAGE Homo sapiens cDNA
8548	21516	34934	0.49	4.2E-01	4758039	NT	Homo sapiens cytochrome c oxidase subunit Vlc (COX8C), nuclear gene encoding mitochondrial protein, mRNA
10329	23253		0.72	4.2E-01	AA705007.1	EST_HUMAN	285507.s1 Soares fetal liver spleen_INFLS_S1 Homo sapiens cDNA clone IMAGE:462649 3'
10541	23463	36958	0.43	4.2E-01	AF181854.1	NT	Leassa virus strain 803213 glycoprotein precursor and nucleoprotein genes, complete cds
10862	23782	37283	1.53	4.2E-01	AW863666.1	EST_HUMAN	MF3-SN0010-280300-103-n07 SN0010 Homo sapiens cDNA
11382	24329	37558	2.39	4.2E-01	AB023489.1	NT	Oryzias latipes OIGC7 mRNA for membrane guanylyl cyclase, complete cds
11723	24609	38185	1.77	4.2E-01	BE966485.2	EST_HUMAN	601660352R1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3906085 3'
13090	25618		1.4	4.2E-01	A392837.1	EST_HUMAN	ig10c05.x1 NCI_CGAP_CLL1 Homo sapiens cDNA clone IMAGE:2108360 3'
1096	14140	27090	1.96	4.1E-01	A1905481.1	EST_HUMAN	RC-BT091-210198-142 BT091 Homo sapiens cDNA
1105	14149	27099	1.33	4.1E-01	AV705243.1	EST_HUMAN	AV705243 ADB Homo sapiens cDNA clone ADBAHF08 5'
1105	14149	27100	1.33	4.1E-01	AV705243.1	EST_HUMAN	AV705243 ADB Homo sapiens cDNA clone ADBAHF08 5'
2722	15716	28734	1.43	4.1E-01	7705283	NT	Homo sapiens anaphase-promoting complex subunit 7 (APC7), mRNA
2951	16008	28932	2.07	4.1E-01	AL161536.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 36
2951	16008	28933	2.07	4.1E-01	AL161536.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 36
3314	16367	29287	0.69	4.1E-01	AA906344.1	EST_HUMAN	g194b08.s1 Soares_NFL_I_GBC_S1 Homo sapiens cDNA clone IMAGE:1505943 3'
4303	17332	30212	2.54	4.1E-01	AJ249207.1	NT	Rhodococcus sp. AD45_IsoB, IsoC, IsoD, IsoE and IsoF genes
4334	17362		0.84	4.1E-01	AA909257.1	EST_HUMAN	oms33d02.s1 Soares_NFL_I_GBC_S1 Homo sapiens cDNA clone IMAGE:1542819 3'
4694	17715	30610	1.71	4.1E-01	AV747880.1	EST_HUMAN	AV747880 NPC Homo sapiens cDNA clone NPCBDF10 5'
6103	19182	32401	4.57	4.1E-01	BF681393.1	EST_HUMAN	602156560F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4297319 5'
6877	19930	33227	0.58	4.1E-01	U02298.1	NT	Mus musculus NIH 3T3 chemokine rantes (Scyts) gene, complete cds
7666	20825	33989	2.96	4.1E-01	U07535.1	NT	Methanococcus jannaschii section 77 of 150 of the complete genome
8370	21339	34750	1.16	4.1E-01	BF574604.1	EST_HUMAN	602133281F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4288238 5'

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9445	22409	35846	1.45	4.1E-01	6755521	NT	Mus musculus signaling intermediate in Toll pathway-evolutionarily conserved (Slpec-pending), mRNA
9823	22807		0.58	4.1E-01	AF160597.1	NT	Vallato gymnocaudus Vgym560 cytochrome b (cytb) gene, complete cds; mitochondrial gene for mitochondrial product
10626	23548		1.18	4.1E-01	AL139076.2	NT	Campylobacter jejuni NCTC11168 complete genome, segment 3/8
10775	23696	37194	1.1	4.1E-01	AV649579.1	EST_HUMAN	AV649579 GLC Homo sapiens cDNA clone GLCBVD12.3
10873	23793	37294	0.51	4.1E-01	P18584	SWISSPROT	PROBABLE SERINE PROTEASE DO-LIKE PRECURSOR (59 KDA IMMUNOGENIC PROTEIN) (SK59)
10873	23793	37295	0.51	4.1E-01	P18584	SWISSPROT	PROBABLE SERINE PROTEASE DO-LIKE PRECURSOR (59 KDA IMMUNOGENIC PROTEIN) (SK59)
10943	23863		2.1	4.1E-01	BF349382.1	EST_HUMAN	CM2-HT0137-200989-010-e08 HT0137 Homo sapiens cDNA
11188	24144	37677	39.55	4.1E-01	X58700.1	NT	Zea mays ZMPMS2 gene for 19 kDa zein protein
12751	25931		3	4.1E-01	D87875.1	NT	Homo sapiens DNA for amyloid precursor protein, complete cds
142	18833		0.65	4.1E-01	AW847123.1	EST_HUMAN	RC2-CT0201-290899-012-d10 CT0201 Homo sapiens cDNA
1040	14065	27036	0.71	4.0E-01	8404656	NT	Laqueus rubellus mitochondrion, complete genome
1342	14377	27346	1.17	4.0E-01	AF203478.1	NT	Drosophila melanogaster Dalmation (dmt) mRNA, complete cds
1481	14514		5.11	4.0E-01	6679258	NT	Mus musculus platelet derived growth factor receptor, beta polypeptide (Pdgfrb), mRNA
2022	16883	28064	1.12	4.0E-01	Z96933.1	NT	Ascaris lumbricoides msc2 gene
2022	16883	28065	1.12	4.0E-01	Z96933.1	NT	Ascaris lumbricoides msc2 gene
2167	16183	28203	1.09	4.0E-01	AE001931.1	NT	Deinococcus radiodurans R1 section 68 of 229 of the complete chromosome 1
2167	16183	28204	1.09	4.0E-01	AE001931.1	NT	Deinococcus radiodurans R1 section 68 of 229 of the complete chromosome 1
2816	13248	26176	1.27	4.0E-01	6678490	NT	Mus musculus ubiquitin-protein ligase e3 componen n-recoglin (Ubr1), mRNA
2979	16037	28959	1.34	4.0E-01	AL163280.2	NT	Homo sapiens chromosome 21 segment HS21C080
2979	16037	28960	1.34	4.0E-01	AL163280.2	NT	Homo sapiens chromosome 21 segment HS21C080
3709	16752	29668	2.32	4.0E-01	AF069903.1	NT	Streptococcus pneumoniae Y1C (y1C), Y1D (y1D), penicillin-binding protein 2x (pbp2x), and undecaprenyl-phosphate-UDP-MurNAc-pentapeptide phospho-MurNAc-pentapeptide transferase (mraY) genes, complete cds
3840	16880	29783	3.28	4.0E-01	AJ277511.1	NT	Ovis aries partial JD2 gene for T cell receptor delta chain (TCRDJ2), exon 1
3840	16880	29784	3.28	4.0E-01	AJ277511.1	NT	Ovis aries partial JD2 gene for T cell receptor delta chain (TCRDJ2), exon 1
4855	17872		9.36	4.0E-01	Q31849	SWISSPROT	NADH-PLASTOQUINONE OXIDOREDUCTASE CHAIN 5; CHLOROPLAST
6015	19098	32299	1.14	4.0E-01	AW970610.1	EST_HUMAN	EST382891 MAGE resequences, MAGEK Homo sapiens cDNA
6226	19300	32533	0.51	4.0E-01	BF243741.1	EST_HUMAN	60187783F1 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:4106221 5'
6578	19638	32904	0.92	4.0E-01	P27285	SWISSPROT	STRUCTURAL POLYPEPTIDE (P130) [CONTAINS: COAT PROTEIN C; SPIKE GLYCOPROTEINS E3, E2 AND E1; 6 KD PEPTIDE]
8345	21314	34729	0.8	4.0E-01	AB016625.1	NT	Homo sapiens OCTN2 gene, complete cds
9360	22325	35753	0.98	4.0E-01	AA323289.1	EST_HUMAN	EST26066 Cerebellum II Homo sapiens cDNA 5' end similar to EST containing Alu repeat

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Single Exon Probes Expressed In Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
11895	24776		2	4.0E-01	BF030282.1	EST_HUMAN	601658283F1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:3828092 5'
12030	24906		1.75	4.0E-01	L76080.1	NT	Synechocystis sp. PCC 9413 transposase gene, complete cds
12448	25793		3.03	4.0E-01	AL163300.2	NT	Homo sapiens chromosome 21 segment HS21C100
12868	25536		1.6	4.0E-01	P36049	SWISSPROT	HYPOTHEICAL 49.7 KD PROTEIN IN GIN2-STE3 INTERGENIC REGION
1378	14412	27383	1.65	3.9E-01	AF206618.1	NT	Gorilla gorilla carboxyl-ester lipase (CEL) gene, complete cds
2650	15647	28870	3.62	3.9E-01	AB033019.1	NT	Homo sapiens mRNA for KIAA1183 protein, partial cds
2716	15710	28726	4.28	3.9E-01	X82032.1	NT	H. sapiens B-myb gene
2716	15710	28727	4.26	3.9E-01	X82032.1	NT	H. sapiens B-myb gene
3113	16170	29080	4.56	3.9E-01	AJ225896.1	NT	Sinorhizobium meliloti egl, syrB2, cys3 genes and orf3
4106	17140	30035	1.25	3.9E-01	BF582611.1	EST_HUMAN	761d01.x1 NCI_CGAP_B16 Homo sapiens cDNA clone IMAGE:3339169 3'
5027	18041	30924	1.74	3.9E-01	BE728667.1	EST_HUMAN	601563948F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3833699 5'
6042	19124	32329	5.65	3.9E-01	BF208036.1	EST_HUMAN	601862362F1 NIH_MGC_53 Homo sapiens cDNA clone IMAGE:4082055 5'
6411	19479	32726	0.66	3.9E-01	U82695.2	NT	Homo sapiens zinc finger protein 92 (ZFP92), expressed-Xq28STS protein (XQ28ORF), and biglycan (BGN) genes, complete cds; and plasma membrane calcium ATPase isoform 3 (PMCA3) gene, partial cds
8286	21255	34664	0.8	3.9E-01	U79415.1	NT	Homo sapiens prepro dipeptidyl peptidase I (DPP-I) gene, complete cds
9213	22179	35610	0.73	3.9E-01	AW177011.1	EST_HUMAN	CM3-CT0105-170898-004-008 CT0105 Homo sapiens cDNA
9222	22188		0.68	3.9E-01	BF348634.1	EST_HUMAN	602019844F1 NCI_CGAP_Bm67 Homo sapiens cDNA clone IMAGE:4155322 5'
9590	22552	36003	1.41	3.9E-01	AW196888.1	EST_HUMAN	xn86d04.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2701351 3' similar to TR:Q94821 O94821 KIAA0713 PROTEIN
9903	22855	36316	1.83	3.9E-01	AI837337.1	EST_HUMAN	wp76a02.x1 NCI_CGAP_Bm25 Homo sapiens cDNA clone IMAGE:2467658 3' similar to SW:RFX5_HUMAN P48382 BINDING REGULATORY FACTOR
10237	23162	36650	2.99	3.9E-01	M19879.1	NT	Human diabinin 27 gene, exons 10 and 11, and L1 and Alu repeats
10305	23230		0.46	3.9E-01	11465620	NT	Porphyria purpurea mitochondrion, complete genome
10527	23449	36947	0.62	3.9E-01	D86722.1	NT	Nicotiana tabacum mRNA for TATA binding protein (TBP), complete cds
10965	23885	37397	0.48	3.9E-01	M18440.1	NT	Human beta-B2-crystallin (B2-1) gene, exon 4, partial cds
12219	25868		4.08	3.9E-01	AF304354.1	NT	Homo sapiens proteoglycan 3 (PRG3) gene, complete cds
12344	25142		2.01	3.9E-01	Q61670	SWISSPROT	HOMEOBOX PROTEIN HLX1
12840	25462		1.49	3.9E-01	11433335	NT	Homo sapiens hypothetical protein FLJ10583 (FLJ10583), mRNA
161	13284		9.02	3.8E-01	7019488	NT	Homo sapiens protein kinase PKNbeta (pknbeta), mRNA
506	13577		0.8	3.8E-01	AB029291.1	NT	Mus musculus pom-1 mRNA for pericentriolar material-1, complete cds
1856	14911		1.19	3.8E-01	AE003870.1	NT	Xylella fastidiosa, section 16 of 228 of the complete genome
2465	15469	28493	1.24	3.8E-01	U41848.1	NT	Oeanorhabdus briggsae acetylcholinesterase (ace-1) gene, complete cds
2577	15578	28597	2.26	3.8E-01	AF214117.1	NT	Arabidopsis thaliana putative c-myb-like transcription factor (MYB3R-3) mRNA, complete cds

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2640	15900	28662	4.89	3.8E-01	6678002	NT	Mus musculus solute carrier family 1, member 6 (Slc1a6), mRNA
3015	16073		0.88	3.8E-01	AJ251087.1	NT	Human immunodeficiency virus type 1 complete genome (isolate 98SE-MP1213)
3061	16118	29033	2.11	3.8E-01	AF043383.1	NT	Pleuroctes americanus aminopeptidase N (ampN) gene, partial cds
3495	16542	29466	9.24	3.8E-01	AL161618.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 30
3549	16595		0.75	3.8E-01	AI807219.1	EST_HUMAN	wf38b12.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2357855 3'
3566	16595		0.97	3.8E-01	AI807219.1	EST_HUMAN	wf38b12.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2357855 3'
3769	16811	29720	0.99	3.8E-01	BE154080.1	EST_HUMAN	PMQ-HT0339-200400-070-G01 HT0339 Homo sapiens cDNA
5691	18796	31957	1.08	3.8E-01	Q04888	SWISSPROT	TRANSCRIPTION FACTOR SOX-10
6473	19538		0.8	3.8E-01	S46825.1	NT	prion protein (mink, Genomic, 2446 nt)
6779	19834	33117	5.49	3.8E-01	BE072399.1	EST_HUMAN	QV3-BT0537-271299-049-e02 BT0537 Homo sapiens cDNA
6824	20148	33468	4.76	3.8E-01	AI374601.1	EST_HUMAN	ts64f11.x1 Soares_fetal Testis_Nb2-IF8_9w Homo sapiens cDNA clone IMAGE:2047917 3' similar to contains Alu repetitive element;
7126	20059	33365	1.24	3.8E-01	AL161513.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 25
7743	20697	34063	0.51	3.8E-01	AAG26274.1	EST_HUMAN	zu88c05.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:745064 3'
7759	20712		4.27	3.8E-01	X61597.1	NT	M.musculus gene for kallikrein-binding protein
7998	20937	34331	0.49	3.8E-01	V00683.1	NT	Yeast mitochondrial gene for ATPase (genes cit-2 and cit-4)
8640	21608	35031	0.45	3.8E-01	MB1385.1	NT	Mouse liver receptor homologous protein (LRH-1) mRNA, complete cds
8903	21869	35294	2.04	3.8E-01	AB046651.1	NT	Homo sapiens mRNA for KIAA1631 protein, partial cds
8972	21938	35363	0.79	3.8E-01	11441264	NT	Homo sapiens FOS-like antigen-1 (FOSL1), mRNA
9169	22135	35561	1.47	3.8E-01	AL163279.2	NT	Homo sapiens chromosome 21 segment HS21C079
9919	22740		6.02	3.8E-01	T95413.1	EST_HUMAN	y643h06.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:120539 5' similar to contains Alu repetitive element; contains PTR6 repetitive element ;
11862	24744		3.41	3.8E-01	BE719219.1	EST_HUMAN	RCO-HT0841-040800-032-b12 HT0841 Homo sapiens cDNA
12000	24877	38473	2.61	3.8E-01	R42550.1	EST_HUMAN	y62h11.s1 Soares infant brain 1NIB Homo sapiens cDNA clone IMAGE:30289 3'
12000	24877	38474	2.61	3.8E-01	R42550.1	EST_HUMAN	y62h11.s1 Soares infant brain 1NIB Homo sapiens cDNA clone IMAGE:30289 3'
12433	25199		4.23	3.8E-01	AE001124.1	NT	Borrelia burgdorferi (section 10 of 70) of the complete genome
12557	25689		2.63	3.8E-01	U94788.1	NT	Human p53 (TP53) gene, complete cds
12667	25343		2.84	3.8E-01	BE829256.1	EST_HUMAN	QV3-ET0063-190700-271-e05 ET0063 Homo sapiens cDNA
13056	25864		2.03	3.8E-01	AF291483.1	NT	Mus musculus vomeronasal receptor V1RA4 (V1ra4) gene, complete cds
13063	25905	31422	1.4	3.8E-01	T54787.1	EST_HUMAN	y642b11.s1 Stragene fetal spleen (#837205) Homo sapiens cDNA clone IMAGE:73821 3' similar to similar to gb:A06977 SERUM ALBUMIN PRECURSOR (HUMAN)
13080	25611	31690	1.57	3.8E-01	AF194972.1	NT	Mus musculus developmental control protein mRNA, partial cds
2490	15493	28518	12.56	3.7E-01	AB037831.1	NT	Homo sapiens mRNA for KIAA1410 protein, partial cds
3474	16520	29442	11.71	3.7E-01	AF066336.1	NT	Danio rerio bone morphogenetic protein 4 precursor (BMP4) gene, complete cds

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3884	16924	29833	0.7	3.7E-01	AA319482.1	EST_HUMAN	EST121715 Adrenal gland tumor Homo sapiens cDNA 5' end
4257	17286	30168	6.92	3.7E-01	AI218707.1	EST_HUMAN	ok3907.x1 Soares NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:1610188 3'
4348	17375	30255	1.64	3.7E-01	AW878037.1	EST_HUMAN	MR3-OT0007-080300-104-502 OT0007 Homo sapiens cDNA
4416	17443	30334	3	3.7E-01	AE002408.1	NT	Neisseria meningitidis serogroup B strain MC58 section 50 of 206 of the complete genome
5857	18947	32132	1.18	3.7E-01	AF136187.1	NT	Homo sapiens interferon-induced protein p78 (MX1) gene, complete cds
6060	19141	32353	1.35	3.7E-01	AL163278.2	NT	Homo sapiens chromosome 21 segment HS21C078
6659	19716	32993	0.66	3.7E-01	MT0806.1	NT	Chicken (White leghorn) delta-1 and delta-2 crystallin genes, complete cds
6690	19737		0.77	3.7E-01	L10353.1	NT	Mus saxicola haptoglobin mRNA, complete cds
7350	20320	33667	3.48	3.7E-01	11525843	NT	Homo sapiens tumor endothelial marker 7 precursor (TEM7), mRNA
7658	20618	33983	0.65	3.7E-01	BE873743.1	EST_HUMAN	601483887F1 NIH_MGC_69 Homo sapiens cDNA clone IMAGE:3886652 5'
7658	20618	33984	0.65	3.7E-01	BE873743.1	EST_HUMAN	601483887F1 NIH_MGC_69 Homo sapiens cDNA clone IMAGE:3886652 5'
8069	21006	34404	0.71	3.7E-01	T66802.1	EST_HUMAN	ye50a07.r3 Soares fetal liver spleen 1NPLS Homo sapiens cDNA clone IMAGE:66324 5'
8672	21640	35064	1.93	3.7E-01	11436739	NT	Homo sapiens chromosome 12 open reading frame 4 (C12ORF4), mRNA
8672	21640	35065	1.93	3.7E-01	11436739	NT	Homo sapiens chromosome 12 open reading frame 4 (C12ORF4), mRNA
8708	21878	35101	0.69	3.7E-01	AA902812.1	EST_HUMAN	ok43b11.s1 NCI_CGAP_Le12 Homo sapiens cDNA clone IMAGE:1616701 3'
9556	22518		3.78	3.7E-01	AJ271386.1	NT	Gallus gallus mRNA for beta-carotene 15,15'-dioxygenase (bcdo gene)
10530	23452		0.52	3.7E-01	K00691.1	NT	mouse Ig germline alpha membrane exon region
10570	23492	36984	3.65	3.7E-01	AJ336411.1	EST_HUMAN	q146b07.x1 Soares fetal lung_NbHL19W Homo sapiens cDNA clone IMAGE:1950997 3'
11205	24159	37689	1.9	3.7E-01	X05958.1	NT	Rabbit mRNA for fast skeletal muscle myosin heavy chain (MHC)
11369	24316	37842	2.81	3.7E-01	AJ297357.1	NT	Homo sapiens partial LIMD1 gene for LIM domains containing protein 1 and KIAA0851 gene
11369	24316	37843	2.81	3.7E-01	AJ297357.1	NT	Homo sapiens partial LIMD1 gene for LIM domains containing protein 1 and KIAA0851 gene
11794	23949	37470	2.34	3.7E-01	X04122.1	NT	Bovine mRNA for terminal deoxynucleotidyltransferase (TdT) (EC 2.7.7.31)
12014	24891		1.53	3.7E-01	AA973540.1	EST_HUMAN	cc46d03.s1 NCI_CGAP_Lu5 Homo sapiens cDNA clone IMAGE:1566221 3' similar to gb:M77698
12060	24933		3.22	3.7E-01	6677678	NT	TRANSITIONAL REPRESSOR PROTEIN YY1 (HUMAN);
12138	25501		2.6	3.7E-01	J04982.1	NT	Mus musculus retinoblastoma 1 (Rb1), mRNA
12309	25117		4.23	3.7E-01	AJ245525.1	NT	Human heart/skeletal muscle ATP/ADP translocator (ANT1) gene, complete cds
12764	25406		1.86	3.7E-01	AL121154.1	EST_HUMAN	Chlamydomonas reinhardtii partial omp1 gene for outer membrane protein 1
12829	25447	31722	2.71	3.7E-01	Y18000.1	NT	DKFZp782K075.1 762 (synonym: hme2) Homo sapiens cDNA clone DKFZp782K075 5'
997	14048		11.36	3.6E-01	U89241.1	NT	Homo sapiens NF2 gene
1317	14352	27320	2.66	3.6E-01	T80255.1	EST_HUMAN	Human mlb gene, partial cds
1317	14352	27321	2.66	3.6E-01	T80255.1	EST_HUMAN	yd03e05.r1 Soares infant brain 1NIB Homo sapiens cDNA clone IMAGE:24443 5'
1331	14955	27951	6.09	3.6E-01	AW590184.1	EST_HUMAN	yd03e05.r1 Soares infant brain 1NIB Homo sapiens cDNA clone IMAGE:24443 5'
1931	14955	27952	6.09	3.6E-01	AW590184.1	EST_HUMAN	hg33f02.x1 NCI_CGAP_GC8 Homo sapiens cDNA clone IMAGE:2947419 3'
1931	14955	27952	6.09	3.6E-01	AW590184.1	EST_HUMAN	hg33f02.x1 NCI_CGAP_GC8 Homo sapiens cDNA clone IMAGE:2947419 3'

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1968	14989	27992	8.4	3.6E-01	AF216207.1	NT	Mus musculus ribosomal protein S19 (Rps19) gene, complete cds
2399	15406		3.58	3.6E-01	X76725.1	NT	P. irregularis (P3804) gene for actin
2483	15487	28510	1.29	3.6E-01	L05435.1	NT	Rattus norvegicus synaptic vesicle protein (SV2) mRNA, complete cds
2483	15487	28511	1.29	3.6E-01	L05435.1	NT	Rattus norvegicus synaptic vesicle protein (SV2) mRNA, complete cds
2495	15498	28524	1.63	3.6E-01	AW812033.1	EST_HUMAN	RC5-ST0171-181099-011-g07 ST0171 Homo sapiens cDNA
							PROTEIN-L-ISOASPARTATE O-METHYLTRANSFERASE (PROTEIN-BETA-ASPARTATE METHYLTRANSFERASE) (PIMT) (PROTEIN L-ISOASPARTYL METHYLTRANSFERASE) (ISOASPARTYL PROTEIN CARBOXYL METHYLTRANSFERASE)
2638	18637	28660	1.23	3.6E-01	P24206	SWISSPROT	Drosophila melanogaster sugar transporter 3 (sug3) mRNA, complete cds
2910	18322		5.89	3.6E-01	AF199485.1	NT	H. sapiens serotonin transporter gene, exons 9 and 10
3483	18529	29453	2.01	3.6E-01	X76758.1	NT	H. sapiens serotonin transporter gene, exons 9 and 10
3483	16529	29454	2.01	3.6E-01	X76758.1	NT	H. sapiens serotonin transporter gene, exons 9 and 10
4438	17462	30351	1.14	3.6E-01	BE707883.1	EST_HUMAN	RC1-HT0545-150600-014-b12 HT0545 Homo sapiens cDNA
4787	17805	30697	0.72	3.6E-01	Y11526.1	NT	Z. mays mRNA for casein kinase II alpha subunit
5045	18058	30937	2.61	3.6E-01	AW339393.1	EST_HUMAN	ha02g04.x1 NCI CGAP Lu24 Homo sapiens cDNA clone IMAGE:2872566 3'
5136	18145	31025	0.65	3.6E-01	BE067699.1	EST_HUMAN	MR4-BT0358-270300-005-c10 BT0358 Homo sapiens cDNA
5274	18280	31143	0.91	3.6E-01	AF067959.1	NT	Gallus gallus homeodomain protein HOXD-3 mRNA, complete cds
5274	18280	31144	0.91	3.6E-01	AF067959.1	NT	Gallus gallus homeodomain protein HOXD-3 mRNA, complete cds
5456	18558	31469	0.71	3.6E-01	AJ005565.1	NT	Homo sapiens lipase gene Intron 5
							FORMATE HYDROGENLYASE SUBUNIT 5 PRECURSOR (FHL SUBUNIT 5) (HYDROGENASE-3 COMPONENT E)
6205	19279	32512	1.1	3.6E-01	P18431	SWISSPROT	Homo sapiens PHEX gene
6823	19681	32958	1.8	3.6E-01	Y10196.1	NT	X74906.r1 Soares fetal liver spleen 1NfLS Homo sapiens cDNA clone IMAGE:275987 5'
7355	20325		3.63	3.6E-01	R94090.1	EST_HUMAN	w72c10.x1 Soares thymus_NHfth Homo sapiens cDNA clone IMAGE:2513010 3' similar to TR:O15117
7500	20465	33828	1.86	3.6E-01	AW027174.1	EST_HUMAN	O15117 FYN BINDING PROTEIN. [1];
8568	21534	34954	0.64	3.6E-01	P98167	SWISSPROT	SCO-SPONDIN
8622	21590	35008	14.05	3.6E-01	AL161583.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 79
9330	22295	35724	0.53	3.6E-01	U91328.1	NT	Human hereditary haemochromatosis region, histone 2A-like protein gene, hereditary haemochromatosis (HLA-H) gene, RoRet gene, and sodium phosphate transporter (NPT3) gene, complete cds
9330	22295	35725	0.53	3.6E-01	U91328.1	NT	Human hereditary haemochromatosis region, histone 2A-like protein gene, hereditary haemochromatosis (HLA-H) gene, RoRet gene, and sodium phosphate transporter (NPT3) gene, complete cds
9355	22320	35746	2.84	3.6E-01	4504956	NT	Homo sapiens lysosomal-associated membrane protein 2 (LAMP2), transcript variant LAMP2A, mRNA

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9355	22320	35747	2.84	3.6E-01	4504956	NT	Homo sapiens lysosomal-associated membrane protein 2 (LAMP2), transcript variant LAMP2A, mRNA
9547	22510	35959	1.12	3.6E-01	AL183204.2	NT	Homo sapiens chromosome 21 segment HS21C004
9754	22695	36151	0.93	3.6E-01	X17550.1	NT	D. melanogaster singed gene, exons 3, 4, 5 & 8
9754	22695	36152	0.93	3.6E-01	X17550.1	NT	D. melanogaster singed gene, exons 3, 4, 5 & 8
9824	22673		0.54	3.6E-01	X62825.1	NT	C. perfringens plc gene for phospholipase C upstream region containing bent DNA fragment
10222	23147	36836	10.66	3.6E-01	Q83194	SWISSPROT	PROBABLE PEPTIDE ABC TRANSPORTER ATP-BINDING PROTEIN Y4TS
10352	23276	36750	0.48	3.6E-01	AW752901.1	EST_HUMAN	MR2-CT0222-211099-002-b10 CT0222 Homo sapiens cDNA
10352	23276	36751	0.48	3.6E-01	AW752901.1	EST_HUMAN	MR2-CT0222-211099-002-b10 CT0222 Homo sapiens cDNA
11292	24242	37769	3.04	3.6E-01	BE902390.1	EST_HUMAN	601876418F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3658997 5'
11442	24385	37925	3.26	3.6E-01	AB004293.1	NT	Arabidopsis thaliana mRNA for StpB, complete cds
11772	23927	37448	5.83	3.6E-01	AE000856.1	NT	Methanobacterium thermoautotrophicum from bases 702375 to 714311 (section 62 of 148) of the complete genome
12174	25989		2.05	3.6E-01	Y19210.1	NT	Homo sapiens hrb5 gene for hair keratin, exons 1 to 9
12247	25076		1.42	3.6E-01	D60901.1	NT	Synechocystis sp. PCC6803 complete genome, 3/27, 271600-402289
12257	25083		6.35	3.6E-01	AE000335.1	NT	Escherichia coli K-12 MG1655 section 225 of 400 of the complete genome
12417	25187		6.26	3.6E-01	U66883.1	NT	Mus musculus Emr1 mRNA, complete cds
12770	25410		1.97	3.6E-01	11432598	NT	Homo sapiens myeloid/lymphoid or mixed-lineage leukemia (trithorax (Drosophila) homolog); translocated to, 10 (AF10), mRNA
13033	25934		3.33	3.6E-01	AW190229.1	EST_HUMAN	x60911.x1 NCL CGAP_Pan1 Homo sapiens cDNA clone IMAGE:2679116 3' similar to gb:K00558 TUBULIN
115	13226	26150	1.42	3.5E-01	AL161636.2	NT	ALPHA-1 CHAIN (HUMAN);
210	13311	26238	3.29	3.5E-01	6678933	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 36
728	13787	26722	1.48	3.5E-01	7706136	NT	Mus musculus mannose receptor, C type 2 (Mrc2), mRNA
726	13787	26723	1.48	3.5E-01	7706136	NT	Homo sapiens GAP-like protein (LOC51306), mRNA
760	13940	26785	4.95	3.5E-01	BF129796.1	EST_HUMAN	Homo sapiens GAP-like protein (LOC51306), mRNA
1623	14656	27634	0.96	3.5E-01	BF310688.1	EST_HUMAN	601811060R1 NIH_MGC_48 Homo sapiens cDNA clone IMAGE:4053951 3'
1646	14678	27651	2.57	3.5E-01	U35776.1	NT	601894653F2 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4124244 5'
2291	15303	28328	1.28	3.5E-01	P08796	SWISSPROT	Rattus norvegicus ADP-ribosylation factor-directed GTPase activating protein mRNA, complete cds
2613	15899	28636	1.13	3.5E-01	AA223252.1	EST_HUMAN	HOMEOBOX PROTEIN HOX-A4 (HOX-1.4) (MH-3)
3818	16858		7.27	3.5E-01	AA642138.1	EST_HUMAN	zr08a09.s1 Stralagene NT2 neuronal precursor 937230 Homo sapiens cDNA clone IMAGE:650872 3'
4291	17320	30199	2.18	3.5E-01	AF071253.1	NT	nr60403.s1 NCL CGAP_Lym3 Homo sapiens cDNA clone IMAGE:1172357 3'
							Danio rerio homeobox protein (hoxb5b) gene, complete cds

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4922	17939	30831	0.7	3.5E-01	N81203.1	EST_HUMAN	788IE1 fetal brain cDNA Homo sapiens cDNA clone 788IE1-K similar to R07879, Z40498
4969	17984	30874	6.46	3.5E-01	M18349.1	NT	Rat leukocyte common antigen (L-CA) gene, exons 1 through 5
5407	18510	31387	0.84	3.5E-01	Q96687	SWISSPROT	EARLY E2A DNA-BINDING PROTEIN
5407	18510	31388	0.84	3.5E-01	Q96687	SWISSPROT	EARLY E2A DNA-BINDING PROTEIN
5629	18725	31886	1.36	3.5E-01	D42045.1	NT	Human mRNA for KIAA0086 gene, complete cds
6365	19434		0.77	3.5E-01	AW863916.1	EST_HUMAN	PMAS-SN0012-030400-001-a11 SN0012 Homo sapiens cDNA
6548	19609	32871	0.62	3.5E-01	AA431833.1	EST_HUMAN	zvf79f03.r1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:782429 5' similar to TR:G1066935
6593	19653	32925	0.68	3.5E-01	U37150.1	NT	G1066935 F10F2.1;
6821	19875	33164	0.92	3.5E-01	O24357	SWISSPROT	Bos taurus peptide methionine sulfoxide reductase (msrA) mRNA, complete cds
7257	19992	34115	0.81	3.5E-01	X98505.1	NT	GLUCOSE-6-PHOSPHATE 1-DEHYDROGENASE, CHLOROPLAST PRECURSOR (G6PD)
7789	20742	34116	0.81	3.5E-01	P47281	SWISSPROT	S. scrofa mRNA for CD31 protein (PECAM-1)
8023	20960	34356	0.7	3.5E-01	X06091.1	NT	HISTIDYL-TRNA SYNTHETASE (HISTIDINE--TRNA LIGASE) (HISRS)
8408	21375	34784	0.67	3.5E-01	BF358871.1	EST_HUMAN	HISTIDYL-TRNA SYNTHETASE (HISTIDINE--TRNA LIGASE) (HISRS)
8409	21378	34784	0.67	3.5E-01	BF358871.1	EST_HUMAN	HISTIDYL-TRNA SYNTHETASE (HISTIDINE--TRNA LIGASE) (HISRS)
8810	21777		0.58	3.5E-01	AF051561.1	NT	E. coli L-arabinose transport operon with genes araF, araG and araH
9279	22245	35674	1.14	3.5E-01	4507610	NT	Homo sapiens tumor protein p53-binding protein, 2 (TP53BP2), mRNA
10093	23019	36494	6.94	3.5E-01	Q02294	SWISSPROT	RC4-ET0024-260600-014-007 ET0024 Homo sapiens cDNA
10246	23171	36680	5.51	3.5E-01	Z26825.1	NT	Rattus norvegicus Na,K-Cl cotransporter (Nkcc1) mRNA, complete cds
10326	23250	36729	1.01	3.5E-01	BE174784.1	EST_HUMAN	Homo sapiens tyrosine kinase non-receptor 1 (TNK1), mRNA
11086	24047	37569	2.48	3.5E-01	X81084.1	NT	VOLTA-DEPENDENT N-TYPE CALCIUM CHANNEL ALPHA-1B SUBUNIT (CALCIUM CHANNEL, L
11362	24311	37838	1.68	3.5E-01	AJ243178.1	NT	TYPE, ALPHA-1 POLYPEPTIDE ISOFORM 5) (BRAIN CALCIUM CHANNEL III) (BIII)
11362	24311	37839	1.68	3.5E-01	AJ243178.1	NT	X. laevis gene for albumin including HP1 enhancer
11919	24800	38391	1.67	3.5E-01	N77597.1	EST_HUMAN	C. griseus rhodopsin gene for opsin protein
11940	24820		1.77	3.5E-01	M82885.1	NT	Gallus gallus SPARC gene for osteonectin, promoter and exon 1
11991	24868	38463	1.6	3.5E-01	L05145.1	NT	Gallus gallus SPARC gene for osteonectin, promoter and exon 1
12289	25891		1.8	3.5E-01	AF297468.1	NT	yz90h12.r1 Soares_multiple_sclerosis_2NBMSP Homo sapiens cDNA clone IMAGE:280375 5'
12341	25139		1.31	3.5E-01	X64565.1	NT	Drosophila melanogaster dual bar protein (BarH2) gene, exon 1
12501	25240		2.56	3.5E-01	AE001774.1	NT	Human glucokinase (GCK) gene, repeat polymorphism
13085	25842	31430	3.37	3.5E-01	H80814.1	EST_HUMAN	Schistosoma mansoni strain NMR1 chromatin assembly factor 1 small subunit-like protein (RBAP48) mRNA, complete cds
13085	25842	31431	3.37	3.5E-01	H80814.1	EST_HUMAN	B. taurus atpA1 gene for F(0)/F(1) ATP synthase alpha-subunit
							Thermotoga maritima section 86 of 136 of the complete genome
							ys64f11.r1 Soares retina N2b4HR Homo sapiens cDNA clone IMAGE:218597 5'
							ys64f11.r1 Soares retina N2b4HR Homo sapiens cDNA clone IMAGE:218597 5'

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
13106	25627		1.57	3.5E-01	4758297	NT	Homo sapiens v-erb-b2 avian erythroblastic leukemia viral oncogene homolog 2 (neurofiblastoma derived oncogene homolog) (ERBB2), mRNA
708	13770		1.97	3.4E-01	AJ242956.1	NT	Homo sapiens partial N-myc (exon 3), HPV45 L2, HPV45 L1, HPV45 E6, HPV45 E7 and HPV45 E1 genes isolated from IC4 cervical carcinoma cell line
977	14028	26982	9.08	3.4E-01	Y09798.2	NT	Pseudomonas fluorescens colR, cdiS genes, orf222 and partial inxA gene
1329	14384	27332	2.79	3.4E-01	Y00554.1	NT	Azotobacter vinelandii nifA gene for NifA protein (positive regulatory element)
2410	15417	28441	2.01	3.4E-01	D90909.1	NT	Synechocystis sp. PCC6803 complete genome, 11/27, 1311235-1430418
3014	16072	28992	0.88	3.4E-01	AL163210.2	NT	Homo sapiens chromosome 21 segment HS21C010
3014	16072	28993	0.88	3.4E-01	AL163210.2	NT	Homo sapiens chromosome 21 segment HS21C010
3175	16230	29146	6.62	3.4E-01	U83905.1	NT	Canis familiaris rod photoreceptor cGMP-gated channel alpha-subunit (CNGC1) mRNA, complete cds
3354	16405	29326	0.94	3.4E-01	AF034862.1	NT	Homo sapiens pulmonary surfactant protein D, promoter region and exon 1
3542	16588	29512	3.42	3.4E-01	AF106835.1	NT	Methylovorus sp. strain SS1 putative GrpE (grpE), DnaK (dnaK), and putative DnaJ (dnaJ) genes, complete cds
3804	16844		1.78	3.4E-01	BF449010.1	EST_HUMAN	7n94a01.x1 NCI_CGAP_Ov18 Homo sapiens cDNA clone IMAGE:3572232 3' similar to TR:Q9UJ15 Q9UJ15 DJ18C9.1
4082	17116		1.48	3.4E-01	AA584196.1	EST_HUMAN	nc11b10.s1 NCI_CGAP_Phe1 Homo sapiens cDNA clone IMAGE:1100347 3'
4674	17695	30582	1.72	3.4E-01	BE069912.1	EST_HUMAN	MR4-BT0403-230200-202-c01 BT0403 Homo sapiens cDNA
4899	18004		4.71	3.4E-01	AI240973.1	EST_HUMAN	q95c05.x1 NCI_CGAP_Kid3 Homo sapiens cDNA clone IMAGE:1867208 3' similar to contains Alu repetitive element
5768	18860	32040	2.74	3.4E-01	AL161594.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 90
5909	18995		5.14	3.4E-01	AA085313.1	EST_HUMAN	zn12d11.s1 Striatogene HNT neuron (#937233) Homo sapiens cDNA clone IMAGE:547221 3'
6122	19200		1.74	3.4E-01	IL02971.1	NT	Echovirus 22 1AB, 1C, 1D, 2A, 2B, 2C, 3A, 3B, 3C, 3D proteins RNA, complete mature peptides and cds
6146	19221	32451	0.8	3.4E-01	BE748912.1	EST_HUMAN	60157181T1 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:3838826 3'
6228	19303	32535	1.91	3.4E-01	AW204505.1	EST_HUMAN	UHH-B11-eel-e-12-UJ.s1 NCI_CGAP_Sub3 Homo sapiens cDNA clone IMAGE:2719582 3'
6362	19431	32674	1.78	3.4E-01	AL120944.1	EST_HUMAN	DKFZp761A249_r1 761 (synonym: hamy2) Homo sapiens cDNA clone DKFZp761A249 5'
6907	19959		1.19	3.4E-01	N65225.1	EST_HUMAN	zb53e12.s1 Soares_fejal_Jung_NbHL19W Homo sapiens cDNA clone IMAGE:307342 3'
7135	20111	33424	1.14	3.4E-01	AI468082.1	EST_HUMAN	hm63g05.x1 NCI_CGAP_Brn25 Homo sapiens cDNA clone IMAGE:2162840 3' similar to gb:S37431 LAMININ RECEPTOR (HUMAN)
7261	19998	33283	0.61	3.4E-01	BF678702.1	EST_HUMAN	602085283F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4249365 5'
8238	21207		0.54	3.4E-01	AE000493.1	NT	Escherichia coli K-12 MG1655 section 383 of 400 of the complete genome
8578	21547	34966	0.55	3.4E-01	Y14930.1	NT	Homo sapiens TORAV28 gene, allele A4, partial
8832	21799		1.8	3.4E-01	AA337063.1	EST_HUMAN	EST14766 Endometrial tumor Homo sapiens cDNA 5' end

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8909	21875	35301	0.64	3.4E-01	L04690.1	NT	Orcetulus griseus cholesterol 7-alpha-hydroxylase gene, complete cds
9204	22170	35600	1.89	3.4E-01	9633624	NT	Bovine enterovirus strain K2577, complete genome
9567	22529	35978	4.43	3.4E-01	P26013	SWISSPROT	INTEGRIN BETA-8 PRECURSOR
9567	22529	35979	4.43	3.4E-01	P26013	SWISSPROT	INTEGRIN BETA-8 PRECURSOR
9776	22717		0.49	3.4E-01	AB017510.1	NT	Ephydratia fluviatilis mRNA for PLC-gammaS, complete cds
9801	21124	34527	6.03	3.4E-01	U19492.1	NT	Saccharomyces cerevisiae Maf1p (MAF1) gene, complete cds
9801	21124	34528	6.03	3.4E-01	U19492.1	NT	Saccharomyces cerevisiae Maf1p (MAF1) gene, complete cds
9855	22791	36243	0.43	3.4E-01	AF183857.1	NT	Dicotyledon discoidium putative CMF receptor CMFR1 mRNA, complete cds
10054	22981	36449	1.09	3.4E-01	U68763.1	NT	Glycine max putative transcription factor SCOF-1 (scot-1) mRNA, complete cds
10249	23174	36684	2.14	3.4E-01	AJ225084.1	NT	Homo sapiens FAA gene, exon 16, 17 and 18
10843	23763		0.88	3.4E-01	AE004096.1	NT	Vibrio cholerae chromosome I, section 4 of 251 of the complete chromosome
11357	24307		3.51	3.4E-01	AE000881.1	NT	Methanobacterium thermoautotrophicum from bases 1018444 to 1029212 (section 87 of 148) of the complete genome
11393	24339	37869	4.96	3.4E-01	P08925	SWISSPROT	PROBABLE E4 PROTEIN
11427	24371	37909	1.67	3.4E-01	AF045981.1	NT	Rutillus arcasii cytochrome b (cytb) gene, mitochondrial gene encoding mitochondrial protein, partial cds
11828	24711	38295	1.58	3.4E-01	AB035507.1	NT	Rattus norvegicus mRNA for s-glycerin/MUC18, complete cds
11856	24738	38323	3.3	3.4E-01	AL161515.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 27
12099	24970	38567	1.9	3.4E-01	AI559985.1	EST_HUMAN	lq77g06.x1 NCI_CGAP_U11 Homo sapiens cDNA clone IMAGE:2214874 3' similar to contains L1.b1 L1 repetitive element
12149	25008		2.08	3.4E-01	U93604.1	NT	Citrus variegation virus putative replicase gene, partial cds
12261	25085		1.59	3.4E-01	Z21621.1	NT	S. cerevisiae RIB5 gene encoding Riboflavin synthase
12485	25231		13.04	3.4E-01	L28339.1	NT	Human autoantigen mRNA, complete cds
12512	25761		3.88	3.4E-01	BE218652.1	EST_HUMAN	hw42h08.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3176127 3' similar to contains PTR5.13
12567	25865		2.19	3.4E-01	9638361	NT	PTR5 repetitive element
12673	25345	31763	3.46	3.4E-01	AJ297131.1	NT	Beta vulgaris mitochondrion, complete genome
12872	25538		1.94	3.4E-01	AF019413.1	NT	Mus musculus SIL, MAP_17, CYP_a, SCL & CYP_b genes
16	13135	26033	10.37	3.3E-01	X07990.1	NT	Homo sapiens HLA class III region containing tenascin X (tenascin-X) gene, partial cds; cytochrome P450 21-hydroxylase (CYP21B), complement component C4 (C4B) G11, helicase (SK2W), RD, complement factor B (Bf), and complement component C2 (C2) genes>
106	13135	26033	4.34	3.3E-01	X07990.1	NT	Rhizobium leguminosarum sym plasmid pRL5.1i nodX gene
448	13521	26454	1.3	3.3E-01	AL161545.2	NT	Rhizobium leguminosarum sym plasmid pRL5.1i nodX gene
634	13700	26621	2.26	3.3E-01	7562485	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 45
							Homo sapiens KIAA1100 protein (KIAA1100), mRNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1205	14244	27203	3.29	3.3E-01	Q12448	SWISSPROT	PROLINE-RICH PROTEIN LAS17
1310	14346	27312	2.44	3.3E-01	BF568880.1	EST_HUMAN	602184016T1 NIH_MGC_42 Homo sapiens cDNA clone IMAGE:4300251 3'
1610	14842	27618	1.55	3.3E-01	6753685	NT	Mus musculus disintegrin 5 (Dign5), mRNA
1752	14781		1.13	3.3E-01	AA332734.1	EST_HUMAN	EST36722 Embryo, 8 week 1 Homo sapiens cDNA 5' end
2043	15082		1.01	3.3E-01	AF031148.1	NT	Methylococcus capsulatus strain Bath outer membrane protein MopB (mcpB) gene, complete cds
2414	15421		4.45	3.3E-01	4507834	NT	Homo sapiens uridine monophosphate synthetase (urotate phosphoribosyl transferase and orotidine-5'- decarboxylase) (UMPS) mRNA
2960	16018	28945	1.76	3.3E-01	AJ251806.1	NT	Bacteriophage phi-YeQ3-12 complete genome
3028	16088		0.8	3.3E-01	O02743	SWISSPROT	INTERLEUKIN-12 ALPHA CHAIN PRECURSOR (IL-12A) (CYTOTOXIC LYMPHOCYTE MATURATION FACTOR 35 KD SUBUNIT) (CLMF P35)
3068	16125	29038	0.91	3.3E-01	AJ007932.2	NT	Streptomyces argillaceus mitramycin biosynthetic genes
3506	16553	29479	1.27	3.3E-01	AB012922.1	NT	Homo sapiens MTA1-1.1 gene, complete cds
3822	16862	29766	2.18	3.3E-01	O84645	SWISSPROT	EXODEOXYRIBONUCLEASE V BETA CHAIN
3832	16872	29773	0.8	3.3E-01	P22602	SWISSPROT	GENOME POLYPROTEIN [CONTAINS: N-TERMINAL PROTEIN (P1); HELPER COMPONENT PROTEINASE (HC-PRO); PROTEIN P3]
3989	17029	29939	1.54	3.3E-01	AL161488.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 10
4026	17064	29965	2.02	3.3E-01	AF200446.1	NT	Hypoxylon fragiforme chitin synthase gene, partial cds
4395	17423		1.51	3.3E-01	D37692.1	NT	Rattus norvegicus DNA for regucalcin, partial cds
4715	17735		1.41	3.3E-01	AI539114.1	EST_HUMAN	lp78b12.x1 NCL_CGAP_U13 Homo sapiens cDNA clone IMAGE:2205407 3' similar to gb:X57922 ANTIGEN PEPTIDE TRANSPORT 1 (HUMAN).
4875	17892	30781	1.33	3.3E-01	D64003.1	NT	Synechocystis sp. PCC6803 complete genome, 22/27, 2755703-2868766
5397	18500	31377	2.48	3.3E-01	X89819.1	NT	R.norvegicus mRNA for 3'UTR of ubiquitin-like protein
5397	18500	31378	2.48	3.3E-01	X89819.1	NT	R.norvegicus mRNA for 3'UTR of ubiquitin-like protein
5664	18759	31928	0.55	3.3E-01	P39055	SWISSPROT	DYNAMIN
5664	18759	31929	0.55	3.3E-01	P39055	SWISSPROT	DYNAMIN
5884	18973	32166	0.61	3.3E-01	BF213873.1	EST_HUMAN	601848090F1 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:4078823 5'
6056	19137	32347	1.75	3.3E-01	BE019850.1	EST_HUMAN	601472768T1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3875753 3'
6056	19137	32348	1.75	3.3E-01	BE019850.1	EST_HUMAN	601472768T1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3875753 3'
6154	19229	32459	0.82	3.3E-01	P05691	SWISSPROT	CIRCUMSPOROZITE PROTEIN (CS)
6960	20185	33508	0.63	3.3E-01	AB034233.1	NT	Flexibacter littoralis gyrB gene for DNA gyrase B subunit, partial cds
6960	20185	33509	0.63	3.3E-01	AB034233.1	NT	Flexibacter littoralis gyrB gene for DNA gyrase B subunit, partial cds
7073	20095	33404	4.16	3.3E-01	AI628131.1	EST_HUMAN	hg44h01.x1 NCL_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2285808 3' similar to contains Alu repetitive element; contains element L1 repetitive element;

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7073	20095	33405	4.16	3.3E-01	AB28131.1	EST_HUMAN	h84h01.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2285809 3' similar to contains Alu repetitive element; contains element L1 repetitive element ;
8052	20999	34395	1.81	3.3E-01	N85146.1	EST_HUMAN	J2498F Human fetal heart, Lambda ZAP Express Homo sapiens cDNA clone J2498 5' similar to TEGT
8908	21874	35300	22.63	3.3E-01	BF683954.1	EST_HUMAN	602140372F1 NIH_MGC_46 Homo sapiens cDNA clone IMAGE:4301800 5'
9080	22046	35469	0.66	3.3E-01	BF210322.1	EST_HUMAN	601873281F1 NIH_MGC_54 Homo sapiens cDNA clone IMAGE:4097180 5'
9469	22433	35871	0.85	3.3E-01	Q62925	SWISSPROT	MITOGEN-ACTIVATED PROTEIN KINASE KINASE 1 (MAPK/ERK KINASE 1) (MEK KINASE 1) (MEKK 1)
9733	22761	36215	0.98	3.3E-01	BE828481.1	EST_HUMAN	GM3-ET0041-180500-187-d10 ET0041 Homo sapiens cDNA
9733	22761	36216	0.98	3.3E-01	BE828481.1	EST_HUMAN	GM3-ET0041-180500-187-d10 ET0041 Homo sapiens cDNA
9869	22805	36258	2.8	3.3E-01	N69866.1	EST_HUMAN	za67h01.s1 Soares_fetal_lung_NHL19W Homo sapiens cDNA clone IMAGE:297649 3'
9910	22731	36186	2.61	3.3E-01	BF376745.1	EST_HUMAN	RC4-TN007-250800-011-g04 TN0077 Homo sapiens cDNA
10350	23274		2.12	3.3E-01	L41044.1	NT	Homo sapiens high-mobility group phosphoprotein (HMGI-C) gene, exons 1-3, complete cds
11076	24038	37561	2.85	3.3E-01	X63953.1	NT	D.mauritiana Adh gene
11076	24038	37562	2.85	3.3E-01	X63953.1	NT	D.mauritiana Adh gene
11365	24313		2.16	3.3E-01	BF528499.1	EST_HUMAN	602070802F1 NCI_CGAP_Brn64 Homo sapiens cDNA clone IMAGE:4213585 5'
11565	24505	38062	8.16	3.3E-01	BE219351.1	EST_HUMAN	hw51g02.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3176978 3'
							GALECTIN-3 (GALACTOSE-SPECIFIC LECTIN 3) (MAC-2 ANTIGEN) (IGE-BINDING PROTEIN) (35 KD LECTIN) (CARBOHYDRATE BINDING PROTEIN 35) (CBP 35) (LAMININ-BINDING PROTEIN) (LECTIN L-29) (CBP30)
11673	24639	38218	3.19	3.3E-01	P47983	SWISSPROT	ob71g02.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1336850 3'
12027	24903		3.43	3.3E-01	AA806621.1	EST_HUMAN	Rhizobium leguminosarum syn plasmid pRL5J ncdX gene
12044	13135	26033	1.97	3.3E-01	X07990.1	NT	Homo sapiens aldehyde oxidase 1 (AOX1), mRNA
12246	25075	38170	1.84	3.3E-01	6598319	NT	Pyrococcus horikoshii OT3 genomic DNA, 287001-544000 nt. position (2/7)
12658	25530		4.92	3.3E-01	AP000002.1	NT	601146730F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:3162006 5'
13113	25632	31621	1.59	3.3E-01	BE312920.1	EST_HUMAN	Rattus norvegicus EH domain binding protein Epsln mRNA, complete cds
457	13530		2.08	3.2E-01	AF018281.1	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 61
719	13781		0.76	3.2E-01	AL161581.2	NT	Fusarium poae virus 1 RNA2 putative RNA dependent RNA polymerase gene, complete cds
1186	14207	27161	10.6	3.2E-01	AF047013.1	NT	P. vulgaris arc5-1 gene
1287	14322	27285	1.77	3.2E-01	Z80202.1	NT	LACTOSE PERMEASE (LACTOSE-PROTON SYMPORT) (LACTOSE TRANSPORT PROTEIN)
1391	14425	27394	5.96	3.2E-01	Q48624	SWISSPROT	Arabidopsis thaliana cultivar Columbia RPP13 (RPP13) gene, complete cds
1639	14671		0.9	3.2E-01	AF209730.1	NT	S. cerevisiae chromosome II reading frame ORF YBR172c
1789	14818	27803	1.5	3.2E-01	Z36041.1	NT	EST369284 IMAGE resequences, MAGD Homo sapiens cDNA
1798	14828	27815	5.47	3.2E-01	AW957194.1	EST_HUMAN	EST369284 IMAGE resequences, MAGD Homo sapiens cDNA
1799	14828	27816	5.47	3.2E-01	AW957194.1	EST_HUMAN	EST369284 IMAGE resequences, MAGD Homo sapiens cDNA

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Table 4
Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1860	14886	27882	1.03	3.2E-01	AL111655.1	NT	Botrytis cinerea strain T4 cDNA library under conditions of nitrogen deprivation
2168	15184	28205	2.33	3.2E-01	BF203817.1	EST_HUMAN	601868804F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4111512 5'
2548	15549		2.3	3.2E-01	7710079	NT	Mus musculus Pbx/knotted 1 homeobox (Pbxk1), mRNA
2720	15714	28732	1.56	3.2E-01	AF080568.1	NT	Homo sapiens promyelocytic leukemia zinc finger protein (PLZF) gene, complete cds
3622	16665		0.79	3.2E-01	D10872.1	NT	Human h NAT allele 3-2 gene for ankyrin N-acetyltransferase
4367	17394	30273	0.93	3.2E-01	4759195	NT	Homo sapiens symplekin (SYM) mRNA
4422	17449	30340	1.62	3.2E-01	M18818.1	NT	Rabbit beta-like globin gene cluster encoding the epsilon, gamma, delta (pseudogene) and beta globin polypeptides, complete cds
4526	17551	30439	1.3	3.2E-01	Q10268	SWISSPROT	HYPOTHETICAL 81.7 KD PROTEIN C13G7 04C IN CHROMOSOME 1 PRECURSOR
4767	17787		8.32	3.2E-01	BF683617.1	EST_HUMAN	602081972F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4246505 5'
4915	17932	30823	0.69	3.2E-01	Q57081	SWISSPROT	CYTADHERENCE HIGH MOLECULAR WEIGHT PROTEIN 3 (CYTADHERENCE ACCESSORY PROTEIN 3) (ACCESSORY ADHESIN PROTEIN 3) (P69)
5250	18258	31127	0.96	3.2E-01	AY008847.1	NT	Homo sapiens interleukin 12 p40 subunit (IL12B) gene, IL12B-1 allele, complete cds
5280	18288		4.18	3.2E-01	A1989472.1	EST_HUMAN	ws2506x1 NCI_CGAP GC8 Homo sapiens cDNA clone IMAGE:2488195 3' similar to contains Alu repetitive element; contains element PTR7 repetitive element;
5344	18449	31320	2.71	3.2E-01	BE173964.1	EST_HUMAN	CMD-H10569-060300-269-110 HT0569 Homo sapiens cDNA
6068	19149	32361	1.36	3.2E-01	L27221.1	NT	Giardia intestinalis pyruvate:flavodoxin oxidoreductase and flanking genes
6436	19502	32763	0.68	3.2E-01	AF016494.1	NT	Fugu rubripes gamma-aminobutyric acid receptor beta subunit gene, partial cds; 55kd erythrocyte membrane protein (P55), synaptic vesicle-associated integral membrane protein (VAMP-1), procollagen C-proteinase enhancer protein (PCOLCE) genes, complete c>
6749	19803	33084	0.91	3.2E-01	AV178037.1	EST_HUMAN	AV178037 FHTA Homo sapiens cDNA clone FHTAABH01 5'
6897	19949		1.03	3.2E-01	AB002359.1	NT	Human mRNA for KIAA0361 gene, KIAA0361 protein
8189	21159	34568	0.44	3.2E-01	AJ277661.1	NT	Homo sapiens partial LMO1 gene for LIM domain only 1 protein, exon 1
8512	21480	34894	1.43	3.2E-01	M60266.1	NT	Rat ISO-atrial natriuretic factor gene, complete cds
8609	21577	34993	0.45	3.2E-01	AJ231001.1	NT	Rattus norvegicus repeat; map NOS-D12Wα1
8710	21678	35103	16.12	3.2E-01	X02508.1	NT	H. sapiens gene fragment for acetylcholine receptor (AChR) alpha subunit exons 8, 9 and 3' flanking region
8713	21681	35108	17.12	3.2E-01	BF311635.1	EST_HUMAN	601897107F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4126633 5'
8805	21772		1.54	3.2E-01	AL161574.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 70
8845	21812	35231	1.13	3.2E-01	BF246771.1	EST_HUMAN	601855580F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4075627 5'
8845	21812	35232	1.13	3.2E-01	BF246771.1	EST_HUMAN	601855580F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4075627 5'
8819	21886	35311	2.13	3.2E-01	AE002015.1	NT	Deinococcus radiodurans R1 section 152 of 229 of the complete chromosome 1
9019	21985	35405	0.83	3.2E-01	U51026.1	NT	Oryctolagus cuniculus Ig H-chain pseudogene, V-region (VH6-a2) gene, partial cds
9019	21985	35406	0.83	3.2E-01	U51026.1	NT	Oryctolagus cuniculus Ig H-chain pseudogene, V-region (VH6-a2) gene, partial cds

Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9422	22387	35826	0.49	3.2E-01	AL163204.2	NT	Homo sapiens chromosome 21 segment HS21C004
9432	22396		2.28	3.2E-01	M86511.1	NT	Human monocyte antigen CD14 (CD14) mRNA, complete cds
9505	22468	35911	0.45	3.2E-01	AF041829.1	NT	Homo sapiens 6-phosphofructo-2-kinase/fructose-2,6-bisphosphatase (PF2K) gene, exons 12 and 13
9505	22468	35912	0.45	3.2E-01	AF041829.1	NT	Homo sapiens 6-phosphofructo-2-kinase/fructose-2,6-bisphosphatase (PF2K) gene, exons 12 and 13
10353	23277	36752	3.37	3.2E-01	U44914.1	NT	Borrelia burgdorferi plasmid cp32-2, erpC and erpD genes, complete cds; and unknown genes
10559	23481	36976	0.5	3.2E-01	BE326230.1	EST_HUMAN	h68905.x1 NCJ_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3181569 3'
10674	23596		3.71	3.2E-01	AB011399.1	NT	Homo sapiens gene for AF-6, complete cds
11028	23962	37519	3.03	3.2E-01	T06813.1	EST_HUMAN	EST04702 Fetal brain, Stratagene (cat#836206) Homo sapiens cDNA clone HFB0221
12286	25890		3.67	3.2E-01	L07288.1	NT	Drosophila melanogaster laminin A (Lam-A) mRNA, complete cds
12674	25943		1.39	3.2E-01	BE88846.1	EST_HUMAN	601507820F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3909632 5'
12804	25431		4.84	3.2E-01	O83217	SWISSPROT	ELONGATION FACTOR TU (EF-TU)
12890	25719		1.48	3.2E-01	AF157625.1	NT	Bos taurus Inositol 1,4,5-trisphosphate receptor type I mRNA, complete cds
12936	25516		1.57	3.2E-01	L39874.1	NT	Homo sapiens deoxydicylate deaminase gene, complete cds
13001	25925	31305	1.33	3.2E-01	BE388776.1	EST_HUMAN	601275480F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3616746 5'
13108	25628	31646	1.38	3.2E-01	A1745111.1	EST_HUMAN	t21c06.x1 NCJ_CGAP_Ov23 Homo sapiens cDNA clone IMAGE:2218954 3' similar to contains MER10.11 MER10 repetitive element:
2679	15675	28696	3.02	3.1E-01	R18051.1	EST_HUMAN	y680h06.r1 Scores fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:125051 5' similar to gb:M64241 QM PROTEIN (HUMAN):
2708	15828	28717	4.64	3.1E-01	7661971	NT	Homo sapiens KIAA0174 gene product (KIAA0174), mRNA
2708	15828	28718	4.64	3.1E-01	7661971	NT	Homo sapiens KIAA0174 gene product (KIAA0174), mRNA
2869	15929		1.63	3.1E-01	AW629036.1	EST_HUMAN	h146f08.x1 Scores_NFL_T_GBC_ST Homo sapiens cDNA clone IMAGE:2975391 3'
3188	16243		4.03	3.1E-01	AB029069.1	NT	Mus musculus gene for Ser/Thr Kinase KKIAMRE, exon 6
3927	16967	29880	0.93	3.1E-01	AJ251586.1	NT	Daucus carota mRNA for transcription factor E2F (E2F gene)
4999	18014	30901	1.25	3.1E-01	AE003984.1	NT	Xylella fastidiosa, section 130 of 229 of the complete genome
5239	18247	31119	0.79	3.1E-01	AF130370.1	NT	Rattus norvegicus MEN1 tumor suppressor (Men1) mRNA, alternative splice product, complete cds
5297	18320	31162	2.69	3.1E-01	AL163203.2	NT	Homo sapiens chromosome 21 segment HS21C003
5555	18652	31566	0.78	3.1E-01	AF176111.1	NT	Homo sapiens hepatocyte nuclear factor-3 alpha (HNF3A) gene, exon 1
5681	18776	31948	0.65	3.1E-01	P44132	SWISSPROT	HYPOTHETICAL PROTEIN HIT238
5682	18777	31949	0.87	3.1E-01	Z74883.1	NT	S.cerevisiae chromosome XV reading frame ORF YOL141w
5693	18788		1.01	3.1E-01	Y13278.1	NT	Mus musculus mRNA for polycystin
5696	18955	32142	2.3	3.1E-01	AF184122.1	NT	Homo sapiens filamin 2 (FLN2) gene, exons 10 through 22

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Table 4
Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6416	25660	32732	0.61	3.1E-01	R94322.1	EST_HUMAN	y44104.1 Soares fetal liver spleen 1NFS Homo sapiens cDNA clone IMAGE:188367 5'
6610	19668	32944	2.69	3.1E-01	AW983549.1	EST_HUMAN	RC3-HN0001-310300-011-b04 HN0001 Homo sapiens cDNA
6683	19740	33015	0.85	3.1E-01	A1264488.1	EST_HUMAN	q39401.x1 NCI_CGAP_Co8 Homo sapiens cDNA clone IMAGE:1874689 3'
6840	19893	33188	0.88	3.1E-01	X71887.1	NT	H.sapiens gene for immunoglobulin kappa light chain variable region A8 and A9
6830	20154		0.7	3.1E-01	AW377354.1	EST_HUMAN	MR2-CT0222-281089-005-h05 CT0222 Homo sapiens cDNA
7162	25634	31238	2.55	3.1E-01	BE737392.1	EST_HUMAN	601306121F1 NIH_MGC 39 Homo sapiens cDNA clone IMAGE:3640420 5'
7942	20884	34275	0.56	3.1E-01	4865390	NT	Homo sapiens hyaluronan synthase 2 (HAS2), mRNA
8038	20975	34371	0.49	3.1E-01	AF242431.1	NT	Mus musculus neuronal apoptosis inhibitory protein 6 (Naip6) gene, complete cds; and Naip3 gene, exons 2-9 and 11-16
8166	21104	34502	0.54	3.1E-01	AW850168.1	EST_HUMAN	IL3-CT0219-271099-022-E03 CT0219 Homo sapiens cDNA
8166	21104	34503	0.54	3.1E-01	AW850168.1	EST_HUMAN	IL3-CT0219-271099-022-E03 CT0219 Homo sapiens cDNA
8995	21981	35386	0.83	3.1E-01	R45318.1	EST_HUMAN	y44601.s1 Soares infant brain 1NIB Homo sapiens cDNA IMAGE:35639 3'
10262	23187	36871	0.52	3.1E-01	6679322	NT	Mus musculus phosphatidylinositol-4-phosphate 5-kinase, type 1 gamma (Pip5k1c), mRNA
10427	23349	36833	1	3.1E-01	BF696639.1	EST_HUMAN	602124743F1 NIH_MGC 56 Homo sapiens cDNA clone IMAGE:4281611 5'
10427	23349	36834	1	3.1E-01	BF696639.1	EST_HUMAN	602124743F1 NIH_MGC 56 Homo sapiens cDNA clone IMAGE:4281611 5'
10488	23410	36907	1.73	3.1E-01	A1244001.1	EST_HUMAN	q161e11.x1 NCI_CGAP_Kid3 Homo sapiens cDNA clone IMAGE:1863980 3' similar to gp.S55700 HYDROXYMETHYLGLUTARYL-COA LYASE PRECURSOR (HUMAN);
10666	23588		0.56	3.1E-01	T55325.1	EST_HUMAN	y447n08.s1 Stratagene fetal spleen (#937205) Homo sapiens cDNA clone IMAGE:74367 3' similar to similar to gb:M91036_m22 HEMOGLOBIN GAMMA-A AND GAMMA-G CHAINS (HUMAN)
11186	24142	37676	2.35	3.1E-01	BF216117.1	EST_HUMAN	60188352F1 NIH_MGC 57 Homo sapiens cDNA clone IMAGE:4095814 5'
11864	24746	38328	2.3	3.1E-01	7662291	NT	Homo sapiens KIAA0764 gene product (KIAA0764), mRNA
12133	25002	38608	1.68	3.1E-01	AF048693.1	NT	Homo sapiens transcription factor forkhead-like 7 (FKHL7) gene, complete cds
12133	25002	38609	1.68	3.1E-01	AF048693.1	NT	Homo sapiens transcription factor forkhead-like 7 (FKHL7) gene, complete cds
12415	25198		1.57	3.1E-01	AF294308.1	NT	Anolis opalinus isolate QS NADH dehydrogenase subunit 2 (ND2) gene, complete cds; mitochondrial gene for mitochondrial product
12451	25210		4.84	3.1E-01	AF304182.1	NT	Stizostedion vitreum 40S ribosomal protein S11 mRNA, partial cds
12592	25296		4.19	3.1E-01	AF195963.1	NT	Homo sapiens membrane-bound aminopeptidase P (XNPEP2) gene, complete cds
12944	25523		3.39	3.1E-01	AF196779.1	NT	Homo sapiens transcription factor IGHM enhancer 3, JM11 protein, JM4 protein, JM5 protein, T54 protein, JM10 protein, A4 differentiation-dependent protein, triple LIM domain protein 6, and synapophysin genes, complete cds; and L-type calcium channel a2
73	15808	26112	1.78	3.0E-01	6755083	NT	Mus musculus protein kinase C, epsilon (Pkc), mRNA
254	13351	26277	8.98	3.0E-01	AJ271735.1	NT	Homo sapiens Xq pseudautosomal region; segment 1/2
1227	14285	27222	2.16	3.0E-01	AW300400.1	EST_HUMAN	xs63008.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2774343 3'
1508	14541	27512	5.96	3.0E-01	AJ006755.1	NT	Balaenoptera physalus gene encoding atrial natriuretic peptide

Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2146	15162	28178	1.13	3.0E-01	AF237778.1	NT	Rattus norvegicus Ca2+/calmodulin-dependent protein kinase II, alpha subunit mRNA, 3' untranslated region
3225	16280		1.26	3.0E-01	AB030481.1	NT	Corynebacterium sp. ALY-1 alyPG gene for polyglutamate lyase, complete cds
3879	16918	29827	1.46	3.0E-01	AW817786.1	EST_HUMAN	PM1-ST0262-261199-001-g01 ST0262 Homo sapiens cDNA
3998	17037	29844	1.02	3.0E-01	AJ271736.1	NT	Homo sapiens Xq pseudocentromeric region; segment 2/2
4541	17564	30451	2.17	3.0E-01	AJ006755.1	NT	Balaenoptera physalus gene encoding atrial natriuretic peptide
5425	18528	31407	5.19	3.0E-01	BE741629.1	EST_HUMAN	601594960F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3948734 5'
5506	18606	31536	0.56	3.0E-01	AF224669.1	NT	Homo sapiens mannosidase, beta A, lysosomal (MANBA) gene, and ubiquitin-conjugating enzyme E2D 3 (UBE2D3) genes, complete cds
5510	18610	31541	0.78	3.0E-01	AF229247.1	NT	Cantagalo orthopoxvirus hemagglutinin gene, complete cds
5582	18678	31641	3.81	3.0E-01	BE693575.1	EST_HUMAN	RC3-BT0333-180700-111-a03 BT0333 Homo sapiens cDNA
5582	18678	31642	3.81	3.0E-01	BE693575.1	EST_HUMAN	RC3-BT0333-180700-111-a03 BT0333 Homo sapiens cDNA
5619	18715	31874	4.05	3.0E-01	U01247.1	NT	Mus musculus 129/sv Clara cell 10 kd protein (mCC10) gene, complete cds
7005	20131	33446	2.86	3.0E-01	D16313.1	NT	Mouse cyclokeratin 15 gene, complete cds
7041	18373	31261	0.71	3.0E-01	U02369.1	NT	Strongyloides purpuratus 34/67 kDa laminin-binding protein mRNA, partial cds
7111	20045	33347	0.96	3.0E-01	AF229247.1	NT	Cantagalo orthopoxvirus hemagglutinin gene, complete cds
7195	20219	33551	0.59	3.0E-01	X63941.1	NT	S Cerevisiae GAC1
7328	20299	33643	0.82	3.0E-01	AL163206.2	NT	Homo sapiens chromosome 21 segment HS21C006
7549	20512	33870	4.88	3.0E-01	10947007	NT	Mus musculus midnolin (Midn-pending), mRNA
7744	20698	34084	1.33	3.0E-01	AF071810.1	NT	Streptococcus pneumoniae strain DBL 5 PspA (pspA) gene, partial cds
8259	21228	34638	1.28	3.0E-01	AE001755.1	NT	Thermotoga maritima section 67 of 136 of the complete genome
8716	21684		4.13	3.0E-01	9910161	NT	Mus musculus C-type (calcium dependent, carbohydrate recognition domain) lectin, superfamily member 9 (Clec4e9), mRNA
8819	21786	35210	1.34	3.0E-01	BE566083.1	EST_HUMAN	601339079F1 NIH_MGC_53 Homo sapiens cDNA clone IMAGE:3681594 5'
9181	22147	35574	0.74	3.0E-01	AF141676.1	NT	Streptomyces sulfonolactams isopenicillin N synthase (pcbC) gene, partial cds
9223	22189		0.71	3.0E-01	7681685	NT	Homo sapiens DKFZP586M0122 protein (DKFZP586M0122), mRNA
9573	22535	35986	0.95	3.0E-01	AF220507.1	NT	Anabaena PCC7120 cytosine-specific DNA methyltransferase (dmnB) gene, complete cds; putative anthranilate phosphoribosyltransferase gene, partial cds; and unknown gene
9932	22859	36320	0.51	3.0E-01	P76399	SWISSPROT	HYPOTHETICAL 59.5 KD PROTEIN IN WZA-ASMA INTERGENIC REGION
10327	23251	36730	0.73	3.0E-01	BF574612.1	EST_HUMAN	602133271F1 NIH_MGC_81-Homo sapiens cDNA clone IMAGE:4286336 5'
10501	23423	36922	0.47	3.0E-01	AF152598.3	NT	Actinobacillus actinomycetomorans Tada (tadA), TadB (tadB), TadC (tadC), TadD (tadD), TadE (tadE), TadF (tadF), and TadG (tadG) genes, complete cds
10501	23423	36923	0.47	3.0E-01	AF152598.3	NT	Actinobacillus actinomycetomorans Tada (tadA), TadB (tadB), TadC (tadC), TadD (tadD), TadE (tadE), TadF (tadF), and TadG (tadG) genes, complete cds

Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10760	23681	37177	0.85	3.0E-01	AW18111.1	EST_HUMAN	xe03d10.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2606035 3'
10762	23683	37179	2.14	3.0E-01	AB030231.1	NT	Aspergillus oryzae b1p4 gene for ER chaperone BIP, complete cds
10782	23703	37201	0.82	3.0E-01	BF683841.1	EST_HUMAN	602140133F1 NIH_MGC_46 Homo sapiens cDNA clone IMAGE:4301097 5'
10782	23703	37202	0.82	3.0E-01	BF683841.1	EST_HUMAN	602140133F1 NIH_MGC_46 Homo sapiens cDNA clone IMAGE:4301097 5'
12061	24934	38529	2.5	3.0E-01	H51029.1	EST_HUMAN	y84b10.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:194107 5'
12061	24934	38530	2.5	3.0E-01	H51029.1	EST_HUMAN	y84b10.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:194107 5'
12696	25875		1.57	3.0E-01	AJ287631.1	NT	Rattus norvegicus mRNA for glyceraldehyde-3-phosphate dehydrogenase type 2 (gapdh-2 gene)
12979	25917		2.52	3.0E-01	6677766	NT	Mus musculus ribose 5-phosphate isomerase A (Rplia), mRNA
1747	14776		0.92	2.9E-01	AJ249895.1	NT	Mus musculus mas proto-oncogene and lgf2 gene for insulin-like growth factor type 2 and L41ps and Au76 pseudogenes
2039	15058	28077	1.19	2.9E-01	AE000736.1	NT	Aquifex aeolicus section 88 of 109 of the complete genome
2260	15274	28298	1.2	2.9E-01	AF222718.1	NT	Chrysothymus synuroides mitochondrion, complete genome
3265	16319	29240	1.92	2.9E-01	AW754239.1	EST_HUMAN	PM1-CT0326-171299-001-f12 CT0326 Homo sapiens cDNA
3265	16319	29241	1.92	2.9E-01	AW754239.1	EST_HUMAN	PM1-CT0326-171299-001-f12 CT0326 Homo sapiens cDNA
3912	16952	29863	1.03	2.9E-01	AI610836.1	EST_HUMAN	lp21a11.x1 NCI_CGAP_Gas4 Homo sapiens cDNA clone IMAGE:2188412 3' similar to gb:D15050 NIL-2-A
3955	16995	29911	0.81	2.9E-01	AI769472.1	EST_HUMAN	ZINC FINGER PROTEIN (HUMAN) contains element L1 repetitive element ;
4112	17146		0.7	2.9E-01	AW002802.1	EST_HUMAN	wj14d10.x1 NCI_CGAP_Kid12 Homo sapiens cDNA clone IMAGE:2402803 3' similar to WP:C34F8.7 CE15676 :
4511	17536	30420	1.24	2.9E-01	AA284468.1	EST_HUMAN	w02f10.x1 NCI_CGAP_G08 Homo sapiens cDNA clone IMAGE:2480395 3'
4710	17731		1.5	2.9E-01	AL163207.2	NT	zs57d12.r1 NCI_CGAP_G081 Homo sapiens cDNA clone IMAGE:701591 5' similar to contains Alu repetitive element;
5156	18166		1.25	2.9E-01	AI670898.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C007
5275	18281	31145	3.3	2.9E-01	AJ131017.1	NT	wa06f03.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2297309 3' similar to contains L1.12 L1 repetitive element ;
5277	18283	31146	1.12	2.9E-01	BE741380.1	EST_HUMAN	Mus musculus SCL gene locus
5330	18436		1.49	2.9E-01	R37485.1	EST_HUMAN	601594241F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3948178 5'
5469	20065	33372	0.75	2.9E-01	AF321001.1	NT	y77e12.s1 Soares infant brain TNIB Homo sapiens cDNA clone IMAGE:28291 3'
5858	19948	32133	5.1	2.9E-01	X56098.1	NT	Suaeda maritima subsp. salsa S-adenosylmethionine synthetase 2 mRNA, complete cds
5858	19948	32134	5.1	2.9E-01	X56098.1	NT	B subtilis levansucrase operon levD, levE, levF, levG and sacC (partial) genes for fructose phosphotransferase
5871	19960	32149	6.12	2.9E-01	6679662	NT	B subtilis levansucrase operon levD, levE, levF, levG and sacC (partial) genes for fructose phosphotransferase
6174	19249	32482	1.35	2.9E-01	AA418145.1	EST_HUMAN	Mus musculus Eph receptor A8 (EphA8), mRNA
							2697b12.r1 Soares_NHIMPu_S1 Homo sapiens cDNA clone IMAGE:767711 5'

Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6412	19480	32727	1.05	2.9E-01	AI797128.1	EST_HUMAN	we27c05.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:2342312 3' similar to contains L1.11 L1
6439	19524	32775	2.3	2.9E-01	U03420.1	NT	repetitive element;
6599	19659	32931	0.6	2.9E-01	R69194.1	EST_HUMAN	Bos taurus myosin I mRNA, complete cds
6599	19659	32932	0.6	2.9E-01	R69194.1	EST_HUMAN	y39408.r1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:141615 5'
6883	19635	33372	0.84	2.9E-01	Z50156.1	NT	y39408.r1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:141615 5'
7043	20065	33372	0.58	2.9E-01	AF321001.1	NT	D. discoideum gene for 34 kD actin binding protein
7179	18410	31211	1.57	2.9E-01	AF142329.1	NT	Suaeda maritima subsp. salsa S-adenosylmethionine synthetase 2 mRNA, complete cds
7303	20274	33810	2.99	2.9E-01	Q04399	SWISSPROT	Mus musculus Filin protein (Filin) gene, complete cds; and Ughn protein (Ughn) gene, partial cds
7387	20937	33887	1.68	2.9E-01	AF100958.1	NT	PUTATIVE MULTICOPPER OXIDASE YDR506C
8252	21221	34630	1.67	2.9E-01	BE540422.1	EST_HUMAN	Mus musculus major histocompatibility locus class II region; Fas-binding protein Daxx (DAXX) gene, partial cds; Bing1 (BING1), leucine (leucine), RalGDS-like factor (RLF), KE2 (KE2), BING4 (BING4), beta1, 3-galactosyl transferase (beta1,3-galactosyl tr>
8252	21221	34631	1.67	2.9E-01	BE540422.1	EST_HUMAN	601065830F1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3452287 5'
8489	21457	34874	0.49	2.9E-01	AJ237937.1	NT	601065830F1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3452287 5'
8489	21457	34875	0.49	2.9E-01	AJ237937.1	NT	Bos taurus partial stat5A gene, exons 5-19
8502	21470		1.16	2.9E-01	BF217743.1	EST_HUMAN	Bos taurus partial stat5A gene, exons 5-19
8682	21650		0.45	2.9E-01	AF197456.1	NT	601882570F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4095113 5'
8942	21908	35333	0.77	2.9E-01	AU150970.1	EST_HUMAN	Buchnera aphidicola plasmid pLau isolate M1 2-isopropylmalate synthase (leuA) gene, partial cds; 3-isopropylmalate dehydrogenase (leuB) gene, complete cds; and isopropylmalate dehydratase subunit (leuC) gene, partial cds
9277	22243	35672	1.01	2.9E-01	AF225908.1	NT	AU150970 NT2RP2 Homo sapiens cDNA clone NT2RP2003901 3'
9388	22353	35784	0.6	2.9E-01	M22452.1	NT	Arabidopsis thaliana sulfurylase receptor-like protein mRNA, complete cds
9601	22605	36053	0.76	2.9E-01	AJ248287.1	NT	Baboon lymphocyte homing/adhesion receptor mRNA, complete cds
9601	22605	36054	0.76	2.9E-01	AJ248287.1	NT	Pyrococcus abyssi complete genome; segment 5/6
11240	24193	37711	1.7	2.9E-01	AF128843.1	NT	Pyrococcus abyssi complete genome; segment 5/6
11497	24440	37989	1.86	2.9E-01	V01394.1	NT	Typanosoma cruzi stage-specific surface glycoprotein gp82 (gp82) mRNA, partial cds
11497	24440	37989	1.86	2.9E-01	V01394.1	NT	Torpedo californica mRNA encoding acetylcholine receptor gamma subunit
11913	24794	38365	2.95	2.9E-01	AL139078.2	NT	Torpedo californica mRNA encoding acetylcholine receptor gamma subunit
12109	24979	38579	2.1	2.9E-01	AW294742.1	EST_HUMAN	Campylobacter jejuni NCTC11168 complete genome; segment 5/6
12651	25334	31760	1.47	2.9E-01	AW005671.1	EST_HUMAN	U1-H-BW6-aim-f10-0-U1.s1 NCI_CGAP_Sub6 Homo sapiens cDNA clone IMAGE:2726984 3'
12728	25381	31747	4	2.9E-01	AF092453.1	NT	wz8805.x1 NCI_CGAP_Bm25 Homo sapiens cDNA clone IMAGE:2565921 3' similar to contains element
13025	25573	31694	1.35	2.9E-01	Y08937.1	NT	MER28 repetitive element;
							Homo sapiens TNF-alpha-inducible RNA binding protein (TIRP) gene, complete cds
							Chlamydomonas reinhardtii mRNA for nitrite reductase structural locus

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
13025	25573	31695	1.35	2.9E-01	Y0937.1	NT	Chlamydomonas reinhardtii mRNA for nitrite reductase structural locus
570	13640		2.2	2.8E-01	U67136.1	NT	Rattus norvegicus A-kinase anchoring protein AKAP150 mRNA, complete cds
575	13644		1.41	2.8E-01	U28145.1	NT	Prune dwarf virus movement protein, complete cds; coat protein, complete cds
1085	14129	27083	3.9	2.8E-01	AF168050.1	NT	Guinea guinea oocyte maturation factor Mos (c-mos) gene, partial cds
1282	14317	27279	1.06	2.8E-01	BE313442.1	EST_HUMAN	601148733F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:3163688 5'
1282	14317	27280	1.06	2.8E-01	BE313442.1	EST_HUMAN	601148733F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:3163688 5'
1295	14330	27291	2.65	2.8E-01	D86550.1	NT	Human mRNA for serine/threonine protein kinase, complete cds
1740	14770	27758	2.22	2.8E-01	AW860020.1	EST_HUMAN	QV1-CT0364-120200-065-505 CT0364 Homo sapiens cDNA
2028	15048	28082	2.08	2.8E-01	AL047620.1	EST_HUMAN	DKFZp566l2321_r1 586 (synonym: lute1) Homo sapiens cDNA clone DKFZp566l2321
2141	15158	28174	1.51	2.8E-01	AW511195.1	EST_HUMAN	hd44503.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2912333 3'
2479	15483	28507	2.18	2.8E-01	AE000494.1	NT	Escherichia coli K-12 MG1655 section 384 of 400 of the complete genome
2479	15483	28508	2.18	2.8E-01	AE000494.1	NT	Escherichia coli K-12 MG1655 section 384 of 400 of the complete genome
2554	15558		3.07	2.8E-01	AL161565.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 65
2674	15671	28689	1.35	2.8E-01	AB020975.1	NT	Arabidopsis thaliana mRNA for lipoyltransferase, complete cds
2982	16040		1.48	2.8E-01	AF179480.1	NT	Toxoplasma gondii 90kDa heat-shock protein (HSP90) mRNA, partial cds
2983	16041	28963	2.57	2.8E-01	Z14037.1	NT	B. taurus microsatellite (ETH121)
2983	16041	28964	2.57	2.8E-01	Z14037.1	NT	B. taurus microsatellite (ETH121)
3390	16439	29365	1.16	2.8E-01	AP000004.1	NT	Pyrococcus horikoshii OT3 genomic DNA, 777001-994000 nt, position (47)
4021	17059	29960	1.72	2.8E-01	AE001180.1	NT	Borrelia burgdorferi (section 66 of 70) of the complete genome
4150	17181		0.67	2.8E-01	AE004450.1	NT	Pseudomonas aeruginosa PA01, section 11 of 528 of the complete genome
4226	17255		2.41	2.8E-01	A090868.1	EST_HUMAN	ov44g10.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1640228 3' similar to contains Alu repetitive element; contains element MER22 repetitive element;
4488	17513	30401	2.62	2.8E-01	P13615	SWISSPROT	RNA POLYMERASE BETA SUBUNIT (LARGE STRUCTURAL PROTEIN)(L PROTEIN)
4822	17839	30737	0.92	2.8E-01	D15050.1	NT	Human mRNA for transcription factor AREB6, complete cds
4822	17839	30738	0.92	2.8E-01	D15050.1	NT	Human mRNA for transcription factor AREB6, complete cds
4866	17883	30771	2.71	2.8E-01	AF030154.1	NT	Bovine adenovirus 3 complete genome
4897	17914	30804	1.37	2.8E-01	BF528186.1	EST_HUMAN	602042601F1 NCL_CGAP_Bn67 Homo sapiens cDNA clone IMAGE:4180129 5'
4920	17937	30829	1.69	2.8E-01	A1272699.1	EST_HUMAN	q159c11.x1 Soares_NHMPu_S1 Homo sapiens cDNA clone IMAGE:1876628 3' similar to contains Alu repetitive element; contains element L TRS repetitive element;
5384	25637	31362	23.73	2.8E-01	AA349997.1	EST_HUMAN	EST57072 Infant brain Homo sapiens cDNA 5' end
5687	18782	31954	2.52	2.8E-01	AB016825.1	NT	Human sapiens OCTN2 gene, complete cds
5915	19001		1.04	2.8E-01	AW992583.1	EST_HUMAN	GM1-BN0024-150200-118-g12 BN0024 Homo sapiens cDNA
6028	19111	32313	0.57	2.8E-01	AA765296.1	EST_HUMAN	oa01d06.s1 NCL_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1303691 3' similar to gb:M34539 FK506-BINDING PROTEIN (HUMAN);

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Table 4
Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6048	19129		0.49	2.8E-01	AA04576.1	EST_HUMAN	z41101.1 Soares ovary tumor NBH0T Homo sapiens cDNA clone IMAGE:724921 5' similar to contains Alu repetitive element;
6300	25994		0.78	2.8E-01	M36688.1	NT	Bovine 680 bp repeated unit of 1.723 satellite DNA
6343	19412	32653	2.02	2.8E-01	AF003124.1	NT	Mesembryanthemum crystallinum fructose-biphosphate aldolase mRNA, complete cds
6343	19412	32654	2.02	2.8E-01	AF003124.1	NT	Mesembryanthemum crystallinum fructose-biphosphate aldolase mRNA, complete cds
6895	19947	33244	8.31	2.8E-01	BF511215.1	EST_HUMAN	UI-H-B14-act-04-0-UI.s1 NCL CGAP_Sub8 Homo sapiens cDNA clone IMAGE:3085182 3'
7201	20225	33557	0.52	2.8E-01	U66300.1	NT	Orthogeomys heterodus cytochrome b (cytb) gene, mitochondrial gene encoding mitochondrial protein, complete cds
7579	20541	33900	0.51	2.8E-01	BE981455.1	EST_HUMAN	601490157F1 NIH_MGC_69 Homo sapiens cDNA clone IMAGE:3892142 5'
7675	20633		1.03	2.8E-01	U05693.1	NT	Marsilea quadrifolia ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit (rbol) gene, chloroplast gene encoding chloroplast protein, partial cds
7724	20680	34044	0.77	2.8E-01	X69980.1	NT	L. esculentum yps2 mRNA for GTP-binding protein
8429	21398	34808	1.12	2.8E-01	A1346126.1	EST_HUMAN	qp48h01.x1 NCL CGAP_Co8 Homo sapiens cDNA clone IMAGE:1926289 3' similar to gb:X08323_cds1
8429	21398	34809	1.12	2.8E-01	A1346126.1	EST_HUMAN	MITOCHONDRIAL 60S RIBOSOMAL PROTEIN L3 (HUMAN);
8551	21519	34938	2.25	2.8E-01	U57688.1	NT	qp48h01.x1 NCL CGAP_Co8 Homo sapiens cDNA clone IMAGE:1926289 3' similar to gb:X08323_cds1
8859	21826	35249	0.49	2.8E-01	AA911629.1	EST_HUMAN	MITOCHONDRIAL 60S RIBOSOMAL PROTEIN L3 (HUMAN);
8936	21902		7.34	2.8E-01	BF347847.1	EST_HUMAN	Homo sapiens lanosterol 14-alpha demethylase cytochrome P450 (CYP51) gene, exon 5
9821	22670	36127	0.91	2.8E-01	U17251.1	NT	o02h05.s1 NCL CGAP_Co12 Homo sapiens cDNA clone IMAGE:1419893 3' similar to gb:M87789 IG
10069	22996		0.85	2.8E-01	L13654.1	NT	GAMMA-1 CHAIN C REGION (HUMAN);
10248	23173	36662	0.93	2.8E-01	AF132728.1	NT	602022987F1 NCL CGAP_Bm67 Homo sapiens cDNA clone IMAGE:4158525 5'
10248	23173	36663	0.93	2.8E-01	AF132728.1	NT	Neurospora crassa negative regulator sulfur controller-2 (scon-2) gene, complete cds
10310	23234	36716	0.6	2.8E-01	AF294393.1	NT	Lycopersicon esculentum peroxidase (TPX1) mRNA, complete cds
10420	23342	36828	4.98	2.8E-01	7706163	NT	Escherichia coli translocated intimin receptor Tir (tir) gene, complete cds
10676	23598		0.94	2.8E-01	9628154	NT	Escherichia coli translocated intimin receptor Tir (tir) gene, complete cds
10718	23640	37133	0.44	2.8E-01	BE959727.2	EST_HUMAN	Rattus norvegicus glycerol-3-phosphate dehydrogenase gene, promoters A and B and exons 1a and 1b; nuclear gene for mitochondrial product
11095	24055	37578	1.9	2.8E-01	BF241062.1	EST_HUMAN	Homo sapiens hypothetical protein (LOC51319), mRNA
11095	24055	37579	1.9	2.8E-01	BF241062.1	EST_HUMAN	Fujinami sarcoma virus, complete genome
11125	24085	37612	2.96	2.8E-01	BF695970.1	EST_HUMAN	601654822R1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:3839765 3'
11608	24546		4.02	2.8E-01	BF874023.1	EST_HUMAN	601880794F1 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:4109350 5'
12312	25120	31843	1.39	2.8E-01	AF268477.1	NT	601880794F1 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:4109350 5'

Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
12684	25351		23.54	2.8E-01	D83328.1	NT	Mus musculus DNA for prostaglandin D2 synthase, complete cds
12788	25420	31738	3.09	2.8E-01	BE178899.1	EST_HUMAN	PM4-HT0806-030400-001-a07 HT0806 Homo sapiens cDNA
12817	25439	31742	1.37	2.8E-01	BE900116.1	EST_HUMAN	601673020F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3955996 5'
12969	25879		3.15	2.8E-01	11433629	NT	Homo sapiens CDC42-binding protein kinase beta (DMPK-like) (CDC42BPB), mRNA
13097	25973		1.76	2.8E-01	AW025400.1	EST_HUMAN	wu96g05.x1 NCL_CGAP_Kid3 Homo sapiens cDNA clone IMAGE:2627928 3'
477	13549	26477	2.95	2.7E-01	Y17324.1	NT	Rattus norvegicus CDK104 mRNA
615	13680	26598	9.43	2.7E-01	AA450081.1	EST_HUMAN	z39b10.s1 Soares_tctat_fetus_Nb2HF8_gw Homo sapiens cDNA clone IMAGE:788827 3' similar to contains Alu repetitive element
1266	14301	27262	2.18	2.7E-01	AB004906.1	NT	Ipomoea purpurea transposable element T100 gene for transposase, complete cds
1625	14658		2.21	2.7E-01	X79815.1	NT	G.lambila SR2 gene
1742	14772	27757	2.88	2.7E-01	W58067.1	EST_HUMAN	z322h10.r1 Soares_fetal_heart_NbHH19W Homo sapiens cDNA clone IMAGE:341443 5'
1791	14820	27805	2.49	2.7E-01	P0334.1	SWISSPROT	GAG POLYPROTEIN [CONTAINS: INNER COAT PROTEIN P12; CORE PROTEIN P15; CORE SHELL PROTEIN P30; NUCLEOPROTEIN P10]
2145	15885		2.29	2.7E-01	AF047575.1	NT	Rattus norvegicus vesicular monomeric transporter type 2, promoter region and exon 1
2375	15883	28405	9.38	2.7E-01	Y13868.1	NT	Feline immunodeficiency virus env gene, isolate ITT0088PIU (M89), partial repetitive element
2481	15465	28488	3.97	2.7E-01	A1310859.1	EST_HUMAN	ta43c11.x2 NCL_CGAP_Lu25 Homo sapiens cDNA clone IMAGE:2046838 3' similar to contains element L1
2909	15968	28891	1	2.7E-01	AF251278.1	NT	Mus musculus serine protease inhibitor 14 (Spi14) mRNA, complete cds
2997	16055		0.91	2.7E-01	BF088284.1	EST_HUMAN	GM1-HT0875-060900-385-e05 HT0875 Homo sapiens cDNA
4038	17076	29976	1.74	2.7E-01	A1928015.1	EST_HUMAN	w02a11.x1 NCL_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2462828 3'
4053	17090	29985	0.76	2.7E-01	AF216214.1	NT	Drosophila buzzatii alpha-esterase 6 (ae6) gene, partial cds
4053	17090	29986	0.76	2.7E-01	AF216214.1	NT	Drosophila buzzatii alpha-esterase 6 (ae6) gene, partial cds
4061	17097	29991	2.33	2.7E-01	L77569.1	NT	Homo sapiens DiGeorge syndrome critical region, telomeric end
4928	17946	30837	0.76	2.7E-01	L27516.1	NT	Triticum aestivum (Wass86) gene, complete cds
5079	18089		4.11	2.7E-01	AW856131.1	EST_HUMAN	RC1-GT0286-230200-076-e03 G10286 Homo sapiens cDNA
5339	18444	31197	2.13	2.7E-01	P17277	SWISSPROT	HOMEOBOX PROTEIN HOXA4 (CHOX-1.4)
5567	18664		1.11	2.7E-01	AB033171.1	NT	Astrepore myrophthalma mitochondrial cytb gene for cytochrome b, partial cds
6476	19541	32787	0.51	2.7E-01	Q00918	SWISSPROT	LATENT TRANSFORMING GROWTH FACTOR BETA BINDING PROTEIN 1 PRECURSOR (TRANSFORMING GROWTH FACTOR BETA-1 BINDING PROTEIN 1) (TGF-BETA1-BP-1) (TRANSFORMING GROWTH FACTOR BETA-1 MASKING PROTEIN, LARGE SUBUNIT)
6476	19541	32788	0.51	2.7E-01	Q00918	SWISSPROT	LATENT TRANSFORMING GROWTH FACTOR BETA BINDING PROTEIN 1 PRECURSOR (TRANSFORMING GROWTH FACTOR BETA-1 BINDING PROTEIN 1) (TGF-BETA1-BP-1) (TRANSFORMING GROWTH FACTOR BETA-1 MASKING PROTEIN, LARGE SUBUNIT)
6765	19819	33100	1.06	2.7E-01	AE001094.1	NT	Archaeoglobus fulgidus section 13 of 172 of the complete genome

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6765	19819	33101	1.06	2.7E-01	AE001094.1	NT	Archaeoglobus fulgidus section 13 of 172 of the complete genome
6946	20170	33494	2.1	2.7E-01	Q61534	SWISSPROT	FIBRILLIN 1 PRECURSOR
7253	19988		0.64	2.7E-01	A1540070.1	EST_HUMAN	Id08h08.x1 NC1 CGAP_GLI1 Homo sapiens cDNA clone IMAGE:2075103 3'
7580	20542	33901	0.8	2.7E-01	Q11079	SWISSPROT	HYPOTHETICAL 20.9 KD PROTEIN B0563.3 IN CHROMOSOME X
7811	20760	34135	0.86	2.7E-01	Q01168	SWISSPROT	NITROGEN REGULATORY PROTEIN NUT1
7811	20760	34136	0.86	2.7E-01	Q01168	SWISSPROT	NITROGEN REGULATORY PROTEIN NUT1
7952	20893	34285	1.9	2.7E-01	AF248054.1	NT	Bos taurus micromolar calcium activated neutral protease 1 (CAPN1) gene, exons 11-20, and partial cds
7952	20893	34286	1.9	2.7E-01	AF248054.1	NT	Bos taurus micromolar calcium activated neutral protease 1 (CAPN1) gene, exons 11-20, and partial cds
8012	20950	34343	0.86	2.7E-01	AA351121.1	EST_HUMAN	EST58740 Infant brain Homo sapiens cDNA 5' and similar to myosin-binding protein H
8012	20950	34344	0.86	2.7E-01	AA351121.1	EST_HUMAN	EST58740 Infant brain Homo sapiens cDNA 5' and similar to myosin-binding protein H
8084	21021	34421	0.63	2.7E-01	L01081.1	NT	Oryctolagus cuniculus UDP-glucuronosyltransferase (UGT2B13) mRNA, complete cds
8196	21166	34576	0.86	2.7E-01	AA013147.1	EST_HUMAN	z635b11.s1 Scores retina N2b4-IR Homo sapiens cDNA clone IMAGE:360957 3' similar to contains Aliu repetitive element;
8360	21329		0.52	2.7E-01	AF048820.1	NT	Carassius auratus pituitary adenylate cyclase activating polypeptide type 1 receptor precursor mRNA, complete cds
8475	21444	34861	0.43	2.7E-01	AW888503.1	EST_HUMAN	MR1-SN0062-100500-002-009 SN0062 Homo sapiens cDNA
8527	21495	34909	0.52	2.7E-01	R39257.1	EST_HUMAN	yc91h06.s1 Scores Infant brain 1N1B Homo sapiens cDNA clone IMAGE:23511 3'
8634	21602	35025	0.74	2.7E-01	AL161952.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 52
9112	22078	35503	0.52	2.7E-01	Q14764	SWISSPROT	MAJOR VAULT PROTEIN (MVP) (LUNG RESISTANCE-RELATED PROTEIN)
9382	22347	35779	0.51	2.7E-01	X03216.1	NT	Staphylococcus aureus transposon Tn554
9688	22641	36098	11.09	2.7E-01	O83809	SWISSPROT	THREONYL-TRNA SYNTHETASE (THREONINE-TRNA LIGASE) (THRRS)
9688	22641	36099	11.09	2.7E-01	O83809	SWISSPROT	THREONYL-TRNA SYNTHETASE (THREONINE-TRNA LIGASE) (THRRS)
9681	22644		2.17	2.7E-01	P37928	SWISSPROT	FIMBRIAE W PROTEIN
10160	23085	36562	0.64	2.7E-01	D89660.1	NT	Rattus norvegicus DNA for peroxisome assembly factor-2, exon 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17 and complete cds
10441	23363	36853	0.85	2.7E-01	AF091848.1	NT	Oryctolagus cuniculus calgranulin C mRNA, partial cds
10477	23399	36896	2.83	2.7E-01	AF087434.1	NT	Mus musculus transcription factor NF-ATc isoform a (NF-ATc) mRNA, complete cds
10611	23533	37029	1.06	2.7E-01	AF156539.1	NT	Homo sapiens xeroderma pigmentosum complementation group C (XPC) gene, intron 9
10611	23533	37030	1.06	2.7E-01	AF156539.1	NT	Homo sapiens xeroderma pigmentosum complementation group C (XPC) gene, intron 9
11163	24121	37648	4.87	2.7E-01	AV705043.1	EST_HUMAN	AV705043 ADB Homo sapiens cDNA clone ADBCOD05 5'
11163	24121	37649	4.87	2.7E-01	AV705043.1	EST_HUMAN	AV705043 ADB Homo sapiens cDNA clone ADBCOD05 5'

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
11171	24128	37658	2.31	2.7E-01	AJ133269.1	NT	Homo sapiens cavedin-1/-2 locus, Contig1, D7S522, genes CAV2 (exons 1, 2a, and 2b), CAV1 (exons 1 and 2)
12066	24939		2.08	2.7E-01	BE141035.1	EST_HUMAN	MR0-HT0067-201099-002-c10 HT0067 Homo sapiens cDNA
12090	24981		1.52	2.7E-01	O14181	SWISSPROT	PUTATIVE 60S RIBOSOMAL PROTEIN C4F8.05C
12509	25244	31802	1.39	2.7E-01	AL163281.2	NT	Homo sapiens chromosome 21 segment HS21C081
12757	25758		1.46	2.7E-01	AB008782.1	NT	Arabidopsis thaliana mRNA for sulfate transporter, complete cds
12851	25480		1.63	2.7E-01	Q63627	SWISSPROT	CTD-BINDING SR-LIKE PROTEIN RA4
12948	25526		3.16	2.7E-01	AF217491.1	NT	Homo sapiens fragile 16D oxido reductase (FOR) gene, exon 6
470	15841	26470	1.97	2.6E-01	P78411	SWISSPROT	IROQUOIS-CLASS HOMEODOMAIN PROTEIN IRX-2
481	13554		1.5	2.6E-01	D16459.1	NT	Bos taurus mRNA for mb-1, complete cds
1394	14428	27397	1.96	2.6E-01	BE85087.1	EST_HUMAN	601510838F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3912345 5'
1431	14465	27441	1.36	2.6E-01	AB013280.1	NT	Glycine max pseudogene for mb-1, complete cds
1912	14938	27931	6.4	2.6E-01	AL161472.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 2
1912	14938	27932	6.4	2.6E-01	AL161472.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 2
2104	15121		7.48	2.6E-01	AW733192.1	EST_HUMAN	bb04d10.x1 NIH_MGC_14 Homo sapiens cDNA clone IMAGE:2958451 3' similar to gb:M36072 80S RIBOSOMAL PROTEIN L7A (HUMAN); gb:M14689_cds1 Mouse surfeit locus surfeit 3 protein gene (MOUSE);
2480	15484		0.99	2.6E-01	Y12996.1	NT	B. maritimus tbcL gene
2553	15555		8.24	2.6E-01	BE272440.1	EST_HUMAN	601126016F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:2990043 5'
3108	16165		1.02	2.6E-01	AW974531.1	EST_HUMAN	EST386635 MAGE resequences, MAGM Homo sapiens cDNA
3594	16639	29559	1.02	2.6E-01	M22342.1	NT	Bacteriophage T2 DNA-(adenine-N0)methyltransferase (dam) gene, complete cds
3657	16700	29616	2.11	2.6E-01	AF229118.1	NT	Homo sapiens acetylcholinesterase collagen-like tail subunit (COLQ) gene, exons 1A, 2, 3, 4, and 5
3982	17022	29932	0.77	2.6E-01	AJ012174.2	NT	Chlamydia pneumoniae partial rnpB gene for RNase P RNA subunit
3982	17022	29933	0.77	2.6E-01	AJ012174.2	NT	Chlamydia pneumoniae partial rnpB gene for RNase P RNA subunit
4181	17212	30100	17.99	2.6E-01	BE080598.1	EST_HUMAN	QV1-BT0630-040400-132-e03 BT0630 Homo sapiens cDNA
4384	17412	30296	1.39	2.6E-01	AF175293.1	NT	Enterococcus faecium strain N97-330 vanD glycopeptide resistance gene cluster, complete cds; and unknown gene
4522	17547	30434	0.82	2.6E-01	AB021180.1	NT	Gallus gallus mRNA for skeletal myosin heavy chain, complete cds
4522	17547	30435	0.82	2.6E-01	AB021180.1	NT	Gallus gallus mRNA for skeletal myosin heavy chain, complete cds
4578	17501	30497	1.47	2.6E-01	AA457617.1	EST_HUMAN	aa89d07.r1 Stradagene fetal retina 937202 Homo sapiens cDNA clone IMAGE:338477 5'
4677	17698	30585	2.31	2.6E-01	U01103.1	NT	Arabidopsis thaliana PSI type III chlorophyll a/b-binding protein (Lhca3') mRNA, complete cds
4745	17765	30659	1.46	2.6E-01	AF142703.1	NT	Ophrestia radicata maturase-like protein (matK) gene, complete cds; chloroplast gene for chloroplast product

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5007	18021	30909	4.38	2.8E-01	H04858.1	EST_HUMAN	y51e05.t1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:152288 5'
5081	18091		0.76	2.8E-01	AA884625.1	EST_HUMAN	am33b71.t1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1468605 3'
5414	18517		1.08	2.8E-01	AB036972.1	NT	Parametrium caudatum gene for PAP, complete cds
5524	18623	31558	0.89	2.8E-01	M96080.1	NT	Acetobacter xylinum cellulose synthase (bcsA) gene, partial cds, CMCax and CcpAx genes, complete cds
5651	18747		0.71	2.8E-01	A1862398.1	EST_HUMAN	tt16a03.x1 NCL_CGAP_Co18 Homo sapiens cDNA clone IMAGE:2075788 3' similar to contains element
5889	18958	32146	0.68	2.8E-01	AF207550.1	NT	Homo sapiens protein translocase, JM28 protein, UDP-galactose translocator, pim-2 protooncogene homolog
6189	25993		2.61	2.8E-01	AE001811.1	NT	pim-2h, and shal-type potassium channel genes, complete cds; JM12 protein and transcription factor IGHM
6325	19395	32637	1.81	2.8E-01	A1582557.1	EST_HUMAN	enhancer 3 genes, partial cds; and unknown gp Thermotoga maritima section 123 of 136 of the complete genome
6325	18395	32638	1.81	2.8E-01	A1582557.1	EST_HUMAN	ts02e12.x1 NCL_CGAP_Pan1 Homo sapiens cDNA clone IMAGE:2227438 3' similar to SW:NDP1_RAT
6562	19622	32887	1.01	2.8E-01	AL162757.2	NT	Q64289 NEUROGENIC DIFFERENTIATION FACTOR 1 ; contains element LTR1 repetitive element ;
6825	19879	33169	0.6	2.8E-01	BE792052.1	EST_HUMAN	y37a03.s1 Soares fetal liver spleen 1NFS Homo sapiens cDNA clone IMAGE:3936156 5'
6825	19879	33170	0.6	2.8E-01	BE792052.1	EST_HUMAN	601581754F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3936156 5'
7238	20259	33593	0.75	2.8E-01	A1914380.1	EST_HUMAN	wd48c04.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2331366 3' similar to gb:M37721
7620	20580	33944	0.72	2.8E-01	BE148961.1	EST_HUMAN	PEPTIDYL-GLYCINE ALPHA-AMIDATING MONOOXYGENASE PRECURSOR (HUMAN);
7663	25696		0.73	2.8E-01	AL139077.2	NT	GM0-HT0245-031199-085-f04 HT0245 Homo sapiens cDNA
7700	20668		0.61	2.8E-01	AA190149.1	EST_HUMAN	Campylobacter jejuni NCTC11168 complete genome; segment 4/6
8013	20951	34345	1.53	2.8E-01	R10365.1	EST_HUMAN	zp92a01.r1 Stralagene HeLa cell s3 937216 Homo sapiens cDNA clone IMAGE:627672 5'
8071	21008	34408	0.85	2.8E-01	Q09835	SWISSPROT	y37a03.s1 Soares fetal liver spleen 1NFS Homo sapiens cDNA clone IMAGE:129004 3' similar to
8182	21152	34559	1.13	2.8E-01	R02411.1	EST_HUMAN	gb:X12517.U1 SMALL NUCLEAR RIBONUCLEOPROTEIN C (HUMAN);
8236	21205	34610	1.17	2.8E-01	BE144331.1	EST_HUMAN	HYPOTHETICAL TRP-ASP REPEATS CONTAINING PROTEIN C29E6.01 IN CHROMOSOME I
8480	21449	34866	0.62	2.8E-01	X8264.1	NT	y82a07.r1 Soares fetal liver spleen 1NFS Homo sapiens cDNA clone IMAGE:124212 5'
8480	21449	34867	0.62	2.8E-01	X8264.1	NT	MR0-HT0106-181199-003-d12 HT0106 Homo sapiens cDNA
8677	21645	35099	2.87	2.8E-01	BF345688.1	EST_HUMAN	D.melanogaster mRNA for alpha 1,2 mannosidase (Berlin)
8753	21721	35143	1.92	2.8E-01	Q10199	SWISSPROT	D.melanogaster mRNA for alpha 1,2 mannosidase (Berlin)
							602014422F1 NC1_CGAP_Bm64 Homo sapiens cDNA clone IMAGE:4150386 5'
							HYPOTHETICAL 76.2 KD PROTEIN C11C11.02 IN CHROMOSOME II

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9042	22008	35428	4.09	2.6E-01	BE830339.1	EST_HUMAN	RC6-ET0082-310600-021-F10 ET0082 Homo sapiens cDNA
9042	22008	35428	4.09	2.6E-01	BE830339.1	EST_HUMAN	RC6-ET0082-310600-021-F10 ET0082 Homo sapiens cDNA
9822	22671	36128	0.89	2.6E-01	X17604.1	NT	S. occidentalis INV gene for invertase (EC 3.2.1.26)
10096	23022		0.63	2.6E-01	AF057121.1	NT	Lontra canadensis cytochrome b (cyb) gene, mitochondrial gene encoding mitochondrial protein, complete cds
10227	23152	36641	1.08	2.6E-01	P87366	SWISSPROT	GREEN-SENSITIVE OPSIN (GREEN CONE PHOTORECEPTOR PIGMENT) (KHFH-G)
10227	23152	36642	1.08	2.6E-01	P87366	SWISSPROT	GREEN-SENSITIVE OPSIN (GREEN CONE PHOTORECEPTOR PIGMENT) (KHFH-G)
10350	23472		0.61	2.6E-01	Q28295	SWISSPROT	VON WILLEBRAND FACTOR PRECURSOR (VWF)
10875	23795		0.91	2.6E-01	Y10190.1	NT	Homo sapiens PHEX gene
10978	23898		0.48	2.6E-01	Y15874.2	NT	Danio rerio mRNA for RPTP-alpha protein
11854	24736		32.27	2.6E-01	X51765.1	NT	Human lambda-immunoglobulin constant region complex (germline)
12268	25091		2.77	2.6E-01	10190655	NT	Mus musculus Jerky (Jrk), mRNA
12464	25683		3.3	2.6E-01	BE883491.1	EST_HUMAN	601517052F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3912612 5'
12828	25257	31806	4.42	2.6E-01	AF316998.1	NT	Homo sapiens Nark-ATPase gamma subunit (FXVD2) gene, complete cds, alternatively spliced
12846	25456		2.01	2.6E-01	D88425.1	NT	Cavia cobaya mRNA for serine/threonine kinase, complete cds
12874	25539		1.74	2.6E-01	AF141325.2	NT	Homo sapiens inositol polyphosphate 1-phosphatase (INPP1) gene, complete cds
13010	25562		3.07	2.6E-01	P47285	SWISSPROT	HYPOTHETICAL PROTEIN MG039
241	13340	26265	2.33	2.5E-01	4502298	NT	Homo sapiens ATP synthase, H+ transporting, mitochondrial F1 complex, delta subunit (ATP5D), nuclear gene encoding mitochondrial protein, mRNA
242	13340	26265	1.97	2.5E-01	4502298	NT	Homo sapiens ATP synthase, H+ transporting, mitochondrial F1 complex, delta subunit (ATP5D), nuclear gene encoding mitochondrial protein, mRNA
255	13352		4.63	2.5E-01	M26601.1	NT	Starfish (P. ochraceus) cytoplasmic actin gene, complete cds
833	13890	26844	1.87	2.5E-01	U09964.1	NT	Mus musculus (CR/Swiss) glyceraldehyde 3-phosphate dehydrogenase (Gapd-S) gene, complete cds
1123	14167	27119	9.8	2.5E-01	T88837.1	EST_HUMAN	ye11g07.r1 Stratagene lung (#837210) Homo sapiens cDNA clone IMAGE:117488 5'
1522	14564	27525	1.55	2.5E-01	AL115624.1	NT	Botrytis cinerea strain T4 cDNA library under conditions of nitrogen deprivation
1741	14771		5.06	2.5E-01	4885406	NT	Homo sapiens hyperpolarization activated cyclic nucleotide-gated potassium channel 4 (HCN4) mRNA
1900	15880	27920	0.94	2.5E-01	BE69604.1	EST_HUMAN	PM4-CT0400-310700-005-008 CT0400 Homo sapiens cDNA
1900	15880	27921	0.94	2.5E-01	BE69604.1	EST_HUMAN	PM4-CT0400-310700-005-008 CT0400 Homo sapiens cDNA
2417	15424		13.96	2.5E-01	AE000675.1	NT	Aquifex aeolicus section 7 of 109 of the complete genome
2503	15506		1.09	2.5E-01	AA251987.1	EST_HUMAN	zs11a12.r1 NCL_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:884862 5'
2844	15641	28665	0.94	2.5E-01	X95310.1	NT	B. laurus mRNA for D-aspartate oxidase
3423	16471		2.83	2.5E-01	AW073471.1	EST_HUMAN	EST385464 IMAGE resequences, MAGM Homo sapiens cDNA

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3545	16591	29516	0.87	2.5E-01	AF233875.1	NT	Danio rerio peptide YY precursor gene, complete cds
3560	16606	29528	7.94	2.5E-01	AL161517.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 29
3881	16900	29803	1.15	2.5E-01	AI741483.1	EST_HUMAN	wg11c07.x1 Soares NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:2364780 3'
3881	16900	29804	1.15	2.5E-01	AI741483.1	EST_HUMAN	wg11c07.x1 Soares NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:2364780 3'
4096	17130		1.76	2.5E-01	P32323	SWISSPROT	A-AGGLUTININ ATTACHMENT SUBUNIT PRECURSOR
4346	17373		0.99	2.5E-01	Q03314	SWISSPROT	RHIB PROTEIN
4780	17800		1.34	2.5E-01	Q27225	SWISSPROT	MOLT-INHIBITING HORMONE PRECURSOR (MIH)
4788	17806	30698	4.71	2.5E-01	AF007788.1	NT	Choristoneura fumiferana diapause associated protein 2 (DAP2) mRNA, complete cds
4821	17838	30736	2.32	2.5E-01	AE004416.1	NT	Vibrio cholerae chromosome II, section 73 of 93 of the complete chromosome
4840	17857		3.69	2.5E-01	AJ230113.1	NT	Mus musculus annexin V gene, intron 4 segment containing 5' LTR and gag portion of MuERV-L (murine endogenous retrovirus) element
4870	17887	30775	0.84	2.5E-01	BE898785.1	EST_HUMAN	601437488F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3922800 5'
5086	18096	30972	0.84	2.5E-01	AW873588.1	EST_HUMAN	hcd2111.x1 Soares NFL_I_GBC_S1 Homo sapiens cDNA clone IMAGE:3041997 3' similar to WP:Y71F9A_294.D CE22858:
5243	18251		0.96	2.5E-01	AA768389.1	EST_HUMAN	ca63a09.s1 NC1_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1316920 3' similar to contains Alu repetitive element
5399	18502	31380	13.58	2.5E-01	S83390.1	NT	T3 receptor-associated cofactor-1 [human, fetal liver, mRNA, 2880 nt]
6070	19151	32363	0.64	2.5E-01	AJ006345.1	NT	Homo sapiens KVLQT1 gene
6071	19152		0.87	2.5E-01	AL163207.2	NT	Homo sapiens chromosome 21 segment HS21C007
6525	19588	32847	0.49	2.5E-01	P22219	SWISSPROT	PROTEIN KINASE VPS15
6780	19835	33118	0.86	2.5E-01	AJ251973.1	NT	Homo sapiens partial stealin-1 gene
7245	19980	33277	0.8	2.5E-01	8394138	NT	Rattus norvegicus rab3 (RAB3), mRNA
7575	20537	33806	0.79	2.5E-01	U13992.1	NT	Feline calicivirus CF168 RNA helicase/cysteine protease/RNA-dependent RNA polymerase polypeptide precursor and capsid protein precursor, genes, complete cds; and unknown gene
7604	20565		1.13	2.5E-01	AF134119.1	NT	Mus musculus SKD1 (Skd1) gene, complete cds
7852	20798	34174	0.88	2.5E-01	AL161506.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 18
7898	20841	34223	3.88	2.5E-01	AL163282.2	NT	Homo sapiens chromosome 21 segment HS21C082
8177	21147	34555	2.72	2.5E-01	BF109040.1	EST_HUMAN	7157a03.x1 Soares NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:3525389 3'
8188	21158	34587	0.62	2.5E-01	BE960712.1	EST_HUMAN	601653391R2 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:3826198 3'
8568	21536	34956	2.02	2.5E-01	BF038595.1	EST_HUMAN	601459238F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3862809 5'
8740	21708	35131	0.87	2.5E-01	P04492	SWISSPROT	E1B PROTEIN, SMALL T-ANTIGEN (E1B 19K)
8963	21949	35373	3.37	2.5E-01	H53236.1	EST_HUMAN	ykb407.1 Soares fetal liver spleen 1NLS Homo sapiens cDNA clone IMAGE:202501 5'
9227	22163	35623	0.81	2.5E-01	M89526.1	NT	Mouse testis-specific protein (TPX-1) gene, exon 10
9874	22827	36280	16.45	2.5E-01	U89651.2	NT	Homo sapiens matrix metalloproteinase MMP Ras1-1 gene, promoter region

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9874	22827	36281	16.45	2.9E-01	U80651.2	NT	Homo sapiens matrix metalloproteinase MMP Rasi-1 gene, promoter region
9931	22814	36288	2.03	2.9E-01	AF085164.1	NT	Hordeum vulgare receptor-like kinase LRK10 gene, partial cds
9931	22814	36269	2.03	2.9E-01	AF085164.1	NT	Hordeum vulgare receptor-like kinase LRK10 gene, partial cds
10458	23380	36873	1.7	2.9E-01	AW581997.1	EST_HUMAN	RC3-ST0186-130100-015-a07 ST0186 Homo sapiens cDNA
10707	23629	37124	0.44	2.9E-01	11465652	NT	Porphyra purpurea chloroplast complete genome
10909	23829	37342	1.58	2.9E-01	AW152248.1	EST_HUMAN	hg40c10.x1 NCI_CGAP_U11 Homo sapiens cDNA clone IMAGE:2630034 3' similar to contains Alu repetitive element; contains element MSR1 repetitive element ;
10912	23832	37346	1.38	2.9E-01	X98491.1	NT	Mouse L1Md LINE DNA
10992	23912	37427	0.45	2.9E-01	AI934721.1	EST_HUMAN	wp88e11.x1 NCI_CGAP_Bm25 Homo sapiens cDNA clone IMAGE:2468876 3' similar to SW:CEBD_HUMAN P49716 CCAAT/ENHANCER BINDING PROTEIN DELTA ;
10992	23912	37428	0.45	2.9E-01	AI934721.1	EST_HUMAN	wp88e11.x1 NCI_CGAP_Bm25 Homo sapiens cDNA clone IMAGE:2468876 3' similar to SW:CEBD_HUMAN P49716 CCAAT/ENHANCER BINDING PROTEIN DELTA ;
11413	24357	37892	4.47	2.9E-01	D50914.1	NT	Human mRNA for KIAA0124 gene, partial cds
12120	24990	38591	2.34	2.9E-01	AE000711.1	NT	Aquifex aeolicus section 43 of 109 of the complete genome
12204	25048	38625	4.55	2.9E-01	AF200528.1	NT	Zea mays cellulose synthase-4 (CesA-4) mRNA, complete cds
12230	25959		5.87	2.9E-01	AL161541.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 41
12691	25905	31527	1.54	2.9E-01	AF170072.1	NT	Spodoptera frugiperda CALNUC mRNA, complete cds
555	13825	26543	0.88	2.4E-01	AA936316.1	EST_HUMAN	on70d04.s1 Scores_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1562023 3'
849	13905	26964	2.87	2.4E-01	BF576124.1	EST_HUMAN	G02132442FT NIH_MGC_B1 Homo sapiens cDNA clone IMAGE:4271578 5'
1307	14343	27307	15.11	2.4E-01	AJ289880.1	NT	Homo sapiens KIAA0851 gene (partial), XT3 gene and LZTFL1 gene
1307	14343	27308	15.11	2.4E-01	AJ289880.1	NT	Homo sapiens KIAA0851 gene (partial), XT3 gene and LZTFL1 gene
1384	14418	27387	1.01	2.4E-01	Y17283.1	NT	Homo sapiens FLI-1 gene, partial
1868	14893		27.14	2.4E-01	AF267763.1	NT	Mesembryanthemum crystallinum putative potassium channel protein Mkt1p mRNA, complete cds
1916	14940	27936	1.21	2.4E-01	AF251706.1	NT	Zea mays cellulose synthase-1 6-bisphosphatase mRNA, complete cds
2148	15164	28180	0.97	2.4E-01	AF111168.2	NT	Homo sapiens serine palmitoyl transferase, subunit II gene, complete cds; and unknown genes
2178	15193		1.04	2.4E-01	P45384	SWISSPROT	IMMUNOGLOBULIN A1 PROTEASE PRECURSOR (IGAT PROTEASE)
2271	15284	28310	2.23	2.4E-01	AE000680.1	NT	Aquifex aeolicus section 12 of 109 of the complete genome
2391	15399	28424	1.95	2.4E-01	BF002171.1	EST_HUMAN	7h23d04.x1 NCI_CGAP_Co16 Homo sapiens cDNA clone IMAGE:3316807 3' similar to SW:PRSB_XENLA
2544	15546	28569	2.37	2.4E-01	Z36534.1	NT	O42886 26S PROTEASE REGULATORY SUBUNIT 6A ;
2772	15764	28785	2.11	2.4E-01	X71783.1	NT	D.discoideum (Ax3-K) ponA gene
2797	15789	28807	3.03	2.4E-01	AF030154.1	NT	S.pombe swi6 gene
						NT	Bovine adenovirus 3 complete genome
3149	16206		3.16	2.4E-01	U72726.1	NT	Onyza longistaminata receptor kinase-like protein, family member D, and retrofit (gag/pol) genes, complete cds

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3163	16219	29134	1.71	2.4E-01	X74209.1	NT	H.septans AGT gene, Pet1 fragment of intron 4
3675	16718	29632	1	2.4E-01	AF169783.1	NT	Podocarpa anserina HEI-C protein (Hei-c) gene, complete cds
3773	16815	29724	0.95	2.4E-01	AE000312.1	NT	Escherichia coli K-12 MG1655 section 202 of 400 of the complete genome
4082	17098		0.87	2.4E-01	D29960.1	NT	Rattus norvegicus mRNA for alphaB crystallin-related protein, complete cds
4974	17989		0.98	2.4E-01	AL161588.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 85
5089	18099	30975	0.95	2.4E-01	D00944.1	NT	Hepatitis C virus genomic RNA for polyprotein, complete cds
5537	18634	31574	0.77	2.4E-01	A1925707.1	EST_HUMAN	wo33d05.x1 NC1_CGAP_Gas4 Homo sapiens cDNA clone IMAGE:2457129 3'
5537	18634	31575	0.77	2.4E-01	A1925707.1	EST_HUMAN	wo33d05.x1 NC1_CGAP_Gas4 Homo sapiens cDNA clone IMAGE:2457129 3'
5562	18659	31605	0.69	2.4E-01	D50871.1	NT	Glycine max mRNA for mitotic cyclin b1-type, complete cds
5738	18832	32011	9.32	2.4E-01	AF091216.1	NT	Mus musculus Wrm protein (Wrm) gene, complete cds
5738	18832	32012	9.32	2.4E-01	AF091216.1	NT	Mus musculus Wrm protein (Wrm) gene, complete cds
5766	18858		0.65	2.4E-01	M83377.1	NT	Gallus gallus brain-derived neurotrophic factor (BDNF) gene, 5' end
5991	25649		1.03	2.4E-01	AJ133836.2	NT	Branchiostoma floridae mRNA for calmodulin 2 (calM2) gene
5998	19052	32279	2.06	2.4E-01	BF592336.1	EST_HUMAN	754d04.x1 NC1_CGAP_Br16 Homo sapiens cDNA clone IMAGE:3338503 3' similar to SW-SFR4_HUMAN
6098	19177	32395	2.07	2.4E-01	AF035546.1	NT	Q08170 SPLICING FACTOR, ARGININE/SERINE-RICH 4; contains element TAR1 TAR1 repetitive element
6209	19283	32515	2.02	2.4E-01	7661801	NT	Drosophila melanogaster p38a MAP kinase gene, complete cds
6264	19337	32570	0.84	2.4E-01	AV733787.1	EST_HUMAN	Homo sapiens HSPC142 protein (HSPC142), mRNA
6523	19586	32844	0.69	2.4E-01	AA398872.1	EST_HUMAN	AV733787 cda Homo sapiens cDNA clone cdaADE11 5'
6685	19742	33018	1.72	2.4E-01	A1689899.1	EST_HUMAN	z70d02.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:727683 3'
7247	19982	33279	0.54	2.4E-01	AF163863.1	NT	wo62c11.x1 NC1_CGAP_Pan1 Homo sapiens cDNA clone IMAGE:2323220 3' similar to gb.J03464
7566	20529	33898	7.93	2.4E-01	L43001.1	NT	PROCOLLAGEN ALPHA 2(I) CHAIN PRECURSOR (HUMAN);
7748	20701	34088	0.55	2.4E-01	N48732.1	EST_HUMAN	Mustela vison tyrosine aminotransferase gene, complete cds
7994	20933		0.51	2.4E-01	U05013.1	NT	Bos taurus guanylyl cyclase-activating protein 2 (guca2) mRNA, complete cds
7996	20935	34329	0.97	2.4E-01	AF229644.1	NT	yy55c11.1 Soares_multiple_sclerosis_2NBHMS Homo sapiens cDNA clone IMAGE:277460 5'
8416	21385	34792	0.51	2.4E-01	X97262.1	NT	Rattus norvegicus Sprague-Dawley heme oxygenase-2 non-reducing isoform gene, complete cds
8416	21385	34793	0.51	2.4E-01	X97262.1	NT	Mus musculus pah gene and promoter
8692	21660	35083	1.5	2.4E-01	AJ012585.1	NT	M.musculus pah gene and promoter
8948	21912	35337	0.98	2.4E-01	BF242794.1	EST_HUMAN	Tetrahymena thermophila macronuclear gene encoding ribosomal protein L3, exons 1-2
9001	21967		0.57	2.4E-01	BF678275.1	EST_HUMAN	601877679F1 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:4106298 5'
9487	22451	35891	0.51	2.4E-01	AL139077.2	NT	602086189F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4250372 5'
							Campylobacter jejuni NC1C11168 complete genome, segment 4/6

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9487	22451	35892	0.51	2.4E-01	AL139077.2	NT	Campylobacter jejuni NCTC11168 complete genome; segment 4/6
9921	22742	36193	7.63	2.4E-01	AI693515.1	EST_HUMAN	wd43e02.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2330908 3' similar to contains MER22.b1 TAR1 repetitive element;
10062	22989	36457	0.57	2.4E-01	AF220087.1	NT	Drosophila melanogaster SKPB gene, complete cds
10062	22989	36458	0.57	2.4E-01	AF220087.1	NT	Drosophila melanogaster SKPB gene, complete cds
10805	23726	37227	1.69	2.4E-01	Q03692	SWISSPROT	COLLAGEN ALPHA 1(X) CHAIN PRECURSOR
11119	24079	37603	2.88	2.4E-01	AL161494.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 6
11185	24141	37675	1.77	2.4E-01	AF030199.1	NT	Mus musculus type 1 sigma receptor gene, complete cds
11534	24479		1.52	2.4E-01	Z21847.1	NT	P. asiatica mosaic virus genomic RNA
12096	24987	38564	4.88	2.4E-01	P08600	SWISSPROT	PROLINE RICH 33 KD EXTENSIN-RELATED PROTEIN PRECURSOR
12160	25015	38617	2.5	2.4E-01	AF217491.1	NT	Homo sapiens fragile 16D oxidoreductase (FOR) gene, exon 6
12294	25749		1.93	2.4E-01	AF004213.1	NT	Arabidopsis thaliana ethylene-insensitive3-like1 (EIL1) mRNA, complete cds
12361	25150		2.1	2.4E-01	AJ278191.1	NT	Mus musculus mRNA for putative mc7 protein (mc7 gene)
12575	25734		2.27	2.4E-01	V01507.1	NT	Gallus gallus gene coding for a-actin
12782	25945		1.31	2.4E-01	BF229975.1	EST_HUMAN	RC3-CT0413-100800-023-b06 CT0413 Homo sapiens cDNA
13006	25559		8.49	2.4E-01	AL163281.2	NT	Homo sapiens chromosome 21 segment HS21C081
399	13464	26394	0.98	2.3E-01	S75898.1	NT	aromatase [Poephila guttata=zebra finches, ovary, mRNA, 3188 nt]
638	13704		5.85	2.3E-01	U39713.1	NT	Mycoplasma genitalium section 35 of 51 of the complete genome
668	13733	26658	21.34	2.3E-01	U67596.1	NT	Methanococcus jannaschii section 138 of 150 of the complete genome
934	13987	26937	4.19	2.3E-01	BE311893.1	EST_HUMAN	601142073F1 NIH_MGC_14 Homo sapiens cDNA clone IMAGE:3505818 5'
1511	14543	27614	1.33	2.3E-01	6677980	NT	Mus musculus vacuolar protein sorting 4b (Vps4b), mRNA
1568	14801		1.02	2.3E-01	U22897.2	NT	Yersinia pestis HmeH (hmsH), HmsF (hmsF), HmsR (hmsR), and HmsS (hmsS) genes, complete cds
1608	14840	27617	1.21	2.3E-01	AJ246480.1	NT	Brassica napus sig gene for S-locus glycoprotein, cultivar T2
1636	14888	27644	2.52	2.3E-01	Y10887.2	NT	Mus musculus cdh5 gene, exon 1, partial
2091	15079		1.33	2.3E-01	AJ235953.1	NT	Homo sapiens partial intron 3 of the wild type AF-4/JEL gene
2452	15457	28478	2.76	2.3E-01	BE297718.1	EST_HUMAN	601175562F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3531015 5'
2650	15657	28676	1.27	2.3E-01	M11319.1	NT	Human erythropoietin gene, complete cds
2835	14422	27391	2.34	2.3E-01	AB015033.1	NT	Martiniella agerovans gyrB gene for DNA gyrase subunit B, partial cds, strain:FO 14957
2974	16032	28955	1.25	2.3E-01	AA601379.1	EST_HUMAN	no16d06.s1 NCI_LGAP_Phe1 Homo sapiens cDNA clone IMAGE:1100843 3' similar to contains Alu repetitive element/contains element THR repetitive element;
3100	16167		7.15	2.3E-01	R21732.1	EST_HUMAN	Yn21b07.s1 Soares placenta Nb21pF Homo sapiens cDNA clone IMAGE:130357 3'
3383	16432	29360	1.26	2.3E-01	H69836.1	EST_HUMAN	yr97h10.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:213283 5'

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3854	16894	29768	1.06	2.3E-01	S82821.1	NT	GSTA5-glutathione S-transferase Yc2 subunit (5' region, intron 1) [rats, Morris hepatoma cell line, Genomic, 2212 nt, segment 1 of 3]
3956	16996		5.02	2.3E-01	7662133	NT	Homo sapiens KIAA0450 gene product (KIAA0450), mRNA
4212	17241		0.92	2.3E-01	J03267.1	NT	Rat atrial natriuretic factor (ANF) gene, 5' end
4377	17405	30285	0.94	2.3E-01	R62262.1	EST_HUMAN	y17701.r1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:149017 5'
4428	17455		2.24	2.3E-01	L78789.1	NT	Mus musculus renin (Ren-1c) gene, promoter region
4479	17504	30392	1.07	2.3E-01	D60899.1	NT	Synchoecyella sp. POC6803 complete genome, 1/27, 1-133859
4515	17540	30426	1.9	2.3E-01	AF092535.1	NT	Homo sapiens mitogen-activated protein kinase p38delta (PRKM13) mRNA, complete cds
4584	17606	30502	7.42	2.3E-01	5031984	NT	Homo sapiens nuclear transport factor 2 (placental protein 15) (PP15) mRNA
5087	18097	30873	0.65	2.3E-01	AB032400.1	NT	Mus musculus tulip 1 mRNA, complete cds
							Human hereditary haemochromatosis region, histone 2A-like protein gene, hereditary haemochromatosis (HLA-H) gene, RoRet gene, and sodium phosphate transporter (NPT3) gene, complete cds
5200	18209	31083	0.91	2.3E-01	U91328.1	NT	Homo sapiens mRNA for KIAA1512 protein, partial cds
5377	18481	31356	2.19	2.3E-01	AB040945.1	NT	7k30606.x1 NCJ CGAP_Oy18 Homo sapiens cDNA clone IMAGE:3476699 3' similar to SW:GAG SMSAV
							P03330 GAG POLYPROTEIN [CONTAINS: CORE PROTEIN P15; INNER COAT PROTEIN P12; CORE SHELL PROTEIN P30; NUCLEOPROTEIN P10]; ;
5503	18603	31532	2.51	2.3E-01	BF058381.1	EST_HUMAN	C.familialis rom1 gene
5608	18704	31861	4.56	2.3E-01	X86587.1	NT	Vitiforma corneum small subunit ribosomal RNA gene
5733	18827		1.01	2.3E-01	L39112.1	NT	23S rRNA [Leuconostoc carnosum, Genomic, 2868 nt]
5845	18935	32119	0.81	2.3E-01	S60371.1	NT	as27e12.x1 Barstead aorta HPLR86 Homo sapiens cDNA clone IMAGE:2318446 3' similar to gb:X13238
							CYTTOCHROME C OXIDASE POLYPEPTIDE VIC PRECURSOR (HUMAN);
6051	19132	32340	2.02	2.3E-01	A1708840.1	EST_HUMAN	as27e12.x1 Barstead aorta HPLR86 Homo sapiens cDNA clone IMAGE:2318446 3' similar to gb:X13238
							CYTTOCHROME C OXIDASE POLYPEPTIDE VIC PRECURSOR (HUMAN);
6051	19132	32341	2.02	2.3E-01	A1708840.1	EST_HUMAN	Oryctolagus cuniculus cytochrome oxidase subunit 1a (cox1a2) mRNA, complete cds; nuclear gene for mitochondrial product
6812	19856	33154	0.76	2.3E-01	AF198089.1	NT	as42f12.x1 Barstead aorta HPLR86 Homo sapiens cDNA clone IMAGE:2319887 3' similar to contains Alu repetitive element;
7061	20083	33391	5.28	2.3E-01	A1718148.1	EST_HUMAN	Homo sapiens hypothetical protein FLJ20345 (FLJ20345), mRNA
7318	20289	33632	0.69	2.3E-01	8923323	NT	Secale cereale omega zeaxin gene, complete cds
7505	20470	33830	0.78	2.3E-01	AF000227.1	NT	Glycine max resistance protein LM17 precursor RNA, partial cds
7646	20606	33972	2.65	2.3E-01	AF175389.1	NT	AV719681 GLC Homo sapiens cDNA clone GLDGB08 5'
7649	20609	33974	10.72	2.3E-01	AV719681.1	EST_HUMAN	AV719681 GLC Homo sapiens cDNA clone GLDGB08 5'
7649	20609	33975	10.72	2.3E-01	AV719681.1	EST_HUMAN	Mus musculus myosin XV (Myo15), mRNA
7866	20810		3.39	2.3E-01	8754779	NT	

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7871	20816	34193	1.36	2.3E-01	BE888071.1	EST_HUMAN	601611573F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3912859 5'
8028	20865		2.69	2.3E-01	N80983.1	EST_HUMAN	zai2e08.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:282358 5'
8073	21010	34408	0.63	2.3E-01	11416821	NT	Homo sapiens protocadherin alpha cluster (LOC83960), mRNA
8073	21010	34409	0.63	2.3E-01	11416821	NT	Homo sapiens protocadherin alpha cluster (LOC83960), mRNA
8184	21154	34562	0.6	2.3E-01	AL161558.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 58
8326	21295	34710	2.02	2.3E-01	M68931.1	NT	Oxytricha nova macronuclear telomere-binding protein alpha subunit (tel-alpha alanine version) gene, complete cds
8838	21805	35222	0.54	2.3E-01	U67699.1	NT	Mus musculus prosaposin (psap) (SGP-1) gene, complete cds
9125	22091	35519	0.46	2.3E-01	AW090541.1	EST_HUMAN	xc90e06.x1 NCI_CGAP_Bm35 Homo sapiens cDNA clone IMAGE:2591554 3'
9240	22206	35639	0.45	2.3E-01	AW964480.1	EST_HUMAN	EST376533 MAGe resequences, MAGH Homo sapiens cDNA
9496	22460	35900	0.59	2.3E-01	AA372164.1	EST_HUMAN	EST84061 Rhabdomyosarcoma Homo sapiens cDNA 5' end similar to DnaJ homolog (GB:X63368)
9496	22460	35901	0.59	2.3E-01	AA372164.1	EST_HUMAN	EST84061 Rhabdomyosarcoma Homo sapiens cDNA 5' end similar to DnaJ homolog (GB:X63368)
9940	22867	36329	0.63	2.3E-01	6679318	NT	Mus musculus phosphatidylinositol 3-kinase catalytic subunit delta (Pik3cd), mRNA
10086	23013	36486	0.78	2.3E-01	BE277860.1	EST_HUMAN	601120170F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:2966739 5'
10141	23067	36543	0.69	2.3E-01	AW964460.1	EST_HUMAN	EST376533 MAGe resequences, MAGH Homo sapiens cDNA
10191	23116	36600	1.36	2.3E-01	X62124.1	NT	Haemophilus influenzae genes for HincII restriction-modification system (HincII methyltransferase (EC 2.1.1.72) and HincII endonuclease (EC 3.1.21.4))
10226	23151	36640	0.57	2.3E-01	AW364833.1	EST_HUMAN	PM2-DT0036-281299-001-f04 DT0036 Homo sapiens cDNA
10294	23219	36702	2.8	2.3E-01	BE173060.1	EST_HUMAN	MR0-HT0559-240400-014-g11 HT0559 Homo sapiens cDNA
10351	23275	36749	2.33	2.3E-01	AJ293281.1	NT	Rhizobium leguminosarum partial genomic DNA for exopolysaccharide biosynthesis genes
10809	23730	37232	0.8	2.3E-01	AF201929.1	NT	Murine hepatitis virus strain 2, complete genome
10820	23741		6.12	2.3E-01	BF133577.1	EST_HUMAN	601646155R2 NIH_MGC_59 Homo sapiens cDNA clone IMAGE:4102092 3'
11355	24305	37832	1.49	2.3E-01	AF004833.1	NT	Mus musculus tissue factor pathway inhibitor (TFPI) mRNA, complete cds
11355	24305	37833	1.49	2.3E-01	AF004833.1	NT	Mus musculus tissue factor pathway inhibitor (TFPI) mRNA, complete cds
11522	24463	38015	1.69	2.3E-01	AJ250189.1	NT	Mus musculus partial mRNA for muscle protein 534 (mg534 gene)
11522	24463	38016	1.69	2.3E-01	AJ250189.1	NT	Mus musculus partial mRNA for muscle protein 534 (mg534 gene)
11679	24845	38222	2.61	2.3E-01	AE002187.2	NT	Chlamydomonas reinhardtii AR39, section 4 of 94 of the complete genome
12098	24989	38566	1.47	2.3E-01	AE004688.1	NT	Chlamydomonas reinhardtii AR39, section 4 of 94 of the complete genome
12278	25098		5.42	2.3E-01	U45428.1	NT	Pseudomonas aeruginosa PA01, section 229 of 529 of the complete genome
12370	25156		6.49	2.3E-01	T27231.1	EST_HUMAN	Borrelia burgdorferi 2.9-6 locus, ORF-A-D genes, complete cds and REP+ gene, partial cds
12403	25176		2.24	2.3E-01	AW963940.1	EST_HUMAN	HCOEST44 HT29M6 Homo sapiens cDNA clone HCOE44 5'
							PM4-SN0012-030400-001-b08 SN0012 Homo sapiens cDNA
12460	25892	31417	2.82	2.3E-01	AW303623.1	EST_HUMAN	xv21d07.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2813773 3' similar to TR-Q9Z175 Q9Z175 LYSYL OXIDASE-RELATED PROTEIN 2; contains PTR5.b2 TAR1 repetitive element;

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Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
12494	25937	31312	11.07	2.3E-01	BE882464.1	EST_HUMAN	601507202F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3908689 5'
12544	25267		2.36	2.3E-01	BF663319.1	EST_HUMAN	602144459F1 NIH_MGC_48 Homo sapiens cDNA clone IMAGE:4297719 5'
12591	25295		3.71	2.3E-01	AL006519.1	NT	Rattus norvegicus mRNA for acid gated ion channel
12680	25348		2.12	2.3E-01	U49645.1	NT	Pleurodeles waltl distal-less like protein PwDlx-3 (PwDlx-3) mRNA, complete cds
12926	25511		1.49	2.3E-01	BF475611.1	EST_HUMAN	nec39h12.x1 Lupsid_sclatc nerve Homo sapiens cDNA clone IMAGE:3395950 3' similar to contains element
90	13206	26130	0.99	2.2E-01	AI052190.1	EST_HUMAN	MER38 repetitive element;
1567	14600	27576	2.33	2.2E-01	AF187850.1	NT	oz14a10.x1 Soares fetal liver spleen 1NFLS_S1 Homo sapiens cDNA clone IMAGE:1675290 3' similar to
2100	15117	28139	2.2	2.2E-01	M34940.1	NT	TR:Q13040 Q13040 ATP-BINDING CASSETTE PROTEIN ;
2412	15419	28443	8.18	2.2E-01	BF677538.1	EST_HUMAN	Homo sapiens PPAR delta gene, promoter region
2593	15594	28611	2.54	2.2E-01	BE618268.1	EST_HUMAN	Fresh-water sponge Emf1 alpha collagen (COLF1) gene
2593	15594	28612	2.54	2.2E-01	BE618268.1	EST_HUMAN	602085608F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4249969 5'
2893	15952	28868	4.89	2.2E-01	BE155625.1	EST_HUMAN	601462629F1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:3866190 5'
2893	15952	28869	4.89	2.2E-01	BE155625.1	EST_HUMAN	601462629F1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:3866190 5'
2932	15990		1.29	2.2E-01	AF020503.1	NT	PM2-HT0353-281299-003-at12 HT0353 Homo sapiens cDNA
3403	16452		2.28	2.2E-01	AL161562.2	NT	PM2-HT0353-281299-003-at12 HT0353 Homo sapiens cDNA
3827	16967		0.66	2.2E-01	AF155728.1	NT	Homo sapiens FRA3B common fragile region, diadenosine triphosphate hydrolase (FHL1) gene, exon 5
4240	17269		1.2	2.2E-01	AF119102.1	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 62
4247	17276	30158	5.86	2.2E-01	AF155142.1	NT	Xiphophorus maculatus truncated Rex1 retrotransposon reverse transcriptase (RT) pseudogene
4292	17321	30200	2.33	2.2E-01	AF117340.1	NT	Drosophila melanogaster UNC-119 (unc-119) gene, complete cds
4292	17321	30201	2.33	2.2E-01	AF117340.1	NT	Mus musculus mixed lineage kinase 3 (Mlk3) and two pore domain K+ channel subunit (Kcnk6) genes, complete cds
4383	17411	30284	1.21	2.2E-01	U01307.1	NT	Mus musculus MAP kinase kinase 1 (MeKk1) mRNA, complete cds
4383	17411	30295	1.21	2.2E-01	U01307.1	NT	Mus musculus MAP kinase kinase 1 (MeKk1) mRNA, complete cds
4456	17482	30370	23.17	2.2E-01	AW361088.1	EST_HUMAN	Human scRNA (BC200 beta) pseudogene
4863	17890		1.38	2.2E-01	D30604.1	NT	Human scRNA (BC200 beta) pseudogene
4868	17885	30773	1.57	2.2E-01	AA211216.1	EST_HUMAN	Human beta-cytoplasmic actin (ACTBP9) pseudogene
5082	18032		1.34	2.2E-01	L13299.1	NT	Human beta-cytoplasmic actin (ACTBP9) pseudogene
5160	18168	31048	1.22	2.2E-01	BE141035.1	EST_HUMAN	zq87c05.1 Stratagene hNT neuron (#837233) Homo sapiens cDNA clone IMAGE:648986 5'
5181	18190	31066	1.51	2.2E-01	H60548.1	EST_HUMAN	Mus musculus vinculin gene, exon 3
5263	18271		1.05	2.2E-01	AL163206.2	NT	MR0-HT0067-201099-002-c10 HT0067 Homo sapiens cDNA
							yr42h09.1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:208001 5' similar to
							gb:Z14119.nat CD59 GLYCOPROTEIN PRECURSOR (HUMAN);
							Homo sapiens chromosome 21 segment HS21C006

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5838	18928	32112	2.18	2.2E-01	5803002	NT	Homo sapiens diaphanous (Drosophila, homolog) 2 (DIAPH2), transcript variant 156, mRNA
5849	18939		3.59	2.2E-01	D64000.1	NT	Synechocystis sp. PCC6803 complete genome, 19127, 2392729-2538999
6114	19192	32415	0.61	2.2E-01	U67087.1	NT	Gallus gallus T-box containing protein (Ch-Tbx1) mRNA, complete cds
6114	19192	32416	0.61	2.2E-01	U67087.1	NT	Gallus gallus T-box containing protein (Ch-Tbx1) mRNA, complete cds
6864	19917	33211	0.7	2.2E-01	AB038490.1	NT	Homo sapiens gene for fukutin, complete cds
6964	20189	33514	0.58	2.2E-01	AA490106.1	EST_HUMAN	ab02e09.s1 Stratagene fetal retina 937202 Homo sapiens cDNA clone IMAGE:839656 3'
6964	20189	33515	0.58	2.2E-01	AA490106.1	EST_HUMAN	ab02e09.s1 Stratagene fetal retina 937202 Homo sapiens cDNA clone IMAGE:839656 3'
7222	20244	33578	7.76	2.2E-01	AV756238.1	EST_HUMAN	AV756238 BM Homo sapiens cDNA clone BMFAHC08 5'
7336	20307	33650	1.43	2.2E-01	AF082738.1	NT	Streptococcus pyogenes phosphatidylglycerophosphate synthase (pgsA) and ABC transporter ATP-binding protein (spbA) genes, complete cds; and unknown genes
7336	20307	33651	1.43	2.2E-01	AF082738.1	NT	Streptococcus pyogenes phosphatidylglycerophosphate synthase (pgsA) and ABC transporter ATP-binding protein (spbA) genes, complete cds; and unknown genes
7509	20474	33834	2.11	2.2E-01	M24138.1	NT	Human glycophorin B gene, exon 4
7509	20474	33835	2.11	2.2E-01	M24138.1	NT	Human glycophorin B gene, exon 4
7728	20884	34048	0.59	2.2E-01	AE000035.2	NT	Mycoplasma pneumoniae M129 section 45 of 63 of the complete genome
7966	20905	34297	0.8	2.2E-01	AF287967.1	NT	Homo sapiens homeobox B7 (HOXB7) gene, partial cds; and homeobox B6 (HOXB6), homeobox B5 (HOXB5), homeobox B4 (HOXB4), and homeobox B3 (HOXB3) genes, complete cds
8000	20939	34332	0.5	2.2E-01	AB024553.1	NT	Bacillus halodurans DNA, complete and partial cds, strain C-125
8354	21323		2.51	2.2E-01	AF165143.1	NT	Mus musculus nm23-M1 gene, promoter region
8425	21394	34805	1	2.2E-01	Z49933.1	NT	E.coli sepA and sepB genes
8896	21862	35284	0.49	2.2E-01	AJ132918.1	NT	Pan troglodytes MeCP2 gene 3'UTR
9234	22200	35629	0.51	2.2E-01	L23312.1	NT	Mouse HD protein mRNA, complete cds
9234	22200	35630	0.51	2.2E-01	L23312.1	NT	Mouse HD protein mRNA, complete cds
9247	22213	35643	4.12	2.2E-01	AE001713.1	NT	Thermotoga maritima section 25 of 136 of the complete genome
9267	22233	35663	0.47	2.2E-01	U09984.1	NT	Mus musculus ICR/Swiss glyceroldehyde 3-phosphate dehydrogenase (Gapd-S) gene, complete cds
9376	22341		3.89	2.2E-01	AW85039.1	EST_HUMAN	PM3-CT0263-241259-009-607 CT0263 Homo sapiens cDNA
9470	22434	35872	1.4	2.2E-01	8393247	NT	Mus musculus deformed epidermal autoregulatory factor 1 (Drosophila) (Deaf1), mRNA
9553	22515	35966	1.4	2.2E-01	BF376354.1	EST_HUMAN	MR1-TN0045-110900-008-c02 TN0045 Homo sapiens cDNA
9644	22688	36037	1.3	2.2E-01	W02988.1	EST_HUMAN	za04f08.1 Soares melanocyte 2NDHM Homo sapiens cDNA clone IMAGE:281591 5'
9662	22819	36274	15.89	2.2E-01	P48634	SWISSPROT	LARGE PROLINE-RICH PROTEIN BAT2 (HLA-B-ASSOCIATED TRANSCRIPT 2)
9707	22660	36116	0.66	2.2E-01	AJ009839.1	NT	Xenopus laevis mRNA for kinesin-like protein 3 (xklp3)
9718	22748	36197	0.78	2.2E-01	7657428	NT	Mus musculus osteoblast specific factor 2 (OSF-2), mRNA
9731	22759	36212	4.38	2.2E-01	M89643.1	NT	Brachydanio rerio ependymin beta and gamma chains (Epd) gene, complete cds

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9979	22906	36371	0.5	2.2E-01	Q90980	SWISSPROT	CYCLIC NUCLEOTIDE GATED CHANNEL, ROD PHOTORECEPTOR, ALPHA SUBUNIT (CNG CHANNEL 3) (CNG-3) (CNG3)
10174	23099	36579	3.74	2.2E-01	AF167941.1	NT	Funaria hygrometrica chloroplast-localized small heat shock protein (OPSHSP21) mRNA, complete cds;
10313	23237	36719	1.76	2.2E-01	BF206507.1	EST_HUMAN	nuclear gene for chloroplast product
10537	23459	36956	1	2.2E-01	9625671	NT	6018697247-1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4100189 5'
10697	23619	37113	0.52	2.2E-01	T59472.1	EST_HUMAN	Human herpesvirus 5, complete genome
10697	23619	37114	0.52	2.2E-01	T59472.1	EST_HUMAN	y653d08.r1 Stratagene ovary (#937217) Homo sapiens cDNA clone IMAGE:75855 5'
							y653d08.r1 Stratagene ovary (#937217) Homo sapiens cDNA clone IMAGE:75855 5'
							Pseudomonas aeruginosa quinolone protein ethanol dehydrogenase (exaA) gene, partial cds, cytochrome c550 precursor (exaB), NAD+ dependent acetaldehyde dehydrogenase (exaC), and pyrroloquinone quinone synthesis A (pgcA) genes, complete cds; and pyrroloquin
10735	23657	37150	0.51	2.2E-01	AF068284.1	NT	Mus musculus PHR1 (Phr1) gene, partial cds
10810	23731		0.68	2.2E-01	AF071001.1	NT	Helicobacter pylori, strain J99 section 123 of 132 of the complete genome
10856	23776	37274	0.67	2.2E-01	AE001562.1	NT	Helicobacter pylori, strain J99 section 123 of 132 of the complete genome
10856	23776	37275	0.67	2.2E-01	AE001562.1	NT	Helicobacter pylori, strain J99 section 123 of 132 of the complete genome
11751	24636	38215	3.77	2.2E-01	X01918.1	NT	Drosophila 68C glue gene cluster
11789	23944	37466	3.41	2.2E-01	7706215	NT	Homo sapiens H-2K binding factor-2 (LOC51580), mRNA
							Homo sapiens chromosome Xq28 melanoma antigen family A2a (MAGEA2A), melanoma antigen family A12 (MAGEA12), melanoma antigen family A2b (MAGEA2B), melanoma antigen family A3 (MAGEA3), caltractin (CALT), NAD(P)H dehydrogenase-like protein (NSDHL), and L1>
12317	25950		2.32	2.2E-01	U82871.2	NT	Vitis vinifera cultivar Pinot Noir plasma membrane aquaporin (PIP1a) mRNA, complete cds
12406	25179		3.88	2.2E-01	AF188843.1	NT	RC1-CT0249-141199-021-g04 CT0249 Homo sapiens cDNA
12513	17462	30370	6.62	2.2E-01	AW361098.1	EST_HUMAN	h117502.x1 NCI_CGAP_GUT1 Homo sapiens cDNA clone IMAGE:2872523 3'
12514	25246		1.7	2.2E-01	AW661922.1	EST_HUMAN	Phodopus sungorus uncoupling protein 3 mRNA, partial cds
13111	25946		1.36	2.2E-01	AF271265.1	NT	nm31e11.s1 NCI_CGAP_Lip2 Homo sapiens cDNA clone IMAGE:1061804
972	14024	26978	1.58	2.1E-01	AA569289.1	EST_HUMAN	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 16
975	14026	26980	1.06	2.1E-01	AL161504.2	NT	Chlamydia muridarum, section 45 of 85 of the complete genome
1126	14169		2.38	2.1E-01	AE002314.2	NT	Mus musculus interferon (alpha and beta) receptor 2 (Inar2), mRNA
1203	14242	27199	0.88	2.1E-01	6754299	NT	Mus musculus interferon (alpha and beta) receptor 2 (Inar2), mRNA
1203	14242	27200	0.88	2.1E-01	6754299	NT	Mus musculus mas proto-oncogene and Igf2 gene for insulin-like growth factor type 2 and L41ps and Au76 pseudogenes
1512	14544	27515	1.05	2.1E-01	AJ248995.1	NT	gk73e02.s1 NCI_CGAP_GC4 Homo sapiens cDNA clone IMAGE:1510610 3' similar to gbK02765
1929	14953	27949	1.94	2.1E-01	AA908824.1	EST_HUMAN	COMPLEMENT C3 PRECURSOR (HUMAN);
2166	15181	28201	3.26	2.1E-01	BF895073.1	EST_HUMAN	602083129F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4247503 5'
2489	15895	28516	2.19	2.1E-01	HT79968.1	EST_HUMAN	y00407.s1 Soares fetal liver, spleen INFLS Homo sapiens cDNA clone IMAGE:232837 3'

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2489	16896	28517	2.19	2.1E-01	H73968.1	EST_HUMAN	yu04f07.s1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:232837 3'
2838	15994	28914	2	2.1E-01	6912445	NT	Homo sapiens potassium voltage-gated channel, subfamily H (eag-related), member 4 (KCNH4), mRNA
3461	16507	28428	0.92	2.1E-01	AA639482.1	EST_HUMAN	nc90b10.s1 NC1_CGAP_C88 Homo sapiens cDNA clone IMAGE:1159579 3'
3819	16859		6.5	2.1E-01	9838361	NT	Beta vulgaris mitochondrion, complete genome
4045	17083		1.16	2.1E-01	AE001793.1	NT	Thermotoga maritima section 105 of 136 of the complete genome
4084	17118	30013	1.48	2.1E-01	P11675	SWISSPROT	IMMEDIATE-EARLY PROTEIN IE180
4084	17118	30014	1.48	2.1E-01	P11675	SWISSPROT	IMMEDIATE-EARLY PROTEIN IE180
4403	17431		1.62	2.1E-01	AB033041.1	NT	Homo sapiens mRNA for KIAA1215 protein, partial cds
4607	17628	30520	1.75	2.1E-01	AB010273.1	NT	Homo sapiens pshp47 gene, complete cds
5063	18073	30963	5.08	2.1E-01	D13587.1	NT	Lampetra japonica mRNA for alpha-2-macroglobulin, complete cds
5110	18120	30994	1.13	2.1E-01	Q01338	SWISSPROT	ALPHA-2A ADRENERGIC RECEPTOR (ALPHA-2A ADRENOCEPTOR) (ALPHA-2AAR)
5216	18225	31099	0.92	2.1E-01	AE001526.1	NT	Helicobacter pylori, strain J99 section 87 of 132 of the complete genome
5374	18479	31352	5.48	2.1E-01	BF672695.1	EST_HUMAN	602152001F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4293001 5'
7071	20093	33403	1.15	2.1E-01	AJ223392.1	NT	Drosophila melanogaster 16S rRNA gene, partial
7083	20017	33320	1.92	2.1E-01	U04642.1	NT	Human olfactory receptor (OR17-2) gene, partial cds
7636	20596	33959	0.78	2.1E-01	Q01966	SWISSPROT	VOLTAGE-GATED POTASSIUM CHANNEL PROTEIN KV3.3 (KSHIID)
7636	20596	33960	0.78	2.1E-01	Q01966	SWISSPROT	VOLTAGE-GATED POTASSIUM CHANNEL PROTEIN KV3.3 (KSHIID)
7648	20608		2.34	2.1E-01	AE000972.1	NT	Archaeoglobus fulgidus section 135 of 172 of the complete genome
7973	20912	34303	1.77	2.1E-01	AF000948.1	NT	Canis familiaris keratin (KRT9) gene, complete cds
8027	20964	34359	1.08	2.1E-01	AF068687.1	NT	Glycine max malate dehydrogenase (Mdh-2) gene, nuclear gene encoding mitochondrial protein, partial cds
8027	20964	34360	1.08	2.1E-01	AF068687.1	NT	Glycine max malate dehydrogenase (Mdh-2) gene, nuclear gene encoding mitochondrial protein, partial cds
8088	21022		0.51	2.1E-01	T87354.1	EST_HUMAN	yd83501.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:114793 5'
8407	21376		1.04	2.1E-01	7305030	NT	Mus musculus erythrocyte protein band 4.1-like 3 (Epb4.13), mRNA
8847	21814	35234					Haemophilus influenzae hmdD, putative haemoglobin processing protein (hmdC), putative ABC transporter (hmdB), putative haemoglobin structural protein (hmdA), and haemoglobin immunity protein (hmdI) genes, complete cds
9149	22115	35540	0.84	2.1E-01	AL040537.1	EST_HUMAN	DKFZp434H0814.1_1 434 (synonym: hies3) Homo sapiens cDNA clone DKFZp434H0814 5'
9149	22115	35541	0.84	2.1E-01	AL040537.1	EST_HUMAN	DKFZp434H0814.1_1 434 (synonym: hies3) Homo sapiens cDNA clone DKFZp434H0814 5'
9392	22357	35787	6.08	2.1E-01	Z35786.1	NT	S.cerevisiae chromosome II reading frame ORF YBL025w
9862	22798	36251	0.59	2.1E-01	N42536.1	EST_HUMAN	Y11e10.r1 Soares melanocyte 2N1BM Homo sapiens cDNA clone IMAGE:270954 5'
9862	22798	36252	0.59	2.1E-01	N42536.1	EST_HUMAN	Y11e10.r1 Soares melanocyte 2N1BM Homo sapiens cDNA clone IMAGE:270954 5'

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9871	22824	36277	2.77	2.1E-01	X97378.1	NT	A.thaliana mRNA for ARANBP1b protein
9976	22903	36367	1.28	2.1E-01	AB036529.1	NT	Homo sapiens p53R2 gene for ribonucleotide reductase, exon 6
10692	23614	37109	1.13	2.1E-01	Z97067.1	NT	Beta vulgaris mRNA for elongation factor 1-beta
10725	23647	37140	2.89	2.1E-01	P52824	SWISSPROT	DIACYLGLYCEROL KINASE, DELTA (DIGLYCERIDE KINASE) (DGK-DELTA) (DAG KINASE DELTA)
10731	23653	37146	0.93	2.1E-01	BF574254.1	EST_HUMAN	(80 KD DIACYLGLYCEROL KINASE)
11009	23974	37498	3.69	2.1E-01	AF294296.1	NT	602131427F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4270831 5'
11890	24771		2.15	2.1E-01	11036647	NT	Anolis lineatopus isolate NG NADH dehydrogenase subunit 2 (ND2) gene, complete cds; mitochondrial gene for mitochondrial product
11905	24786	38376	1.61	2.1E-01	BE180422.1	EST_HUMAN	Homo sapiens pancreatic polypeptide 2 (PPY2), mRNA
12137	25022		1.38	2.1E-01	X57624.1	NT	RC3-H70622-040500-013-b11 HT0622 Homo sapiens cDNA
12660	25339		1.94	2.1E-01	AF217490.1	NT	Drosophila melanogaster ALA-E6 DNA, repeat region
12860	25860		1.8	2.1E-01	L32588.1	NT	Homo sapiens fragile 16D oxidoreductase (FOR) gene, exons 8, 9, and partial cds
12914	25493		2	2.1E-01	BE622149.1	EST_HUMAN	Human granulosa gene
13045	25586	31682	1.62	2.1E-01	BE672330.1	EST_HUMAN	601440712F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3915675 5'
201	13302	26231	1.32	2.0E-01	AB017437.1	NT	7a59a02.x1 NCI_CGAP_GC8 Homo sapiens cDNA clone IMAGE:3223034 3'
535	13606		1.82	2.0E-01	7705601	NT	Gallus gallus mRNA for avena, complete cds
700	13762	26694	1.25	2.0E-01	M77085.1	NT	Homo sapiens CGI-18 protein (LOC51003), mRNA
811	13869	26818	1.96	2.0E-01	AF027895.1	NT	O.cuniculus germline IgH heavy chain V-H pseudogene, allotype VH2
1013	14081	27012	0.72	2.0E-01	D60905.1	NT	Mus musculus Major Histocompatibility Locus class II region
1127	14170	27121	2.93	2.0E-01	AL163213.2	NT	Synechocystis sp. PCC6803 complete genome, 7127, 781449-920915
1259	14294	27258	1.42	2.0E-01	AJ132895.5	NT	Homo sapiens chromosome 21 segment HS21C013
1311	14347	27313	2.04	2.0E-01	AW384937.1	EST_HUMAN	Homo sapiens rac1 gene
1454	14487		1.39	2.0E-01	AJ243967.1	NT	PM11-HT0422-291299-002-c06 HT0422 Homo sapiens cDNA
1483	14516	27490	15.27	2.0E-01	4503408	NT	Plum pox virus strain M, complete genome, isolate PS
1555	14587	27559	2.13	2.0E-01	AB007974.1	NT	Homo sapiens dystrobrein, alpha (DTNA), mRNA
1560	14592	27565	1.52	2.0E-01	AF260700.1	NT	Homo sapiens sodium/iodide symporter mRNA, partial cds
1706	14736	27718	1.38	2.0E-01	U22346.1	NT	Homo sapiens bradykinin B1 receptor (bradyb1) gene, complete cds
1730	14760		2.09	2.0E-01	AF111703.3	NT	Homo sapiens 14q32 Jagged2 gene, complete cds; and unknown gene
1772	14801		3.8	2.0E-01	U67525.1	NT	Methanococcus jannaschii section 67 of 150 of the complete genome
1907	14931	27926	0.94	2.0E-01	BE871330.1	EST_HUMAN	601449441F1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3853330 5'
1907	14931	27927	0.94	2.0E-01	BE871330.1	EST_HUMAN	601449441F1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3853330 5'
2355	15364		1.88	2.0E-01	X82877.1	NT	H.sapiens Na+-D-glucose cotransport regulator gene

Table 4
Single Exon Probes Expressed In Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3499	16546	29472	0.74	2.0E-01	P46607	SWISSPROT	HOMEOBOX PROTEIN GLABRA2 (HOMEOBOX-LEUCINE ZIPPER PROTEIN ATHB-10) (HD-ZIP PROTEIN ATHB-10)
3582	16627		0.82	2.0E-01	AW238005.1	EST_HUMAN	xp15602.x1 NCI_CGAP_HN9 Homo sapiens cDNA clone IMAGE:2740395 3' similar to contains element MER21 repetitive element;
3720	16763	29674	0.79	2.0E-01	P34841	SWISSPROT	CED-11 PROTEIN
3855	16895	29799	1.14	2.0E-01	AL163204.2	NT	Homo sapiens chromosome 21 segment HS21C004
3877	17017	29931	0.7	2.0E-01	Z46906.1	NT	Sus scrofa
4597	17618		10.26	2.0E-01	BE828165.1	EST_HUMAN	QV4-EN0032:190500-223-e03 EN0032 Homo sapiens cDNA
5078	18088	30988	7.06	2.0E-01	8922080	NT	Homo sapiens hypothetical protein ASH1 (ASH1), mRNA
5144	18153	31033	0.97	2.0E-01	Y19216.1	EST_HUMAN	Homo sapiens putative psithbD pseudogene for hair keratin, exons 1 to 9
5298	18302	31163	0.93	2.0E-01	BE439491.1	EST_HUMAN	HTM1-122F1 HTM1 Homo sapiens cDNA
5520	18619	31563	2.31	2.0E-01	X66600.1	NT	Rat SOD-2 gene for manganese-containing superoxide dismutase
5831	18921	32104	1.89	2.0E-01	11432540	NT	Homo sapiens dual oxidase-like domains 2 (DUOX2), mRNA
5940	19026	32220	0.89	2.0E-01	X91856.1	NT	F. rubripes DNA encoding for valyl-tRNA synthetase
6178	19253	32486	5.47	2.0E-01	U15300.1	NT	Saccharomyces cerevisiae Hal5p (HAL5) mRNA, complete cds
6298	19370		0.79	2.0E-01	M79867.1	NT	Human hepatocyte growth factor gene, exon 1
6417	19494	32733	0.56	2.0E-01	P02467	SWISSPROT	COLLAGEN ALPHA 2(I) CHAIN PRECURSOR
6569	19629	32895	3.06	2.0E-01	X61033.1	NT	M. auratus mu class glutathione transferase gene
6678	19736	33012	4.25	2.0E-01	AW360865.1	EST_HUMAN	PM1-CT0247-141099-001-g06 CT0247 Homo sapiens cDNA
7512	20477	33838	1.27	2.0E-01	AF250371.1	NT	Mus musculus phosphofructokinase-1 C isozyme (Pfkc) gene, exons 3 through 7
7679	20637	33989	0.72	2.0E-01	P54422	SWISSPROT	GAMMA-GLUTAMYL TRANSPEPTIDASE PRECURSOR
8054	20991	34389	0.61	2.0E-01	V00726.1	NT	Mouse germ line gene coding for beta-globin (Y2)
8285	21254		6.17	2.0E-01	AF028026.1	NT	Andes virus strain O123133 glycoprotein G1 and G2 precursor, gene, partial cds
8542	21510	34927	3.1	2.0E-01	X91151.1	NT	M. musculus scp2 gene exon 14
9074	22040		0.43	2.0E-01	BE582247.1	EST_HUMAN	601344648F1 NIH_MGC 8 Homo sapiens cDNA clone IMAGE:3677794 5'
9705	22659	36115	1.09	2.0E-01	U82511.1	NT	Dichytellum discoidium random slug cDNA19 protein (rsc19) mRNA, partial cds
9745	22686	36141	0.76	2.0E-01	U71122.1	NT	Arabidopsis pyruvate decarboxylase-2 (Pdc2) gene, complete cds
9914	22735		6.23	2.0E-01	AE001278.1	NT	Chlamydia trachomatis section 5 of 87 of the complete genome
10103	23029	36506	0.62	2.0E-01	P11420	SWISSPROT	DAUGHTERLESS PROTEIN
10103	23029	36507	0.62	2.0E-01	P11420	SWISSPROT	DAUGHTERLESS PROTEIN
10251	23178		1.94	2.0E-01	AF146892.1	NT	Homo sapiens filamin 2 (FLN2) mRNA, complete cds
10401	23323	36807	1.94	2.0E-01	AF086907.1	NT	Arabidopsis thaliana root gravitropism control protein (PIN2) gene, complete cds
10401	23323	36808	1.94	2.0E-01	AF086907.1	NT	Arabidopsis thaliana root gravitropism control protein (PIN2) gene, complete cds
10528	23450	36848	0.64	2.0E-01	AF157814.1	NT	Homo sapiens cAMP specific phosphodiesterase (PDE4C) gene, exons 2 through 12

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10528	23450	36946	0.64	2.0E-01	AF157814.1	NT	Homo sapiens cAMP specific phosphodiesterase (PDE4C) gene, exons 2 through 12
10575	23497		0.78	2.0E-01	X78388.1	NT	D.melanogaster DNA mobile element (hoppe)
10770	23681	37188	0.97	2.0E-01	X97121.1	NT	R.norvegicus mRNA for NTR2 receptor
11189	24145	37678	2.24	2.0E-01	D88088.1	NT	Salvelinus pluvius mRNA for transferrin, complete cds
11189	24145	37679	2.24	2.0E-01	D88088.1	NT	Salvelinus pluvius mRNA for transferrin, complete cds
12641	25325		1.42	2.0E-01	AF206637.2	NT	Pimphales promelas liver glucose-6-phosphate-1-dehydrogenase mRNA, partial cds
12828	25779		1.66	2.0E-01	AF30273.1	NT	Homo sapiens ninein-Lm isoform (ninein) mRNA, complete cds
12837	25711	31609	1.34	2.0E-01	AW975297.1	EST_HUMAN	EST387405 MAGE resequences, MAGN Homo sapiens cDNA
12875	25508	31707	4.12	2.0E-01	AI023592.1	EST_HUMAN	ov60a10.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1643610 3'
12898	25483		2.98	2.0E-01	AF078164.2	NT	Homo sapiens Ku70-binding protein (KUB3) mRNA, partial cds
110	13221		9.9	1.9E-01	7549743	NT	Rattus norvegicus Aryl hydrocarbon receptor nuclear translocator 1 (Arlt1), mRNA
352	13441	26386	6.09	1.9E-01	AF004353.1	NT	Mus musculus pale ear (ep) gene, wild type allele, 3' region, partial cds
657	13723	26847	2.66	1.9E-01	U32581.2	NT	Homo sapiens lamda102a protein kinase C-interacting protein mRNA, complete cds
657	13723	26848	2.66	1.9E-01	U32581.2	NT	Homo sapiens lamda102a protein kinase C-interacting protein mRNA, complete cds
664	13730	26655	8.69	1.9E-01	BE070801.1	EST_HUMAN	RC3-BT0502-25/199-011-d01 BT0502 Homo sapiens cDNA
665	13730	26655	6.99	1.9E-01	BE070801.1	EST_HUMAN	RC3-BT0502-25/199-011-d01 BT0502 Homo sapiens cDNA
988	14039		1.19	1.9E-01	7305180	NT	Mus musculus interleukin 2 receptor, gamma chain (il2rg), mRNA
1108	14150	27101	9.83	1.9E-01	AA358813.1	EST_HUMAN	EST67784 Fetal lung II Homo sapiens cDNA 5' end
1372	14406	27376	2.9	1.9E-01	AF061282.1	NT	Sorghum bicolor 22 kDa kafirin cluster
1430	14484		3.22	1.9E-01	AF184623.1	NT	Plasmodium vivax reticulocyte binding protein-2 (rbp-2) gene, complete cds
2390	15398	28423	3.89	1.9E-01	U66066.1	NT	Homo sapiens hypothetical protein FLJ10581 (FLJ10581), mRNA
2934	15992	28912	3.47	1.9E-01	8922533	NT	Sigmodon hispidus p53 gene, partial cds
2949	16006		4.89	1.9E-01	J00922.1	NT	Gallus gallus ovalbumin (Y) gene, complete cds
3406	16455	29378	4	1.9E-01	D13167.1	NT	Mouse gene for immunoglobulin diversity region D1
3492	16539	29464	5.36	1.9E-01	R19467.1	EST_HUMAN	y42f10.71 Soares fetal liver spleen 1NFSL Homo sapiens cDNA clone IMAGE:129547 5'
3817	16857	29763	0.87	1.9E-01	AF284017.1	NT	Rattus norvegicus arylacetamide deacetylase gene, complete cds
3848	16888	29791	2.26	1.9E-01	P35768	SWISSPROT	PAIR-RULE PROTEIN ODD-PAIRED
4018	17057	29959	3.91	1.9E-01	AB006784.1	NT	Schizosaccharomyces pombe DNA for cytoplasmic dynein heavy chain, complete cds
4110	17144	30038	1.42	1.9E-01	AB0754106.1	EST_HUMAN	CN3-CT0315-271199-045-011 CT0315 Homo sapiens cDNA
4259	17288	30169	1.24	1.9E-01	BE834943.1	EST_HUMAN	MR1-FN0010-290700-007-404 FN0010 Homo sapiens cDNA
4496	17521	30408	0.83	1.9E-01	AL161493.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 5
5047	18060		1.15	1.9E-01	AF223642.1	NT	Rattus norvegicus chemokine receptor CXCR3 mRNA, complete cds
5231	18239		1.01	1.9E-01	AI631198.1	EST_HUMAN	hs3912.x1 NCI_CGAP_G038 Homo sapiens cDNA clone IMAGE:223888 3' similar to gb:M21574 ALPHA PLATELET-DERIVED GROWTH FACTOR RECEPTOR PRECURSOR (HUMAN);

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5685	18780		5.2	1.9E-01	AW130149.1	EST_HUMAN	xf29a07.x1 NCL_CGAP_UH1 Homo sapiens cDNA clone IMAGE:2619444 3' similar to gb:M73779 RETINOIC ACID RECEPTOR ALPHA-1 (HUMAN);
5728	18822	32002	8.11	1.9E-01	AF127937.1	NT	Homo sapiens DNA polymerase epsilon catalytic subunit protein (POLE1) gene, exon 1a
5839	19025	32219	0.71	1.9E-01	AF091216.1	NT	Mus musculus Wm protein (Wm) gene, complete cds
5987	19072		2.15	1.9E-01	AU133116.1	EST_HUMAN	AU133116 N72RP4 Homo sapiens cDNA clone NT2RP4001328 5'
6461	19526	32776	0.95	1.9E-01	AU762391.1	EST_HUMAN	wf54h02.x1 NCL_CGAP_Co18 Homo sapiens cDNA clone IMAGE:2394099 3'
6527	19590	32850	0.88	1.9E-01	AW148452.1	EST_HUMAN	xf14c08.x1 NCL_CGAP_Kid8 Homo sapiens cDNA clone IMAGE:2618030 3' similar to gb:X03559 ATP SYNTHASE BETA CHAIN, MITOCHONDRIAL PRECURSOR (HUMAN);
7164	18395	31240	1.46	1.9E-01	R43212.1	EST_HUMAN	y809a12.s1 Scores Infant brain 1N1B Homo sapiens cDNA clone IMAGE:31663 3' similar to contains MER13 repetitive element;
7193	20217	33547	0.95	1.9E-01	AF034920.1	NT	Homo sapiens tubby like protein 1 (TULP1) gene, exons 9-11
7183	20217	33548	0.95	1.9E-01	AF034920.1	NT	Homo sapiens tubby like protein 1 (TULP1) gene, exons 9-11
7474	20440	33798	0.65	1.9E-01	U73846.1	NT	Drosophila melanogaster testis-specific RNA-binding protein (bruno) mRNA, complete cds
7709	20668	34033	0.75	1.9E-01	U93688.1	NT	Staphylococcus aureus toxic shock syndrome toxin-1 (tsst), enterotoxin (ent), and integrase (int) genes, complete cds
7734	20689	34053	1.35	1.9E-01	U80922.1	NT	Arabidopsis thaliana serine/threonine protein phosphatase type one (TOPPB8) gene, complete cds
7784	20737	34109	2.54	1.9E-01	AF072724.1	NT	Zea mays starch branching enzyme I (sbe1) gene, complete cds
8318	21287	34701	1.41	1.9E-01	AL161557.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 57
9034	22000	35421	12.98	1.9E-01	AB033024.1	NT	Homo sapiens mRNA for KIAA1198 protein, partial cds
9297	22263	35692	1.32	1.9E-01	M14568.1	NT	Marsupial cat beta-globin gene mRNA, partial cds
9297	22263	35693	1.32	1.9E-01	M14568.1	NT	Marsupial cat beta-globin gene mRNA, partial cds
10234	23159	36647	0.67	1.9E-01	AA012486.1	EST_HUMAN	g86g10.s1 NCL_CGAP_PNS1 Homo sapiens cDNA clone IMAGE:1537506 3' similar to contains Alu repetitive element;
10502	23524	37019	0.72	1.9E-01	BE830353.1	EST_HUMAN	RC5-ET0082-060700-022-A02 ET0082 Homo sapiens cDNA
10802	23524	37020	0.72	1.9E-01	BE830353.1	EST_HUMAN	RC5-ET0082-060700-022-A02 ET0082 Homo sapiens cDNA
11106	24066	37588	1.87	1.9E-01	AF223391.1	NT	Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced
11831	24714	38298	1.47	1.9E-01	M22253.1	NT	Rattus norvegicus sodium channel I mRNA, complete cds
12033	24909	38504	3.54	1.9E-01	AJ243213.1	NT	Homo sapiens partial 5-HT4 receptor gene, exons 2 to 5
12049	24922	38519	1.53	1.9E-01	L07344.1	NT	Influenza A/Guangdong/243/72 nucleoprotein (seg 6) gene, 5' end
12975	25540		1.62	1.9E-01	AF036859.1	NT	Rattus norvegicus nuclear serine/threonine protein kinase mRNA, complete cds
34	13154	26055	2.78	1.9E-01	U73200.1	NT	Mus musculus p16Rip mRNA, complete cds
260	15837	26281	1.39	1.8E-01	AB022090.1	NT	Mus musculus Ctg gene for chaperonin containing TCP-1 gamma subunit, partial cds

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370	13456	26386	1.91	1.8E-01	4502532	NT	Homo sapiens calcium channel, voltage-dependent, beta 2 subunit (CACNB2) mRNA, and translated products
983	14034	26986	0.89	1.8E-01	AI912212.1	EST_HUMAN	wd7102.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:2337051 3'
1093	14136	27087	1.05	1.8E-01	AF000580.1	NT	Dichostellum discoideum plasmid Ddp5, complete genome
1293	14328	27290	9.43	1.8E-01	AL117189.1	NT	Yersinia pestis plasmid pCD1
1503	14536	27507	1.17	1.8E-01	6753947	NT	Mus musculus guanylate nucleotide binding protein 1 (Gbp1), mRNA
1503	14536	27508	1.17	1.8E-01	6753947	NT	Mus musculus guanylate nucleotide binding protein 1 (Gbp1), mRNA
1864	14889		1.37	1.8E-01	4505036	NT	Homo sapiens latent transforming growth factor beta binding protein 4 (LTBP4) mRNA
1882	14907		1.47	1.8E-01	AI733708.1	EST_HUMAN	qg22d10.x5 NCI_CGAP_Kid3 Homo sapiens cDNA clone IMAGE:1781811 3' similar to TR:O75938 O75938 GAMMA BUTYROBETAINE HYDROXYLASE :
1930	14954	27950	1.66	1.8E-01	AB051897.1	NT	Mus musculus Soya6, Soya8, Soya16-ps, Soya5 genes for small inducible cytokine A6 precursor, small inducible cytokine A9 precursor, Soya16 pseudogene, small inducible cytokine A5 precursor, complete cds
2702	15598		3.94	1.8E-01	AW935728.1	EST_HUMAN	QV3-DT0018-081299-036-g04 DT0018 Homo sapiens cDNA
2908	15967		1.95	1.8E-01	AF184589.1	NT	Jbrapsidium aculea LEAFY protein (LEAFY2) gene, partial cds
2914	15972	28896	0.85	1.8E-01	AW182300.1	EST_HUMAN	x41a03.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2659756 3'
3141	16198	29108	1.35	1.8E-01	AW995178.1	EST_HUMAN	QV0-BN0041-070300-147-c04 BN0041 Homo sapiens cDNA
3379	16428	29354	0.82	1.8E-01	BF183582.1	EST_HUMAN	601B09723R1 NIH_MGC_18 Homo sapiens cDNA clone IMAGE:4040821 3'
3637	16680	29594	1.69	1.8E-01	H03389.1	EST_HUMAN	y45e01.s1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:151704 3' similar to contains Alu repetitive element;
3637	16680	29595	1.69	1.8E-01	H03389.1	EST_HUMAN	y45e01.s1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:151704 3' similar to contains Alu repetitive element;
4360	17387		0.75	1.8E-01	D37954.1	NT	Bovine NB25 mRNA for MHC class II (Bd.A-DQB), complete cds
4586	17608	30503	6.42	1.8E-01	AL161556.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 56
4806	17823	30718	2.5	1.8E-01	AB051897.1	NT	Mus musculus Soya6, Soya8, Soya16-ps, Soya5 genes for small inducible cytokine A6 precursor, small inducible cytokine A9 precursor, Soya16 pseudogene, small inducible cytokine A5 precursor, complete cds
5051	18063	30941	2.11	1.8E-01	X79794.1	NT	N tabacum mRNA pNL A-35
5084	18094	30970	1.96	1.8E-01	AW814270.1	EST_HUMAN	MR3-ST0203-151239-112-g06 ST0203 Homo sapiens cDNA
5099	18109	30982	0.93	1.8E-01	AF792382.1	EST_HUMAN	an29g07.y5 Gessler Wilms tumor Homo sapiens cDNA clone IMAGE:1700028 5'
5131	18140	31018	2.96	1.8E-01	AF181258.1	NT	Mesorhizetia auratus Na-tetraocholeate cotransporting polypeptide mRNA, partial cds
5214	18223		0.73	1.8E-01	U66150.1	NT	Loligo forbesi TTA repeat microsatellite region Lfor4
5371	18476	31349	0.64	1.8E-01	BE082828.1	EST_HUMAN	RC6-BT0641-300300-011-H03 BT0641 Homo sapiens cDNA
5906	18992	32183	1.91	1.8E-01	AL161594.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 90

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12301	25112	31840	1.88	1.8E-01	BF348623.1	EST_HUMAN	602019928F1 NCI_CGAP_Brm67 Homo sapiens cDNA clone IMAGE:4155318 5'
12752	25398		2.05	1.8E-01	Q86882	SWISSPROT	DNA TERMINAL PROTEIN (BELLETT PROTEIN) (PTP PROTEIN)
12866	25489		1.85	1.8E-01	R24494.1	EST_HUMAN	Yn48h10.1 Scores placenta NB2HP Homo sapiens cDNA clone IMAGE:133027 5'
12907	25489		1.56	1.8E-01	Y11114.1	NT	E displar mRNA for hexokinase (hdx1)
579	13948	26561	1.77	1.7E-01	BE385164.1	EST_HUMAN	601274604F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3816788 5'
806	13864	26514	2.22	1.7E-01	X63330.1	NT	P dimerill histone gene cluster for core histones H2A, H2B, H3 and H4
962	14015		1.93	1.7E-01	P36616	SWISSPROT	NEUROFILAMENT TRIPLET L PROTEIN (NEUROFILAMENT LIGHT POLYPEPTIDE) (NF-L)
1988	15019		3.18	1.7E-01	AF255051.1	NT	Homo sapiens BNIP3H (BNIP3H) gene, complete cds; nuclear gene for mitochondrial product
2871	15931	28848	2.3	1.7E-01	AF000716.1	NT	Vibrio cholerae hypoxanthine phosphoribosyltransferase (hpt) gene, partial cds, hemagglutinin/protease regulatory protein (haptR) gene, complete cds, and YRAL VIBCO gene, partial cds
2871	15931	28849	2.3	1.7E-01	AF000716.1	NT	Vibrio cholerae hypoxanthine phosphoribosyltransferase (hpt) gene, partial cds, hemagglutinin/protease regulatory protein (haptR) gene, complete cds, and YRAL VIBCO gene, partial cds
2938	15996	28917	1.69	1.7E-01	AA336909.1	EST_HUMAN	EST41651 Endometrial tumor Homo sapiens cDNA 5' end
3010	16088	28988	1.22	1.7E-01	AJ238736.1	NT	Naja naja atra cdx-1 gene, exons 1-3
3010	16088	28989	1.22	1.7E-01	AJ238736.1	NT	Naja naja atra cdx-1 gene, exons 1-3
3122	16179	29089	1.68	1.7E-01	AF081514.1	NT	Taxus canadensis geranylgeranyl diphosphate synthase mRNA, complete cds
3376	16427	29353	0.82	1.7E-01	N55763.1	EST_HUMAN	J2348F Human fetal heart, Lambda ZAP Express Homo sapiens cDNA clone J2348 5'
3482	16508	29429	1.48	1.7E-01	AJ269505.1	NT	Anabaena sp. ORF4 (partial), ORF3, ORF2, ORF1, adpA gene, adpB gene, adpC gene, adpD gene, adpE gene and adpF gene
3959	16989	29914	5.69	1.7E-01	AJ235377.1	NT	Homo sapiens derivative 11 breakpoint fragment: partial intron 10 of the ALL-1/MLL/HRX gene fused to intron 5 of the AF-4/FEL gene
4591	17612		1.9	1.7E-01	X52896.1	NT	Schistosoma gregaria alpha repetitive DNA
4876	17893	30782	1.21	1.7E-01	AJ247635.1	EST_HUMAN	qh57e09.x1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:1848908 3' similar to contains OFR.b1 OFR repetitive element;
5165	18174		0.92	1.7E-01	AF072725.1	NT	Zea mays starch branching enzyme IIb (ae) gene, complete cds
5210	18219	31095	0.74	1.7E-01	BF030010.1	EST_HUMAN	601557256F1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:3827197 5'
5482	18582	31493	1.88	1.7E-01	AA470686.1	EST_HUMAN	he13a02.s1 NCI_CGAP_Co3 Homo sapiens cDNA clone IMAGE:881066 3' similar to gb:M17896 60S
5482	18582	31494	1.88	1.7E-01	AA470686.1	EST_HUMAN	he13a02.s1 NCI_CGAP_Co3 Homo sapiens cDNA clone IMAGE:881066 3' similar to gb:M17896 60S
5674	18769	31941	0.74	1.7E-01	U43599.1	NT	ACIDIC RIBOSOMAL PROTEIN P1 (HUMAN);
6463	19528	32777	12.89	1.7E-01	H72118.1	EST_HUMAN	Brugia pahangi microfilarial sheath protein SHP3 (shp3) gene, complete cds
							ys02g06.s1 Soares_fetal_liver_spleen_1NFLS Homo sapiens cDNA clone IMAGE:213658 3'

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Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6526	19589	32848	0.9	1.7E-01	A1370976.1	EST_HUMAN	ta29c11.x1 Soares_fetal_lung_NbHL19W Homo sapiens cDNA clone IMAGE:2045492 3'
6526	19589	32849	0.9	1.7E-01	A1370976.1	EST_HUMAN	ta29c11.x1 Soares_fetal_lung_NbHL19W Homo sapiens cDNA clone IMAGE:2045492 3'
7031	18363	31250	0.78	1.7E-01	BE300286.1	EST_HUMAN	600944067T1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:2960248 3'
7063	20085		1.76	1.7E-01	AF026582.3	NT	Mesocricetus auratus oviductin precursor (OVI) gene, complete cds
7196	20220		0.79	1.7E-01	Z92910.1	NT	Homo sapiens HFE gene
7430	20397	33749	1.56	1.7E-01	AF000422.1	NT	Escherichia coli O157:H7 genomic DNA, Sakai-VT2 prophage inserted region
7515	20480	33841	8.55	1.7E-01	BE734179.1	EST_HUMAN	601569022F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3843964 5'
7721	20678	34043	1.42	1.7E-01	P16724	SWISSPROT	PROBABLE PROCESSING AND TRANSPORT PROTEIN UL56 (HFLP0 PROTEIN)
7739	26688	34057	0.71	1.7E-01	Q01995	SWISSPROT	COLLAGEN ALPHA 3(V) CHAIN PRECURSOR
8194	21164	34573	1.24	1.7E-01	AF000573.1	NT	Homo sapiens homogenitase 1,2-dioxygenase gene, complete cds
8295	21265	34676	0.82	1.7E-01	AF150669.1	NT	Pseudomonas putida long-chain-fatty-acid-CoA ligase (fadD) gene, complete cds
8620	21588	35004	7.37	1.7E-01	7706426	NT	Homo sapiens cleavage and polyadenylation specificity factor 3, 73kD subunit (CPSF3), mRNA
8620	21588	35005	7.37	1.7E-01	7706426	NT	Homo sapiens cleavage and polyadenylation specificity factor 3, 73kD subunit (CPSF3), mRNA
9045	22011	35433	0.6	1.7E-01	AW992873.1	EST_HUMAN	RG2-BN0032-120200-011-a10 BN0032 Homo sapiens cDNA
9079	22045	35468	3.22	1.7E-01	D00384.1	NT	Rat (SHR strain) SX1 gene
9196	22162	35590	0.81	1.7E-01	AF217413.1	NT	Homo sapiens neuroigin 3 isoform gene, complete cds, alternatively spliced
9196	22162	35591	0.81	1.7E-01	AF217413.1	NT	Homo sapiens neuroigin 3 isoform gene, complete cds, alternatively spliced
9349	22314	35739	0.44	1.7E-01	R77002.1	EST_HUMAN	y66g02.r1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:144242 5'
9523	22486	35933	0.43	1.7E-01	BE253142.1	EST_HUMAN	601116672F1 NIH_MGC_18 Homo sapiens cDNA clone IMAGE:3357184 5'
9523	22486	35934	0.43	1.7E-01	BE253142.1	EST_HUMAN	601116672F1 NIH_MGC_18 Homo sapiens cDNA clone IMAGE:3357184 5'
9948	22875	36337	8.16	1.7E-01	AP001508.1	NT	Bacillus halodurans genomic DNA, section 2/14
10056	22983	36451	0.47	1.7E-01	AW977455.1	EST_HUMAN	EST389564 IMAGE resequences, MAGO Homo sapiens cDNA
10056	22983	36452	0.47	1.7E-01	AW977455.1	EST_HUMAN	EST389564 IMAGE resequences, MAGO Homo sapiens cDNA
10073	23000	36470	1.93	1.7E-01	U16288.1	NT	Human class IV alcohol dehydrogenase (ADH7) gene, exon 3
10148	23074	36548	0.59	1.7E-01	Z34508.1	NT	Human immunodeficiency virus type 1 (B7.05) env gene (partial)
10148	23074	36549	0.59	1.7E-01	Z34508.1	NT	Human immunodeficiency virus type 1 (B7.05) env gene (partial)
10167	23092	36570	0.7	1.7E-01	AJ251749.1	NT	Drosophila melanogaster mRNA for serine protease inhibitor (serpin-6), (sp6 gene)
10563	23515		2.43	1.7E-01	AL163284.2	NT	Homo sapiens chromosome 21 segment HS21C084
							Homo sapiens solute carrier family 7 (cationic amino acid transporter, y ⁺ system), member 2 (SLC7A2), mRNA
10759	23680	37176	1.24	1.7E-01	11427203	NT	
10761	23682	37178	1.61	1.7E-01	AA627972.1	EST_HUMAN	hg60e07.s1 NCI_CGAP_Cos8 Homo sapiens cDNA clone IMAGE:1148292 3' similar to gbL25081
10966	23886		0.42	1.7E-01	AL161542.2	NT	TRANSFORMING PROTEIN RHOC (HUMAN);
11040	24004	37530	8.17	1.7E-01	BE330835.1	EST_HUMAN	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 42

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11157	24715	37641	2.51	1.7E-01	AA814617.1	EST_HUMAN	af43a03.s1 NCI_CGAP_CNS1 Homo sapiens cDNA clone IMAGE:142924 3'
11447	24390	37633	8.03	1.7E-01	7106300	NT	Mus musculus adenomatosis polyposis coli binding protein Eb1 (Eb1), mRNA
11447	24390	37634	8.03	1.7E-01	7106300	NT	Mus musculus adenomatosis polyposis coli binding protein Eb1 (Eb1), mRNA
11703	24668	38245	1.6	1.7E-01	AA883375.1	EST_HUMAN	ak4509.s1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1460287 3'
12021	24898		1.66	1.7E-01	P15272	SWISSPROT	AMP NUCLEOSIDASE
12141	25005	38615	1.74	1.7E-01	11418157	NT	Homo sapiens calcium channel, voltage-dependent, alpha 1 subunit (CACNA1L), mRNA
12273	25893		1.54	1.7E-01	AL163278.2	NT	Homo sapiens chromosome 21 segment HS21C078
12437	25736	31618	1.55	1.7E-01	AA847421.1	EST_HUMAN	bet1h02.s1 NCI_CGAP_Ov2 Homo sapiens cDNA clone IMAGE:1386231
12555	25739		1.69	1.7E-01	A1924404.1	EST_HUMAN	b08905.x1 NCI_CGAP_U11 Homo sapiens cDNA clone IMAGE:2274872 3' similar to gb:M73779 RETINOIC ACID RECEPTOR ALPHA-1 (HUMAN);
12833	25450	31723	14.15	1.7E-01	U01317.1	NT	Human beta globin region on chromosome 11
128	13233	26162	2.02	1.6E-01	AF217532.1	NT	Homo sapiens mevalonate kinase gene, exon 6 and 7
680	15814	26670	1.56	1.6E-01	R31497.1	EST_HUMAN	yt75f12.1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:135559 5'
1504	14537	27509	1.4	1.6E-01	AA648963.1	EST_HUMAN	nk28d12.s1 NCI_CGAP_Co11 Homo sapiens cDNA clone IMAGE:1014839 3'
1625	14557	27528	4.54	1.6E-01	AF298117.1	NT	Homo sapiens homeobox protein OTX2 gene, complete cds
1941	14965	27962	1.79	1.6E-01	P22063	SWISSPROT	AXONIN-1 PRECURSOR (AXONAL GLYCOPROTEIN TAG-1)
2001	15022		1	1.6E-01	U10334.1	NT	Crassostrea gigas RNA polymerase II largest subunit mRNA, partial cds
2393	15892	28427	0.99	1.6E-01	X94232.1	NT	H. sapiens mRNA for novel T-cell activation protein
2501	15504	28531	1.19	1.6E-01	AB037729.1	NT	Homo sapiens mRNA for KIAA1308 protein, partial cds
2802	15961	28881	10.42	1.6E-01	AF185589.1	NT	Homo sapiens cytochrome P450 3A4 (CYP3A4) gene, promoter region
2802	15961	28882	10.42	1.6E-01	AF185589.1	NT	Homo sapiens cytochrome P450 3A4 (CYP3A4) gene, promoter region
3649	16692	29607	1.2	1.6E-01	AJ003165.1	NT	Populus trichocarpa cv. Trichobol AB13 gene
3649	16692	29608	1.2	1.6E-01	AJ003165.1	NT	Populus trichocarpa cv. Trichobol AB13 gene
3786	16827	29734	0.76	1.6E-01	AE000962.1	NT	Archaeoglobus fulgidus section 145 of 172 of the complete genome
4025	17063		2.81	1.6E-01	AE004413.1	NT	Vibrio cholerae chromosome II, section 70 of 93 of the complete chromosome
4356	17383	30265	10.43	1.6E-01	AF179080.1	NT	Homo sapiens apelin gene, complete cds
4484	17509		3.1	1.6E-01	AW989601.1	EST_HUMAN	EST380677 IMAGE resequences, MAG, Homo sapiens cDNA
4491	17516		4.57	1.6E-01	8753319	NT	Mus musculus chaperonin subunit 3 (gamma) (Cct3), mRNA
4816	17933	30824	1.43	1.6E-01	Z28330.1	NT	S. cerevisiae chromosome XI reading frame ORF YKR105c
4816	17933	30825	1.43	1.6E-01	Z28330.1	NT	S. cerevisiae chromosome XI reading frame ORF YKR105c
4882	17997	30885	4.36	1.6E-01	AA088943.1	EST_HUMAN	z184h09.s1 Stragane colon (#837204) Homo sapiens cDNA clone IMAGE:511361 3' similar to TR:E221955
5004	18018	30805	1.94	1.6E-01	AJ006356.1	NT	E221955 38,855 BP SEGMENT OF CHROMOSOME XIV. ;
5004	18018	30806	1.94	1.6E-01	AJ006356.1	NT	Lycopodium esculentum Real fragment 2, satellite region

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5069	18079	30960	1.16	1.6E-01	BE018707.1	EST_HUMAN	b883h08.y1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3049023 5' similar to gb:M61715
5461	18563	31475	0.87	1.6E-01	L40508.1	NT	TRYPTOPHANYL-TRNA SYNTHETASE (HUMAN); gb:X98957 M.musculus (MOUSE);
5600	18896	31666	2.82	1.6E-01	AW197496.1	EST_HUMAN	Plasmodium falciparum (strain Dd2) variant-specific surface protein (var-1) gene, complete cds
5900	18896	31667	2.82	1.6E-01	AW197496.1	EST_HUMAN	xm4301.x1 NCI_CGAP_GC6 Homo sapiens cDNA clone IMAGE:2686969 3' similar to TR:O75984 O75984
5612	18708	31865	2.31	1.6E-01	AF034716.1	NT	HYPOPHOSPHATE 127.6 KD PROTEIN ;
6144	19219	32449	0.9	1.6E-01	BE25803.1	EST_HUMAN	HYPOPHOSPHATE 127.6 KD PROTEIN ;
6385	19453	32697	0.57	1.6E-01	BF183584.1	EST_HUMAN	Rattus norvegicus CCAAT/enhancer binding protein epsilon (cebpe) gene, complete cds
6386	19453	32698	0.57	1.6E-01	BF183584.1	EST_HUMAN	RC3-BN0034-310800-113-h01 BN0034 Homo sapiens cDNA
6568	19628	32893	1.99	1.6E-01	AL161588.2	NT	601809725R1 NIH_MGC_18 Homo sapiens cDNA clone IMAGE:4040335 3'
6568	19628	32894	1.99	1.6E-01	AL161588.2	NT	601809725R1 NIH_MGC_18 Homo sapiens cDNA clone IMAGE:4040335 3'
6850	20174	33498	0.55	1.6E-01	AA398047.1	EST_HUMAN	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 84
6969	20192	33519	0.66	1.6E-01	AB046786.1	EST_HUMAN	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 84
7158	18388	31232	4.63	1.6E-01	AW291215.1	EST_HUMAN	289404.r1 Soares testis_NHT Homo sapiens cDNA clone IMAGE:729511 5'
7518	20483	33844	0.61	1.6E-01	Z49632.1	NT	Homo sapiens mRNA for KIAA1566 protein, partial cds
8056	20993	34390	1.59	1.6E-01	AW246359.1	EST_HUMAN	U1H-B12-agi-b-05-0-UI.s1 NCI_CGAP_Sub4 Homo sapiens cDNA clone IMAGE:2724418 3'
8090	21026	34425	0.57	1.6E-01	6753237	NT	S.cerevisiae chromosome X reading frame ORF YJR132w
8102	21038		1.15	1.6E-01	AU136525.1	EST_HUMAN	2822248.5prime NIH_MGC_7 Homo sapiens cDNA clone IMAGE:2822248 5'
8201	21171	34582	1.26	1.6E-01	L49349.1	NT	Mus musculus Cas2>x-dependent activator protein for secretion (Cacps), mRNA
8359	21328		0.51	1.6E-01	BE244087.1	EST_HUMAN	AU136525 PLACE1 Homo sapiens cDNA clone PLACE1004466 5'
8456	21425	34841	0.66	1.6E-01	U38243.1	NT	Gorilla gorilla androgen receptor gene, partial exon
8979	21945	35359	0.85	1.6E-01	Z99119.1	NT	TOBAP1E0607 Pediatric pre-B cell acute lymphoblastic leukemia Baylor-HGSC project=TCBA Homo sapiens cDNA clone TOBAP0607
9178	22144	35571	0.71	1.6E-01	R13673.1	EST_HUMAN	Bacteroides vulgatus beta-lactamase (cbxA) gene, complete cds and mobilization protein (mobA) gene, complete cds
9285	22251		0.63	1.6E-01	L36861.1	NT	Bacillus subtilis complete genome (section 16 of 21): from 2997771 to 3213410
9322	22287	35717	1.9	1.6E-01	Z49501.1	NT	yf60108.r1 Soares infant brain 1N1B Homo sapiens cDNA clone IMAGE:26873 5'
9466	22430		0.63	1.6E-01	AF111167.2	NT	Homo sapiens guanylate cyclase activating protein (GCAP) gene exons 1-4, complete cds
10009	22936		2.05	1.6E-01	BF375171.1	EST_HUMAN	S.cerevisiae chromosome X reading frame ORF YJR001w
10012	22939	36404	2	1.6E-01	Z49501.1	NT	S.cerevisiae chromosome X reading frame ORF YJR001w
10048	22975		0.96	1.6E-01	BE156664.1	EST_HUMAN	PM2-HT0353-270100-004-f11 HT0353 Homo sapiens cDNA

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11017	23982	37509	2.59	1.6E-01	AW850853.1	EST_HUMAN	IL3-CT0220-111199-028-G01 CT0220 Homo sapiens cDNA
11122	24082	37607	1.82	1.6E-01	Z28073.1	NT	S.cerevisiae chromosome XI reading frame ORF YKL073w
11122	24082	37608	1.82	1.6E-01	Z28073.1	NT	S.cerevisiae chromosome XI reading frame ORF YKL073w
11344	24294	37820	1.5	1.6E-01	BE259649.1	EST_HUMAN	601145793F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:3161183 5'
11451	24394		3.84	1.6E-01	AF106064.1	NT	Plasmodium falciparum calcium-dependent protein kinase-3 (cdpk3) gene, complete cds
11740	24625	38204	6.59	1.6E-01	AF106064.1	NT	Mus musculus adaptor-related protein complex AP-1, beta 1 subunit (Ap1b1), mRNA
12155	25906		1.75	1.6E-01	6679466	NT	Mus musculus protein kinase, cGMP-dependent, type II (Phkg2), mRNA
12275	25995	38179	8.75	1.6E-01	AV719585.1	EST_HUMAN	AV719585 GLC Homo sapiens cDNA clone GCEMF07 5'
12608	26307		1.82	1.6E-01	AW839711.1	EST_HUMAN	RC1-L10074-120200-014-H01_1 L10074 Homo sapiens cDNA
12697	26721		22.15	1.6E-01	AB045310.1	NT	Cucumis sativus KS mRNA for anti-kaurene synthase, complete cds
12856	26463		2.73	1.6E-01	AK024496.1	NT	Homo sapiens mRNA for FLJ00104 protein, partial cds
12945	25524		2.56	1.6E-01	AF287344.1	NT	Fuchsia hybrid cultivar Qiu 94208 ribosomal protein S10 gene, partial cds; nuclear gene for mitochondrial product
12971	25537	31716	2.24	1.6E-01	9506522	NT	Rattus norvegicus chondroitin sulfate proteoglycan 5 (neuroglycan C) (Cspg5), mRNA
12978	25543		1.93	1.6E-01	BE267894.1	EST_HUMAN	601125459F1 NIH_MGC_8 Homo sapiens cDNA clone IMAGE:3345038 5'
248	13345	26270	1.73	1.5E-01	BE710087.1	EST_HUMAN	IL3-HT0619-040700-197-E05 HT0619 Homo sapiens cDNA
248	13345	26271	1.73	1.5E-01	BE710087.1	EST_HUMAN	IL3-HT0619-040700-197-E05 HT0619 Homo sapiens cDNA
589	15813		2.4	1.5E-01	AV711698.1	EST_HUMAN	AV711696 DCA Homo sapiens cDNA clone DCAADH06 5'
783	13843	26788	1.51	1.5E-01	AL163284.2	NT	Homo sapiens chromosome 21 segment HS21C084
1094	14136	27089	1.01	1.5E-01	AJ009735.1	NT	Cyprinus carpio mRNA for EGGS22 myosin heavy chain, 3'UTR
1099	14143	27093	2.55	1.5E-01	AJ251885.1	NT	Homo sapiens partial SLG22A2 gene for organic cation transporter (OC12), exon 1
1115	14159		1.57	1.5E-01	L36125.1	NT	Rattus norvegicus insulin-responsive glucose transporter (GLUT4) gene, 5' end
1280	14315	27276	3.58	1.5E-01	D26535.1	NT	Human gene for dihydropyrimidine succinyltransferase, complete cds (exon 1-15)
1280	14315	27277	3.58	1.5E-01	D26535.1	NT	Human gene for dihydropyrimidine succinyltransferase, complete cds (exon 1-15)
1478	14511	27487	2.54	1.5E-01	AF117340.1	NT	Mus musculus MAP kinase kinase 1 (Mekk1) mRNA, complete cds
1923	14947	27943	1.85	1.5E-01	AW444451.1	EST_HUMAN	UJH-B13-akb-b-09-q-UJ.st1 NCJ CGAP Sub6 Homo sapiens cDNA clone IMAGE:2733641 3'
2723	15717	28736	1.47	1.5E-01	BF695381.1	EST_HUMAN	602083269F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4247637 5'
2924	15982		1.1	1.5E-01	AW572516.1	EST_HUMAN	xw56a02.x2 NCJ CGAP_Pan1 Homo sapiens cDNA clone IMAGE:1571337 3' similar to gb:X55072_ma1
3048	16105	29019	0.76	1.5E-01	M81441.1	NT	THYROID HORMONE RECEPTOR ALPHA-1 (HUMAN); Bos taurus factor V variant 2 (factor V) mRNA, complete cds
3363	16413	29338	5.55	1.5E-01	AA935048.1	EST_HUMAN	cc68405.s1 NCJ CGAP_G4 Homo sapiens cDNA clone IMAGE:1571337 3' similar to gb:M11433
3381	16430	29357	0.74	1.5E-01	Z23104.1	NT	RETINOL-BINDING PROTEIN I, CELLULAR (HUMAN); L.stagnalis mRNA for G protein-coupled receptor
3381	16430	29358	0.74	1.5E-01	Z23104.1	NT	L.stagnalis mRNA for G protein-coupled receptor

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3440	16487	29405	0.97	1.5E-01	AW612237.1	EST_HUMAN	h28f02.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:2856539 3' similar to contains element MER16 repetitive element:
3768	16810	28719	2.22	1.5E-01	U09984.1	NT	Mus musculus ICR/Swiss glyceradehyde 3-phosphate dehydrogenase (Gapd-S) gene, complete cds Homo sapiens pyruvate dehydrogenase kinase, isoenzyme 1 (PDK1), nuclear gene encoding mitochondrial protein, mRNA
3782	16823	29731	0.8	1.5E-01	7108358	NT	XYNA; Thermoanaerobacterium; xynA; 4182 base-pairs
3795	16835	29740	0.86	1.5E-01	M97882.1	NT	h10106.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2981411 3'
3881	16920	29829	2.25	1.5E-01	AW665983.1	EST_HUMAN	Populus trichocarpa cv. Trichobol ABI3 gene
3898	16936	29846	0.71	1.5E-01	AJ003165.1	NT	Populus trichocarpa cv. Trichobol ABI3 gene
3896	16936	29847	0.71	1.5E-01	AJ003165.1	NT	Populus trichocarpa cv. Trichobol ABI3 gene
4080	17115	30011	2.53	1.5E-01	AW366659.1	EST_HUMAN	RC2-HT0149-191099-012-c08 HT0149 Homo sapiens cDNA
4213	17242	30127	9.83	1.5E-01	AL163284.2	NT	Homo sapiens chromosome 21 segment HS21C084
4513	17538	30422	0.91	1.5E-01	BE791253.1	EST_HUMAN	601583398F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3938345 5'
4513	17538	30423	0.91	1.5E-01	BE791253.1	EST_HUMAN	601583398F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3938345 5'
4756	17776	30672	1.88	1.5E-01	BF887685.1	EST_HUMAN	602067192F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4066223 5'
4783	15717	28735	2.86	1.5E-01	BF887685.1	EST_HUMAN	602067192F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4247537 5'
4830	17847	30748	1	1.5E-01	BE173796.1	EST_HUMAN	CMD-HT0565-280200-245-b10 HT0565 Homo sapiens cDNA
5034	18048	30928	1.2	1.5E-01	AL161580.2	NT	CMD-HT0565-280200-245-b10 HT0565 Homo sapiens cDNA
5134	18143	31023	1.07	1.5E-01	5579451	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 60
5328	18434	31186	2.46	1.5E-01	P07996	SWISSPROT	Homo sapiens calbindin 1, (28kD) (CALB1), mRNA
5357	18462	31331	1.03	1.5E-01	AF256652.1	NT	THROMBOSPONDIN 1 PRECURSOR
5401	18504		5.5	1.5E-01	P15196	SWISSPROT	Calman crocodilus MHC class II beta chain (hclbeta) gene, complete cds
5616	18712	31870	4.35	1.5E-01	AW850784.1	EST_HUMAN	SEX HORMONE-BINDING GLOBULIN PRECURSOR (SHBG) (SEX STEROID-BINDING PROTEIN) (ABP)
5659	18758	31922	7.17	1.5E-01	U65018.1	NT	IL3-CT0219-160200-064-F10 CT0219 Homo sapiens cDNA
5659	18755	31923	7.17	1.5E-01	U65016.1	NT	Mus musculus transforming growth factor alpha (TGFa) mRNA, complete cds
6012	19095	32285	0.79	1.5E-01	4506810	NT	Mus musculus sodium channel, voltage-gated, type VI, alpha polypeptide (SCN6A) mRNA
6120	19198	32422	1.74	1.5E-01	6753659	NT	Mus musculus DNA methyltransferase 2 (Dnm2), mRNA
6120	19198	32423	1.74	1.5E-01	6753659	NT	Mus musculus DNA methyltransferase 2 (Dnm2), mRNA
6161	19236	32467	1.96	1.5E-01	AJ276505.1	NT	Mus musculus genomic fragment, 279 Kb, chromosome 7
6319	19390	32630	3.25	1.5E-01	BE727658.1	EST_HUMAN	601564322F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3833981 5'
6375	19443		1.86	1.5E-01	4506396	NT	Homo sapiens RAD54 (S.cerevisiae)-like (RAD54L) mRNA

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Table 4
Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6478	19643	32791	1.7	1.5E-01	AF134907.1	NT	Influenza B virus (B/Nanchang/480/94) NB protein gene, complete cds; and neuraminidase gene, partial cds
6651	25664	32985	1.8	1.5E-01	AE001039.1	NT	Archaeoglobus fulgidus section 68 of 172 of the complete genome
6681	19738	33013	4.63	1.5E-01	11417236	NT	Homo sapiens chromosome 5 open reading frame 3 (C5ORF3), mRNA
6692	19749	33028	1.8	1.5E-01	P48508	SWISSPROT	GLUTAMATE-CYSTEINE LIGASE REGULATORY SUBUNIT (GAMMA-GLUTAMYL-CYSTEINE SYNTHETASE) (GAMMA-ECS) (GCS LIGHT CHAIN)
6740	19796	33075	2.35	1.5E-01	Q28462	SWISSPROT	AMELOGENIN
6842	19895	33189	0.85	1.5E-01	AA714760.1	EST_HUMAN	hw30410.s1 NCL_CGAP_GCB0 Homo sapiens cDNA clone IMAGE:1241971 3'
6871	19924	33220	1.8	1.5E-01	P30143	SWISSPROT	HYPOHETICAL 51.7 KD PROTEIN IN THRC-TALB INTERGENIC REGION (ORF8)
7171	18402	31247	5.15	1.5E-01	AW970295.1	EST_HUMAN	EST382376 MAGE resequences, MAGK Homo sapiens cDNA
7214	25678		0.71	1.5E-01	AA811545.1	EST_HUMAN	cb73102.s1 NCL_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1337019 3' similar to contains element LTR2 repetitive element;
7424	20391		1.91	1.5E-01	AF210842.1	NT	Homo sapiens HARP (HARP) gene, exon 17 and complete cds
7621	20581	33945	1.68	1.5E-01	AI973157.1	EST_HUMAN	wf52c08.x1 NCL_CGAP_UH1 Homo sapiens cDNA clone IMAGE:2497310 3'
7846	20763	34169	0.96	1.5E-01	AF299073.1	NT	Bos taurus Niemann-Pick type C1 disease protein (NPC1) mRNA, complete cds
7846	20763	34170	0.96	1.5E-01	AF299073.1	NT	Bos taurus Niemann-Pick type C1 disease protein (NPC1) mRNA, complete cds
7857	20802	34177	1.84	1.5E-01	AW500611.1	EST_HUMAN	UI-HF-BNO-akk-d-05-0-JL1 NIH_MGC_50 Homo sapiens cDNA clone IMAGE:3077409 5'
7857	20802	34178	1.84	1.5E-01	AW500611.1	EST_HUMAN	UI-HF-BNO-akk-d-05-0-JL1 NIH_MGC_50 Homo sapiens cDNA clone IMAGE:3077409 5'
8014	20952	34346	0.71	1.5E-01	U46560.1	SWISSPROT	Saccharomyces cerevisiae weak multicopy suppressor of lost-1 (SOL3) gene, complete cds
8393	21362	34769	1.21	1.5E-01	P21303	SWISSPROT	MEROZOITE RECEPTOR PK86 PRECURSOR (86 KD PROTECTIVE MINOR SURFACE ANTIGEN)
8562	21530	34950	0.97	1.5E-01	AA970317.1	EST_HUMAN	o085g12.s1 NCL_CGAP_Kid5 Homo sapiens cDNA clone IMAGE:1573030 3' similar to gb.M26062
8655	21623		1.01	1.5E-01	BE884799.1	EST_HUMAN	INTERLEUKIN-2 RECEPTOR BETA CHAIN PRECURSOR (HUMAN);
8743	21711		13.33	1.5E-01	C16800.1	EST_HUMAN	601510523F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3912004 5'
8776	21743	35165	1.69	1.5E-01	L27835.1	NT	C16800 Clontech human aorta polyA+ mRNA (#6572) Homo sapiens cDNA clone GEN-529109 5'
8940	21806	35330	1.79	1.5E-01	D84478.1	NT	Pangasinodon gigas growth hormone (GH) mRNA, complete cds
8962	21928		0.74	1.5E-01	P43446	SWISSPROT	Homo sapiens mRNA for ASK1, complete cds
9190	22156	35585	1.31	1.5E-01	4501972	NT	WNT-10A PROTEIN PRECURSOR
9460	22424	35862	3.06	1.5E-01	N74226.1	EST_HUMAN	Homo sapiens adaptor-related protein complex 1, beta 1 subunit (ADTB1), mRNA
9648	22511	35960	1.03	1.5E-01	BF555465.1	EST_HUMAN	z559e06.s1 Scores fetal liver spleen 1N1FLS Homo sapiens cDNA clone IMAGE:286866 3' similar to
9655	22517		2.73	1.5E-01	AV754819.1	EST_HUMAN	PIR-S44443 S44443 RAD23 protein homolog2 - human ;
9760	22701		0.87	1.5E-01	AU130007.1	EST_HUMAN	GV0000404 Human Psoriasis Differential Display Homo sapiens cDNA
9808	21131	34534	6.92	1.5E-01	U00455.1	NT	AV754819 TP Homo sapiens cDNA clone TPAAHB12 5'
							AU130007 NT2RP3 Homo sapiens cDNA clone NT2RP300080 5'
							Adipenser transmontano vitellogenin mRNA, partial cds

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10176	23101	36581	0.58	1.5E-01	M77144.1	NT	Human type II 3-beta hydroxysteroid dehydrogenase/ 5-delta - 4-delta isomerase gene, complete cds
10281	23206	36690	6.22	1.5E-01	AF007570.1	NT	Aplysia californica carboxypeptidase D mRNA, complete cds
10281	23206	36691	6.22	1.5E-01	AF007570.1	NT	Aplysia californica carboxypeptidase D mRNA, complete cds
10563	23485	36979	2.67	1.5E-01	X98852.1	NT	Pleniusculus mRNA for integrin beta subunit
10551	23573		0.62	1.5E-01	AB027759.1	NT	Mesocricetus auratus mRNA for collagen type XVII, complete cds
10871	23593	37089	2.49	1.5E-01	AI814046.1	EST_HUMAN	wk53112.x1 NCI CGAP P122 Homo sapiens cDNA clone IMAGE:2419175 3' similar to gb:M27508 BETA GALACTOSIDASE-RELATED PROTEIN PRECURSOR (HUMAN);
10871	23593	37090	2.49	1.5E-01	AI814046.1	EST_HUMAN	wk53112.x1 NCI CGAP P122 Homo sapiens cDNA clone IMAGE:2419175 3' similar to gb:M27508 BETA GALACTOSIDASE-RELATED PROTEIN PRECURSOR (HUMAN);
10753	23675	37172	2.19	1.5E-01	U40932.1	NT	Danio rerio transcription factor Pax8b (Pax8) mRNA, complete cds
10908	23826	37338	2.14	1.5E-01	AJ011984.1	NT	Claviceps purpurea ps1 gene
10908	23826	37339	2.14	1.5E-01	AJ011984.1	NT	Claviceps purpurea ps1 gene
11173	24130	37659	4.35	1.5E-01	AL163280.2	NT	Homo sapiens chromosome 21 segment HS21C080
11173	24130	37660	4.35	1.5E-01	AL163280.2	NT	Homo sapiens chromosome 21 segment HS21C080
11412	24356	37891	1.71	1.5E-01	AW841815.1	EST_HUMAN	IL5-CN0024-030300-025-D04 CN0024 Homo sapiens cDNA
11449	24392	37937	3.86	1.5E-01	AA425488.1	EST_HUMAN	zw46d02.r1 Soares_tetal_fetus_Nb2HF8_9w Homo sapiens cDNA clone IMAGE:773091 5' similar to contains element MER22 repetitive element
11501	20581	33945	1.69	1.5E-01	AI973157.1	EST_HUMAN	wr62c08.x1 NCI CGAP_U11 Homo sapiens cDNA clone IMAGE:2491310 3'
12229	25769		11.17	1.5E-01	BF700582.1	EST_HUMAN	602128753FT NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4285549 5'
12607	25306		1.82	1.5E-01	AF030358.2	NT	Rattus norvegicus chemokine CX3C mRNA, complete cds
12610	25309		1.81	1.5E-01	AJ238332.1	NT	Mus musculus mRNA for death inducer-obliterat-1 (Dio-1)
12668	25791		12.47	1.5E-01	R83077.1	EST_HUMAN	yp87ec4.r1 Soares fetal liver spleen INFLS Homo sapiens cDNA clone IMAGE:194430 5'
12748	25814		2.45	1.5E-01	AV741272.1	EST_HUMAN	AV741272 CB Homo sapiens cDNA clone CBDA004 5'
12855	25722	31613	7.87	1.5E-01	AL139074.2	EST_HUMAN	Campylobacter jejuni NCTC11188 complete genome; segment 1/6
13073	25606	31689	1.53	1.5E-01	AJ276242.1	NT	Sus scrofa mRNA for sodium iodide symporter
299	13393		2.07	1.4E-01	AF006663.1	NT	Homo sapiens T cell receptor beta locus, TCRBV85P to TCRBV21S2A2 region
911	13966		3.95	1.4E-01	D78638.1	NT	Xenopus laevis mRNA for DNA (cytosine-5-)-methyltransferase, complete cds
1264	14299		2.77	1.4E-01	T91864.1	EST_HUMAN	yd54c01.s1 Soares fetal liver spleen INFLS Homo sapiens cDNA clone IMAGE:112032 3'
1763	14792		1.61	1.4E-01	6679980	NT	Mus musculus growth differentiation factor 5 (Gdf5), mRNA
1766	14795	27780	1.82	1.4E-01	AE001710.1	NT	Thermoloba maritima section 22 of 136 of the complete genome
2002	15023		12.82	1.4E-01	AA720615.1	EST_HUMAN	ny72d07.s1 NCI CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1283821 3'
2482	15486	28509	1.15	1.4E-01	P30706	SWISSPROT	GLYCEROL-3-PHOSPHATE ACYLTRANSFERASE PRECURSOR (GPAT)
2804	15796	28815	7.57	1.4E-01	AI933496.1	EST_HUMAN	wm74d01.x1 NCI CGAP_U12 Homo sapiens cDNA clone IMAGE:2441665 3'

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3914	16954	29865	0.93	1.4E-01	R69232.1	EST_HUMAN	y97a03.r1 Soares Infant brain (NIB) Homo sapiens cDNA clone IMAGE:41467 5'
3914	16954	29866	0.93	1.4E-01	R69232.1	EST_HUMAN	y97a03.r1 Soares Infant brain (NIB) Homo sapiens cDNA clone IMAGE:41467 5'
4202	17233	30120	11.04	1.4E-01	A1699094.1	EST_HUMAN	b56d02.x1 NCL_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:2273570 3'
4202	17233	30121	11.04	1.4E-01	A1699094.1	EST_HUMAN	b56d02.x1 NCL_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:2273570 3'
4265	17284	30173	3.96	1.4E-01	AE001710.1	NT	Thermidoga maritima section 22 of 138 of the complete genome
							z50501.s1 Soares fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:453673 3' similar to gb:X01057_mn1 INTERLEUKIN-2 RECEPTOR ALPHA CHAIN PRECURSOR (HUMAN)/contains Alu repetitive element
4440	17466		0.71	1.4E-01	AA776287.1	EST_HUMAN	Homo sapiens phosphodiesterase 4A, cAMP-specific (dunce) (Drosophila)-homolog phosphodiesterase E2 (PDE4A), mRNA
4703	17724	30618	0.69	1.4E-01	5453861	NT	
4807	17924	30817	0.92	1.4E-01	AV686659.1	EST_HUMAN	AY686659 GKX Homo sapiens cDNA clone GKCDUG09 5'
5379	18483	31358	4.72	1.4E-01	T90677.1	EST_HUMAN	ye15c11.s1 Stragene lung (#937210) Homo sapiens cDNA clone IMAGE:117812 3'
5402	18505	31381	4.06	1.4E-01	AB004556.1	NT	Candida tropicalis DNA for mitochondrial NADP-linked isocitrate dehydrogenase, complete cds
5402	18505	31382	4.06	1.4E-01	AB004556.1	NT	Candida tropicalis DNA for mitochondrial NADP-linked isocitrate dehydrogenase, complete cds
6430	19496	32749	2.9	1.4E-01	BE328891.1	EST_HUMAN	hr67c02.x1 NCL_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:313538 3'
6629	19687	32965	5.1	1.4E-01	AU117147.1	EST_HUMAN	AU117147 HEMBA1 Homo sapiens cDNA clone HEMBA1000769 5'
6629	19687	32966	5.1	1.4E-01	AU117147.1	EST_HUMAN	AU117147 HEMBA1 Homo sapiens cDNA clone HEMBA1000769 5'
6723	19779	33058	3.48	1.4E-01	AW082796.1	EST_HUMAN	xb71d12.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2881751 3'
6737	19793		1.26	1.4E-01	BE266836.1	EST_HUMAN	601193623F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3637681 5'
6759	19813	33093	2.02	1.4E-01	BF376533.1	EST_HUMAN	QV1-UM0036-080300-103-409 UM0036 Homo sapiens cDNA
7333	20304		0.74	1.4E-01	AL118668.1	EST_HUMAN	DKFZ5761A0910_r1 761 (synonym: hemy2) Homo sapiens cDNA clone DKFZp761A0910 5'
7615	20575		1.67	1.4E-01	AW015373.1	EST_HUMAN	U1-H-BIO-eak-c-09-0-UI.s1 NCL_CGAP_Sub1 Homo sapiens cDNA clone IMAGE:2710289 3'
7641	20601	33965	0.51	1.4E-01	F08745.1	EST_HUMAN	HSC1DB011 normalized Infant brain cDNA Homo sapiens cDNA clone c-1db01
							w04f12.x1 NCL_CGAP_CLL1 Homo sapiens cDNA clone IMAGE:2389295 3' similar to SW:ICE4_HUMAN P49662 CASPASE-4 PRECURSOR ;
7694	20652		0.61	1.4E-01	A1762827.1	EST_HUMAN	
7883	20827	34203	0.82	1.4E-01	U85645.1	NT	Oryctolagus cuniculus fructose 1,6-bisphosphate aldolase (AldB) gene, complete cds
8029	20966	34361	1.24	1.4E-01	A1305192.1	EST_HUMAN	gl90b12.x1 Soares_NHMPU_S1 Homo sapiens cDNA clone IMAGE:1879583 3'
8818	21785		1.24	1.4E-01	AV659047.1	EST_HUMAN	AV659047 GLC Homo sapiens cDNA clone GLCF5H08 3'
							th92b12.x1 Soares_NSIF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:2128111 3' similar to TR:002710 Q02710 GAG POLYPROTEIN. ;
9136	22102		0.67	1.4E-01	AI436093.1	EST_HUMAN	EST1178192 Colon carcinoma (HCC) cell line Homo sapiens cDNA 5' end
9264	22230	35681	4.68	1.4E-01	AA307073.1	EST_HUMAN	df58b03.y1 Morton Fetal Cochlea Homo sapiens cDNA clone IMAGE:2487485 5'
9346	22310	35735	0.56	1.4E-01	AW023636.1	EST_HUMAN	Y10h05.r1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:138873 5'
9478	22442	35883	0.94	1.4E-01	R62746.1	EST_HUMAN	Y10h05.r1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:138873 5'
9478	22442	35884	0.94	1.4E-01	R62746.1	EST_HUMAN	Y10h05.r1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:138873 5'

Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9541	22504	35953	9.19	1.4E-01	BF310959.1	EST_HUMAN	601895465F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4124824 5'
9630	22574	36024	1.19	1.4E-01	W83411.1	EST_HUMAN	z184a04.r1 Soares_fetal_heart_NbH119W Homo sapiens cDNA clone IMAGE:357102 5' similar to contains element KER repetitive element:
9702	22655	36109	0.43	1.4E-01	X73293.1	NT	M.vannielii genes rpoH, rpoB and rpoA
9702	22655	36110	0.43	1.4E-01	X73293.1	NT	M.vannielii genes rpoH, rpoB and rpoA
9713	22666	36123	1.44	1.4E-01	Y10196.1	NT	Homo sapiens PHEX gene
9713	22666	36124	1.44	1.4E-01	Y10196.1	NT	Homo sapiens PHEX gene
9805	21128	34532	2.06	1.4E-01	AF121361.1	NT	Drosophila melanogaster signal transducing adaptor protein (STAM), serine threonine kinase lat (IAL), and zinc finger protein (DNZ1) genes, complete cds
10164	23089	36567	0.55	1.4E-01	X66092.1	NT	C.perfringens ORF for putative membrane transport protein
10346	23270	36747	1.12	1.4E-01	AF023813.1	NT	Macromitrium levatum small ribosomal protein 4 (rps4) gene, chloroplast gene encoding chloroplast protein, partial cds
10448	23370	36861	0.57	1.4E-01	AW021908.1	EST_HUMAN	df29h08.y1 Morton Fetal Cochlea Homo sapiens cDNA clone IMAGE:2485094 5'
10448	23370	36862	0.57	1.4E-01	AW021908.1	EST_HUMAN	df29h08.y1 Morton Fetal Cochlea Homo sapiens cDNA clone IMAGE:2485094 5'
10619	23541	37039	0.67	1.4E-01	BF375285.1	EST_HUMAN	MR3-ST0218-211299-013-a08 ST0218 Homo sapiens cDNA
10619	23541	37040	0.67	1.4E-01	BF375285.1	EST_HUMAN	MR3-ST0218-211299-013-a08 ST0218 Homo sapiens cDNA
10829	23750	37395	0.86	1.4E-01	T84293.1	EST_HUMAN	y447d03.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:111365 5'
10862	23882	37395	0.71	1.4E-01	Z99117.1	NT	Bacillus subtilis complete genome (section 14 of 21): from 2599451 to 2812870
11191	24147	37680	2.59	1.4E-01	R53400.1	EST_HUMAN	Integrin alpha-5 precursor (FIBRONECTIN RECEPTOR ALPHA SUBUNIT) (INTEGRIN ALPHA-5) (VLA-5) (CD49E)
11432	24376	37916	2.53	1.4E-01	P08648	SWISSPROT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 8
11752	24637		1.59	1.4E-01	AL161496.2	NT	Borrelia burgdorferi glyceraldehyde-3-phosphate dehydrogenase (GAPDH), phosphoglycerate kinase (PGK), triosephosphate isomerase (TPI) genes, complete cds
11797	23952	37474	2.38	1.4E-01	U28780.1	NT	M.musculus p16K gene for 16 kDa protein
11855	24737		1.55	1.4E-01	X52102.1	NT	P. salina plastid gene secY
12549	25272	31776	2.33	1.4E-01	X74773.1	NT	Rattus norvegicus desmin (Des), mRNA
12562	25280		2.24	1.4E-01	11968117	NT	601315638F1 NIH_MGC_8 Homo sapiens cDNA clone IMAGE:3634329 5'
12605	25984		2.35	1.4E-01	BE513802.1	EST_HUMAN	Synchyocystis sp. PCC8803 complete genome, 23/27, 2868767-3002965
12702	25362		2.29	1.4E-01	D64004.1	NT	TYROSINE-PROTEIN KINASE TRANSFORMING PROTEIN ABL
12776	25981		4.86	1.4E-01	P10447	SWISSPROT	Mus musculus mRNA for prolidase, complete cds
12985	25782		3.72	1.4E-01	D82983.1	NT	MR0-HT0208-221299-204-508 HT0208 Homo sapiens cDNA
13067	25601		2.63	1.4E-01	AW377998.1	EST_HUMAN	Homo sapiens G protein-coupled receptor 50 (GPR50) mRNA
322	13414	26338	2.46	1.3E-01	4758467	NT	Homo sapiens G protein-coupled receptor 50 (GPR50) mRNA
322	13414	26339	2.48	1.3E-01	4758467	NT	Homo sapiens G protein-coupled receptor 50 (GPR50) mRNA

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Table 4
Single Exon Probes Expressed in Bone Marrow.

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
530	13601	26519	2.91	1.3E-01	AB013139.1	NT	Homo sapiens gene for NBS1, complete cds
637	13703	26624	0.78	1.3E-01	AJ277606.1	NT	Human calicivirus HU/NLV/Girlington/93/UK RNA for capsid protein (ORF2), strain HU/NLV/Girlington/93/UK
637	13703	26625	0.78	1.3E-01	AJ277606.1	NT	Human calicivirus HU/NLV/Girlington/93/UK RNA for capsid protein (ORF2), strain HU/NLV/Girlington/93/UK
845	13901	26859	1.04	1.3E-01	X53330.1	NT	P. dumerilii histone gene cluster for core histones H2A, H2B, H3 and H4
895	13950	26908	1.76	1.3E-01	AF139518.1	NT	Rattus norvegicus A-kinase anchor protein mRNA, complete cds
1028	14074	27024	1.8	1.3E-01	AL117078.1	NT	Botrytis cinerea strain T4 cDNA library under conditions of nitrogen deprivation
1129	14172		2.88	1.3E-01	AL115265.1	NT	Botrytis cinerea strain T4 cDNA library under conditions of nitrogen deprivation
1220	14258	27215	1.51	1.3E-01	AV712487.1	EST_HUMAN	AV712487 DCA Homo sapiens cDNA clone DCAAF05 5'
1438	14471		0.93	1.3E-01	AF146277.1	NT	Homo sapiens adapter protein CMS mRNA, complete cds
1876	14997	27999	2.07	1.3E-01	AL117078.1	NT	Botrytis cinerea strain T4 cDNA library under conditions of nitrogen deprivation
2180	15195		1.69	1.3E-01	AJ243578.1	NT	Rhodospirillum rubrum acidoiphila pucB5, pucA5, pucB6, pucA6, pucB7, pucA7, pucB8, pucA8 and pucC genes and ORF151
2298	15310		0.96	1.3E-01	AW812104.1	EST_HUMAN	RC4-ST0173-191099-032-012 ST0173 Homo sapiens cDNA
2389	15397		3.94	1.3E-01	AE001016.1	NT	Archaeoglobus fulgidus section 91 of 172 of the complete genome
2592	15593	28610	2.23	1.3E-01	M89918.1	NT	Carassius auratus keratin type I mRNA, complete cds
3465	16511	29432	0.98	1.3E-01	M21572.1	NT	Bovine branched chain alpha-keto acid dihydrolipoyl transacylase mRNA, complete cds
3735	16777	29689	0.91	1.3E-01	AP000001.1	NT	Pyrococcus horikoshii OT3 genomic DNA, 1-287000 nt. position (177)
3735	16777	29690	0.91	1.3E-01	AP000001.1	NT	Pyrococcus horikoshii OT3 genomic DNA, 1-287000 nt. position (177)
3741	16783	29695	0.89	1.3E-01	AB032159.1	NT	Homo sapiens DD4 gene for dihydrolipoyl dehydrogenase 4 [AKR 1C4], exon 2
3784	16777	29689	0.67	1.3E-01	AP000001.1	NT	Pyrococcus horikoshii OT3 genomic DNA, 1-287000 nt. position (177)
3784	16777	29690	0.67	1.3E-01	AP000001.1	NT	Pyrococcus horikoshii OT3 genomic DNA, 1-287000 nt. position (177)
3816	16856	29762	0.74	1.3E-01	6978840	NT	Rattus norvegicus Fibrinogen, gamma polypeptide (Fgg), mRNA
4014	17053		1.48	1.3E-01	AL161581.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 77
4081	13703	26624	7.11	1.3E-01	AJ277606.1	NT	Human calicivirus HU/NLV/Girlington/93/UK RNA for capsid protein (ORF2), strain HU/NLV/Girlington/93/UK
4081	13703	26625	7.11	1.3E-01	AJ277606.1	NT	Human calicivirus HU/NLV/Girlington/93/UK RNA for capsid protein (ORF2), strain HU/NLV/Girlington/93/UK
4163	17194		1.12	1.3E-01	AF020713.1	NT	Bacteriophage SPBc2 complete genome
4185	17216		4.1	1.3E-01	AW364341.1	EST_HUMAN	QV3-DT0018-081299-036-a03 DT0018 Homo sapiens cDNA
4194	17225	30114	2.47	1.3E-01	AF028805.1	NT	Schistosoma mansoni fructose biphosphate aldolase mRNA, complete cds
4215	17244	30129	20.19	1.3E-01	AW273741.1	EST_HUMAN	xx2310.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2813995 3'
4343	17370		1.49	1.3E-01	AL163280.2	NT	Homo sapiens chromosome 21 segment HS21C080

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4505	17530	30414	0.8	1.3E-01	M21572.1	NT	Bovine branched chain alpha-keto acid dihydrolypolyl transacylase mRNA, complete cds
4564	17587	30479	2.72	1.3E-01	BE272339.1	EST_HUMAN	601126098F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:2990063 5'
5014	18028		0.91	1.3E-01	AU136619.1	EST_HUMAN	AU136619 PLACE1 Homo sapiens cDNA clone PLACE1004693 5'
5060	18070		0.63	1.3E-01	BF091980.1	EST_HUMAN	RC4-TN0077-180900-012-c05 TN0077 Homo sapiens cDNA
							ha07b06.x1 NCI_CGAP_Kid12 Homo sapiens cDNA clone IMAGE:2872979 3' similar to contains L1.b1 L1
							L1 repetitive element
5398	18501	31379	0.76	1.3E-01	AW469988.1	EST_HUMAN	QVQ-UM0093-10040-189-a06 UM0093 Homo sapiens cDNA
5436	18538	31446	1.98	1.3E-01	AW804417.1	EST_HUMAN	Emeritella nidulans DNA-dependent RNA polymerase II RPB140 (RPB2) gene, partial cds
5579	18675		0.91	1.3E-01	AF107783.1	NT	Hepatitis C virus 68 Cl.10 genome polyprotein gene, partial cds
5665	18760		0.68	1.3E-01	AF056880.1	NT	601874591F1 NIH_MGC_54 Homo sapiens cDNA clone IMAGE:4101119 5'
5813	18903	32086	0.85	1.3E-01	BF210920.1	EST_HUMAN	602039337F2 NCI_CGAP_Bm67 Homo sapiens cDNA clone IMAGE:4177233 5'
6099	19178	32396	0.58	1.3E-01	BF527281.1	EST_HUMAN	602039337F2 NCI_CGAP_Bm67 Homo sapiens cDNA clone IMAGE:4177233 5'
6099	19178	32397	0.58	1.3E-01	BF527281.1	EST_HUMAN	602039337F2 NCI_CGAP_Bm67 Homo sapiens cDNA clone IMAGE:4177233 5'
6630	19688	32967	17.29	1.3E-01	AB031326.1	NT	Schizosaccharomyces pombe gene for Alp41, complete cds
6720	19776	33055	2.08	1.3E-01	X88891.1	NT	C.jacchus intron 4 of visual pigment gene (red allele)
6940	20164	33487	0.64	1.3E-01	H73425.1	EST_HUMAN	yu02d01.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:232609 5'
6955	20180		0.82	1.3E-01	W26367.1	EST_HUMAN	2613 Human retina cDNA randomly primed sublibrary Homo sapiens cDNA
7009	20135	33450	1.04	1.3E-01	BE782926.1	EST_HUMAN	601465657F1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:3869079 5'
7009	20135	33451	1.04	1.3E-01	BE782926.1	EST_HUMAN	601465657F1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:3869079 5'
7211	20234		0.72	1.3E-01	BF529560.1	EST_HUMAN	602044345F1 NCI_CGAP_Bm67 Homo sapiens cDNA clone IMAGE:4181866 5'
7477	20443		2.15	1.3E-01	H48664.1	EST_HUMAN	yr33402.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:207075 5'
8292	21281		0.97	1.3E-01	BE272339.1	EST_HUMAN	601126098F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:2990063 5'
8306	21275	34686	1.59	1.3E-01	11423294	NT	Homo sapiens PRO0611 protein (PRO0611), mRNA
8336	21305	34720	1.18	1.3E-01	BF690522.1	EST_HUMAN	602187015T1 NIH_MGC_49 Homo sapiens cDNA clone IMAGE:4299074 3'
8580	21548		0.96	1.3E-01	BE562528.1	EST_HUMAN	601335829F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3689934 5'
8617	21585	35001	0.6	1.3E-01	11421556	NT	Homo sapiens TED protein (TED), mRNA
8688	21656		4.68	1.3E-01	Z74102.1	NT	S.cerevisiae chromosome IV reading frame ORF YDL054c
8729	21697		4.2	1.3E-01	8923919	NT	Homo sapiens core histone macroH2A2.2 (MACROH2A2), mRNA
8873	21840	35263	1.05	1.3E-01	BF690522.1	EST_HUMAN	602187015T1 NIH_MGC_49 Homo sapiens cDNA clone IMAGE:4299074 3'
							yr39g11.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:129284 5' similar to
9300	22265	35694	0.55	1.3E-01	R11172.1	EST_HUMAN	SP:RL2B_RAT P29316 60S RIBOSOMAL PROTEIN ;
9300	22265	35695	0.55	1.3E-01	R11172.1	EST_HUMAN	yr39g11.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:129284 5' similar to
9574	22536	35987	0.65	1.3E-01	11068003	NT	SP:RL2B_RAT P29316 60S RIBOSOMAL PROTEIN ;
9574	22536	35988	0.65	1.3E-01	11068003	NT	Plutella xylostella granulovirus, complete genome

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Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9827	22676	36132	3.9	1.3E-01	AF023129.1	NT	Oryctolagus cuniculus H ₂ K+ATPase alpha 2c subunit mRNA, complete cds
10129	23055		0.74	1.3E-01	N86348.1	EST_HUMAN	J7837F Human fetal heart, Lambda ZAP Express Homo sapiens cDNA clone J7837 5' similar to B-CELL RECEPTOR ASSOCIATED PROTEIN (BAP) 29
10411	23333		0.89	1.3E-01	8393940	NT	Rattus norvegicus peptidyl arginine deiminase, type IV (Pd4), mRNA
10489	23411	36908	0.86	1.3E-01	AW851598.1	EST_HUMAN	MR2-CT0222-201099-001-e01 CT0222 Homo sapiens cDNA
10767	25702	37173	1.06	1.3E-01	AL183246.2	NT	Homo sapiens chromosome 21 segment HS21C046
10891	23811	37318	0.66	1.3E-01	AU121237.1	EST_HUMAN	AU121237 HEMBB1 Homo sapiens cDNA clone HEMBB1002387 5'
10936	23858	37372	0.45	1.3E-01	AW247836.1	EST_HUMAN	2820637.3prime NIH_MGC_7 Homo sapiens cDNA clone IMAGE:2820637 3'
10996	23962		2.67	1.3E-01	BF330999.1	EST_HUMAN	MR4-BT0358-130700-010-H08 BT0358 Homo sapiens cDNA
11581	24519		3.56	1.3E-01	6671745	NT	Mus musculus cofilin 2, muscle (Cif2), mRNA
11670	24606	38182	1.77	1.3E-01	AW082636.1	EST_HUMAN	xc20f09.x1 NCL_CGAP_Cot19 Homo sapiens cDNA clone IMAGE:2584841 3'
11670	24606	38183	1.77	1.3E-01	AW082636.1	EST_HUMAN	xc20f09.x1 NCL_CGAP_Cot19 Homo sapiens cDNA clone IMAGE:2584841 3'
11922	24803	38395	2.33	1.3E-01	BE279449.1	EST_HUMAN	601156052F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3504804 5'
12397	25171	31817	1.83	1.3E-01	BE618346.1	EST_HUMAN	60146274F1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:3866003 5'
12535	25260		3.3	1.3E-01	AJ242790.1	NT	Gallus gallus sox1 gene for lymphotactin, exons 1-3
12692	25357	31766	1.37	1.3E-01	BF572303.1	EST_HUMAN	602077752F1 NIH_MGC_62 Homo sapiens cDNA clone IMAGE:4252082 5'
12865	25475		1.48	1.3E-01	AB026829.1	NT	Echydatta fluviatilis mRNA for sALK-6, complete cds
12915	25494		2.52	1.3E-01	AW001114.1	EST_HUMAN	TR:O60287 O60287 KIAA0539 PROTEIN ;
383	13496	26428	14.66	1.2E-01	AK421744.1	EST_HUMAN	tf39b02.x1 NCL_CGAP_Brn23 Homo sapiens cDNA clone IMAGE:2098539 3' similar to gb:U05760_rna1
424	13119		1.38	1.2E-01	U66912.1	NT	ANNEXIN V (HUMAN);
549	13619		2.78	1.2E-01	AF039442.1	NT	Dictyostelium discoideum ORF DG1016 gene, partial cds
1377	14411	27381	2.19	1.2E-01	AU149146.1	EST_HUMAN	Homo sapiens colon cancer antigen NY-CO-45 mRNA, partial cds
1377	14411	27382	2.19	1.2E-01	AU149146.1	EST_HUMAN	AU149146 NT2RM4 Homo sapiens cDNA clone NT2RM4001691 3'
1383	14417		4.89	1.2E-01	AV735249.1	EST_HUMAN	AU149146 NT2RM4 Homo sapiens cDNA clone NT2RM4001691 3'
1388	14421		0.92	1.2E-01	AL445068.1	NT	AV735249 cda Homo sapiens cDNA clone cdaAJB11 5'
1607	14540		1.23	1.2E-01	AA897474.1	EST_HUMAN	Thermoplasma acidophilum complete genome, segment 4/5
1635	14687	27643	1.82	1.2E-01	Q14934	SWISSPROT	a148909.s1 Soares_NFL_I_GBC_S1 Homo sapiens cDNA clone IMAGE:1460584 3' similar to TR:Q16671
1658	14690	27666	2.89	1.2E-01	AI285402.1	EST_HUMAN	Q16671 ANTI-MULLERIAN HORMONE TYPE II RECEPTOR PRECURSOR ;
1783	14812		18.69	1.2E-01	X89211.1	NT	NUCLEAR FACTOR OF ACTIVATED T-CELLS, CYTOPLASMIC 4 (T CELL TRANSSCRIPTION FACTOR NFAT3) (NF-ATC4) (NF-AT3)
1934	14958		1.76	1.2E-01	AW449368.1	EST_HUMAN	q166f09.x1 NCL_CGAP_Esc2 Homo sapiens cDNA clone IMAGE:1960553 3'
							H.sapiens DNA for endogenous retroviral like element
							U1H-B13-akl-e-10-0-U1.s1 NCL_CGAP_Sub5 Homo sapiens cDNA clone IMAGE:2734554 3'

Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2193	15208	28227	1.65	1.2E-01	BF248490.1	EST_HUMAN	601821587F1 NIH_MGC_62 Homo sapiens cDNA clone IMAGE:4046224 5'
2294	15306	28329	1.21	1.2E-01	AL163213.2	NT	Homo sapiens chromosome 21 segment HS21C013
2595	15596	28614	2.05	1.2E-01	AW966556.1	EST_HUMAN	QV3-BN0046-220300-129-F10 BN0046 Homo sapiens cDNA
2602	15602	28624	1.81	1.2E-01	BE219989.1	EST_HUMAN	h16504.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3178303 3'
							ts18g07.x1 NCI_CGAP_Pan1 Homo sapiens cDNA clone IMAGE:2228988 3' similar to TR:Q14048 Q14048 COLLAGEN VI ALPHA-2 ALTERNATIVE C-TERMINAL DOMAIN. [1] contains element PTR5 repetitive element;
2738	15732	28748	37.99	1.2E-01	AI823388.1	EST_HUMAN	Human E1A enhancer binding protein (E1A-F) mRNA, partial cds
2855	15915	28838	1.4	1.2E-01	U18018.1	NT	es80-c09.x1 Barslead colon HPLRB7 Homo sapiens cDNA clone IMAGE:2335024 3' similar to gb.L05095
2913	15971	28895	2.03	1.2E-01	AI720470.1	EST_HUMAN	80S RIBOSOMAL PROTEIN L30 (HUMAN); Human creatine kinase-B mRNA, complete cds
2948	16004	28929	2.52	1.2E-01	M18364.1	NT	Wheat mRNA for a group 3 late embryogenesis abundant protein (LEA)
3017	16075	28996	0.73	1.2E-01	X56882.1	NT	QV1-BT0259-261099-021-d05 BT0259 Homo sapiens cDNA
3244	16299	29224	1.34	1.2E-01	AW370668.1	EST_HUMAN	Methanococcus jannaschii section 142 of 160 of the complete genome
3271	16325		0.82	1.2E-01	U67600.1	NT	Wheat mRNA for a group 3 late embryogenesis abundant protein (LEA)
3533	16579	29502	0.86	1.2E-01	X56882.1	NT	Wheat mRNA for a group 3 late embryogenesis abundant protein (LEA)
3533	16579	29503	0.86	1.2E-01	X56882.1	NT	Bacillus subtilis complete genome (section 15 of 21): from 2795131 to 3013540
3620	16538		1.05	1.2E-01	Z99118.1	NT	601810786R1 NIH_MGC_46 Homo sapiens cDNA clone IMAGE:4053688 3'
3780	16821		0.7	1.2E-01	BF128551.1	EST_HUMAN	P. clarkii mRNA; repeat region (ID 2MRT7)
4211	17240	30125	2.16	1.2E-01	Z54255.1	NT	P. clarkii mRNA; repeat region (ID 2MRT7)
4211	17240	30126	2.16	1.2E-01	Z54255.1	NT	L. esculentum mRNA for glycylase-1
4751	17771	30667	0.98	1.2E-01	Z48183.1	NT	HEMOLYSIN PRECURSOR
5116	18126		1	1.2E-01	P18466	SWISSPROT	Homo sapiens chromosome 21 segment HS21C027
5150	18159	31038	0.91	1.2E-01	AL163227.2	NT	Homo sapiens chromosome 21 segment HS21C027
5150	18159	31039	0.91	1.2E-01	AL163227.2	NT	Homo sapiens chromosome 4, contig fragment No. 30
5194	18173	31052	1	1.2E-01	AL161518.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 30
5234	18242	31114	0.81	1.2E-01	BE974502.1	EST_HUMAN	601880493R2 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:3950711 3'
5322	18428	31178	0.75	1.2E-01	AA744369.1	EST_HUMAN	ny63c04.s1 NCI_CGAP_G051 Homo sapiens cDNA clone IMAGE:1282950 3'
							Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced
5373	18478	31351	0.91	1.2E-01	AF223391.1	NT	z08cd02.r1 Soares_papillary tumor NblHPA Homo sapiens cDNA clone IMAGE:321699 5'
5383	18487	31361	2.27	1.2E-01	W33035.1	EST_HUMAN	Homo sapiens gene encoding plakophilin (exons 1-13)
5442	18544	31456	2.15	1.2E-01	Z98266.1	NT	M. domestica Borkh. Granny Smith adh mRNA for alcohol dehydrogenase
5583	18679	31643	0.95	1.2E-01	Z48234.1	NT	601493518F1 NIH_MGC_70 Homo sapiens cDNA clone IMAGE:3895613 5'
6324	18934	32636	2.66	1.2E-01	BE620945.1	EST_HUMAN	MATING-TYPE P-SPECIFIC POLYPEPTIDE P1
6376	19444	32686	1.1	1.2E-01	P10842	SWISSPROT	

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Table 4
Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6431	19497	32750	2.19	1.2E-01	AW845275.1	EST_HUMAN	IL0-CT0031-221099-113-e04 CT0031 Homo sapiens cDNA
6499	19593	32815	1.38	1.2E-01	M26925.1	NT	Mouse galactosyltransferase mRNA, complete cds
6804	19888	33145	0.89	1.2E-01	BF347985.1	EST_HUMAN	602023112F1 NCL CGAP_Bm67 Homo sapiens cDNA clone IMAGE:4158386 5'
6966	20190	33517	0.55	1.2E-01	AF295739.1	NT	JC virus agnoprotein VP2, VP3, VP1, large T antigen, and small T antigen genes, complete cds
7210	20233	33567	0.67	1.2E-01	H47789.1	EST_HUMAN	yp80f04.r1 Soares fetal liver spleen 1NF1LS Homo sapiens cDNA clone IMAGE:193759 5'
7210	20233	33568	0.67	1.2E-01	H47789.1	EST_HUMAN	yp80f04.r1 Soares fetal liver spleen 1NF1LS Homo sapiens cDNA clone IMAGE:193759 5'
7854	20799	34175	0.62	1.2E-01	AJ271741.1	NT	Homo sapiens partial ILF3 gene for interleukin enhancer binding factor 3 (alternative transcripts drbp76, drbp76 gamma, drbp76 alpha and ILF3)
8063	21000	34396	0.9	1.2E-01	BF680613.1	EST_HUMAN	602155195F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4296382 5'
8098	21034	34433	0.57	1.2E-01	D87458.1	NT	Human mRNA for KIAA0282 gene, partial cds
8098	21034	34434	0.57	1.2E-01	D87458.1	NT	Human mRNA for KIAA0282 gene, partial cds
8224	21193		1.24	1.2E-01	BE007072.1	EST_HUMAN	PM3-BN0137-290300-002-f09 BN0137 Homo sapiens cDNA
8295	21264	34675	3.1	1.2E-01	AI913753.1	EST_HUMAN	wc9g03.x1 NCL CGAP_Cx3 Homo sapiens cDNA clone IMAGE:2326804 3' similar to SW:GST2_HUMAN
8341	21310	34724	0.76	1.2E-01	Q02369	SWISSPROT	Q99735 MICROSOMAL GLUTATHIONE S-TRANSFERASE II
8652	21620	35040	0.61	1.2E-01	AI832881.1	EST_HUMAN	NADH-UBIQUINONE OXIDOREDUCTASE B22 SUBUNIT (COMPLEX I-B22) (C1-B22)
8739	21707		10.85	1.2E-01	AW083652.1	EST_HUMAN	at71b10.x1 Barslead colon HPLRB7 Homo sapiens cDNA clone IMAGE:2377435 3'
							xc49d07.x1 NCL CGAP_Esc02 Homo sapiens cDNA clone IMAGE:2587597 3' similar to gb:M13452 LAMIN A (HUMAN);
8759	21726						Staphylococcus aureus plasmid pSK23 putative recombinase Sin (sin) gene, partial cds; and transcriptional regulator QacR (qacR) and multidrug efflux protein QacB (qacB) genes, complete cds
8798	21765	35187	3.98	1.2E-01	AF053772.1	NT	N.crassa vacuolar ATPase 57-Kd subunit (vma-2) gene, complete cds
8798	21765	35188	0.99	1.2E-01	J03956.1	NT	N.crassa vacuolar ATPase 57-Kd subunit (vma-2) gene, complete cds
8948	21914		0.81	1.2E-01	AJ271736.1	NT	Homo sapiens Xq pseudautosomal region; segment 2/2
9037	22003		2.01	1.2E-01	U32714.1	NT	Haemophilus influenzae Rd section 29 of 163 of the complete genome
9073	22039		0.64	1.2E-01	X15191.1	NT	M.musculus DNA fragment of Apolipoprotein B gene
9930	22813	36267	1.69	1.2E-01	X77981.1	NT	S.cerevisiae HXT5 gene
10365	23288	36765	1.64	1.2E-01	AV710857.1	EST_HUMAN	AV710857 Cu Homo sapiens cDNA clone CUAAKE08 5'
11232	24185		2.36	1.2E-01	D26184.1	NT	Yeast MPT5 gene for suppressor protein, complete cds
11404	24348		2.55	1.2E-01	BE982324.2	EST_HUMAN	601655578R1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3846283 3'
11482	24425		1.57	1.2E-01	BF314481.1	EST_HUMAN	601900763F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4130103 5'
11584	24522	38077	2.45	1.2E-01	AF190493.1	NT	Homo sapiens dynein intermediate chain DNAIL1 (DNAIL1) gene, exon 17
11738	24823	38201	1.6	1.2E-01	9994174	NT	Homo sapiens UDP-Gal:betaGalNAc beta 1,4-galactosyltransferase, polypeptide 4 (B4GALT4), mRNA

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Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
11836	24719		1.54	1.2E-01	M65109.1	NT	Rabbit glycogen-associated protein phosphatase regulatory subunit (RG1) mRNA, complete cds
12162	25016		3.86	1.2E-01	AV658033.1	EST_HUMAN	AV658033 GLC Homo sapiens cDNA clone GLC1B12 3'
12517	25248		2.78	1.2E-01	AJ271736.1	NT	Homo sapiens Xq pseudautosomal region; segment 2/2
12563	25622	31304	6.17	1.2E-01	Q04912	SWISSPROT	MACROPHAGE-STIMULATING PROTEIN RECEPTOR PRECURSOR (MSP RECEPTOR) (P185-RON) (CDW 136) (CD136 ANTIGEN)
12805	25432		2.66	1.2E-01	X53981.1	NT	R. norvegicus NF68 gene for 68kDa neurofilament
12867	25635	31310	1.58	1.2E-01	BE061418.1	EST_HUMAN	QV4-BT0234-111199-031-g10 BT0234 Homo sapiens cDNA
12889	25477	31731	9.62	1.2E-01	A1298903.1	EST_HUMAN	q20g05.x1 NCL_CGAP_Lu5 Homo sapiens cDNA clone IMAGE:1898840 3'
12911	25490		2.91	1.2E-01	L10187.1	NT	Xenopus laevis integrin alpha 3 subunit mRNA, partial cds
12917	25662		9.28	1.2E-01	O98433	SWISSPROT	GYCLIN T
12948	25525	31712	1.76	1.2E-01	AE004428.1	NT	Vibrio cholerae chromosome II, section 85 of 93 of the complete chromosome
13082	16538		2.08	1.2E-01	Z99118.1	NT	Bacillus subtilis complete genome (section 15 of 21); from 2795131 to 3013540
13098	25623		1.51	1.2E-01	BF314481.1	EST_HUMAN	601900763F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4130103 5'
566	13636	26552	1.01	1.1E-01	AI561003.1	EST_HUMAN	bt18408.x1 NCL_CGAP_Brn25 Homo sapiens cDNA clone IMAGE:2167983 3'
617	13682	26599	1.84	1.1E-01	AA569006.1	EST_HUMAN	hm08g11.s1 NCL_CGAP_Co10 Homo sapiens cDNA clone IMAGE:1059620 3' similar to gb-X06985_rna1
1057	14103	27054	1.55	1.1E-01	BF697308.1	EST_HUMAN	HEME OXYGENASE 1 (HUMAN);
1087	14131		1.48	1.1E-01	AL161560.2	NT	602129847F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4286771 5'
1163	15860	27158	4.6	1.1E-01	AW972158.1	EST_HUMAN	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 60
1254	14290	27255	2.03	1.1E-01	D64004.1	NT	EST384142 IMAGE resequences, MAGL Homo sapiens cDNA
1524	14566	27527	2.46	1.1E-01	AU140363.1	EST_HUMAN	Synechocystis sp. PCC6803 complete genome, 23/27, 2868767-3002965
2322	15333		2.72	1.1E-01	6756215	NT	AL140363 PLACE2 Homo sapiens cDNA clone PLACE2000403 5'
2545	15926		0.93	1.1E-01	6756215	NT	Mus musculus pre T-cell antigen receptor alpha (Pctra) mRNA
2574	15575		0.93	1.1E-01	AW821809.1	EST_HUMAN	Rattus norvegicus Procollagen II alpha 1 (Col2a1) mRNA
3046	16103	28017	0.95	1.1E-01	F03265.1	EST_HUMAN	RCO-ST0379-210100-032-g04 ST0379 Homo sapiens cDNA
3352	16403		1.66	1.1E-01	6753231	NT	HSC1RF022 normalized infant brain cDNA Homo sapiens cDNA clone c-1r02 3'
3432	16480	29399	2.18	1.1E-01	BE383186.1	EST_HUMAN	Mus musculus calcium channel, voltage-dependent, T type, alpha 1G subunit (Ca _v 1g), mRNA
3466	16612	29433	1.3	1.1E-01	X62135.1	NT	601308678F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3627066 5'
3596	16641	29560	0.8	1.1E-01	Y07695.1	NT	C.reinhardtii nuclear gene on linkage group XIX
3715	16758		0.86	1.1E-01	P97384	SWISSPROT	A. limmerus gene for transposase
3722	16765	29676	1.23	1.1E-01	X52708.1	NT	ANNEXIN XI (CALCYCLIN-ASSOCIATED ANNEXIN 50) (CAP-50)
4137	17169	30054	1.14	1.1E-01	AW819412.1	EST_HUMAN	G.gallus gene encoding non-histone chromosomal protein HMG-14b, exons 4 and 5
4137	17169	30055	1.14	1.1E-01	AW819412.1	EST_HUMAN	MR3-ST0280-280100-025-g07 ST0280 Homo sapiens cDNA
4281	17310		9.36	1.1E-01	AF157066.1	NT	MR3-ST0280-280100-025-g07 ST0280 Homo sapiens cDNA
							Drosophila melanogaster klarsicht protein (klar) mRNA, complete cds

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Table 4
Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4316	17345	30229	0.69	1.1E-01	AW802056.1	EST_HUMAN	IL5-UM0070-020500-088-a08 UM0070 Homo sapiens cDNA
4670	17691	30577	1.02	1.1E-01	S44957.1	NT	Tapa-1=Integral membrane protein TAPA-1 [mice, B cell lymphoma line 38C13, Genomic, 1973 nt, segment 1 of 7]
4869	17886	30774	0.98	1.1E-01	Y07695.1	NT	A.immerus gene for transposase
5056	17174		0.78	1.1E-01	AF030001.1	NT	Mus musculus major histocompatibility locus class III region:butyrophilin-like protein gene, partial cds; Notch4, PBX2, RAGE, lysophosphatidic acid acyl transferase-alpha, palmitoyl-protein thioesterase 2 (PPT2), CREB-RP, and tenascin X (TNX) genes, complete>
5753	18847		1.36	1.1E-01	AA747216.1	EST_HUMAN	nx78a03.s1 NCI_CGAP_Ew1 Homo sapiens cDNA clone IMAGE:1268140 similar to contains Alu repetitive element; contains element MER35 repetitive element;
5829	18919	32102	1.16	1.1E-01	AF020927.1	NT	6 Homo sapiens diacylglycerol kinase 3 (DAGK3) gene, exon 6
5886	18957	32145	0.95	1.1E-01	AF110885.1	NT	Botrytis cinerea strain T4 cDNA library under conditions of nitrogen deprivation
5904	18990	32180	0.73	1.1E-01	BF339519.1	EST_HUMAN	602039176F1 NCI_CGAP_Bm64 Homo sapiens cDNA clone IMAGE:4186818 5'
5904	18990	32181	0.73	1.1E-01	BF339519.1	EST_HUMAN	602039176F1 NCI_CGAP_Bm64 Homo sapiens cDNA clone IMAGE:4186818 5'
5935	19021	32215	1.67	1.1E-01	X68851.1	NT	S.pombe ste8 gene encoding protein kinase
5971	19056	32256	4.98	1.1E-01	M86533.1	NT	Providencia rettgeri penicillin G amidase gene
6142	19217	32446	1.63	1.1E-01	AJ007673.1	NT	Homo sapiens LGMD2B gene
6164	19239	32470	1.54	1.1E-01	BE769152.1	EST_HUMAN	PK3-FT0024-130600-004-F12 FT0024 Homo sapiens cDNA
6184	19259	32493	8	1.1E-01	AW853696.1	EST_HUMAN	RC3-CT0254-280999-011-a01 CT0254 Homo sapiens cDNA
6564	19624	32869	0.5	1.1E-01	AL163282.2	NT	Homo sapiens chromosome 21 segment HS21C082
6571	19631	32898	1.28	1.1E-01	AF035746.1	EST_HUMAN	AF035746 Human salivary gland cell line HSG Homo sapiens cDNA clone RL43
6617	19675	32953	0.84	1.1E-01	AI216307.1	EST_HUMAN	qg76d06.x1 Scores_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1841098 3'
6762	19816	33096	6.18	1.1E-01	O69835	SWISSPROT	ACETYL-COENZYME A SYNTHETASE (ACETATE--COA LIGASE) (ACYL-ACTIVATING ENZYME)
6862	19815		2.81	1.1E-01	AF032922.1	NT	Homo sapiens syntaxin 4 binding protein UNC-18c (UNC-18c) mRNA, complete cds
6982	20187	33512	2.23	1.1E-01	11432372	NT	Homo sapiens phosphatidylinositol glycan, class B (PIGB), mRNA
7249	19984	33281	0.65	1.1E-01	AE002155.1	NT	Ureaplasma urealyticum section 56 of 59 of the complete genome
7249	19984	33282	0.65	1.1E-01	AE002155.1	NT	Ureaplasma urealyticum section 56 of 59 of the complete genome
7393	25999		0.94	1.1E-01	BF332758.1	EST_HUMAN	601816524F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4050653 5'
7523	25683	33850	1.59	1.1E-01	AF000006.1	NT	Pyrococcus horikoshii OT3 genomic DNA, 1166001-1485000 nt, position (67)
7781	20734	34105	7.69	1.1E-01	BF684628.1	EST_HUMAN	602140976F1 NIH_MGC_46 Homo sapiens cDNA clone IMAGE:4302019 5'
7781	20734	34106	7.69	1.1E-01	BF684628.1	EST_HUMAN	602140976F1 NIH_MGC_46 Homo sapiens cDNA clone IMAGE:4302019 5'
7839	20786	34161	0.54	1.1E-01	AA96908.1	EST_HUMAN	ou44g03.s1 Scores_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1629172 3'
7917	20860	34249	1.77	1.1E-01	P41067	SWISSPROT	TRAB PROTEIN
7859	20900		0.79	1.1E-01	Z14008.1	NT	B.subtilis gene encoding hypothetical polypeptide synthase

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7961	20902	34294	2.99	1.1E-01	AA788784.1	EST_HUMAN	ah31b08.s1 Soares parathyroid tumor NBHPA Homo sapiens cDNA clone 1240403 3' similar to gb:J03483
8111	21048	34448	0.95	1.1E-01	BE782290.1	EST_HUMAN	CHROMOGHRANIN A PRECURSOR (HUMAN);
8301	21270	34692	0.48	1.1E-01	U67492.1	NT	601470055F1 NIH_MGC_87 Homo sapiens cDNA clone IMAGE:3873229 5'
8550	21518	34936	1.61	1.1E-01	AA493574.1	EST_HUMAN	Malhanococcus jamaerschii section 34 of 150 of the complete genome
8550	21518	34937	1.61	1.1E-01	AA493574.1	EST_HUMAN	h04g10.s1 NCI_CGAP_Thy1 Homo sapiens cDNA clone IMAGE:943362
8598	21566	34982	1.1	1.1E-01	X91233.1	NT	h04g10.s1 NCI_CGAP_Thy1 Homo sapiens cDNA clone IMAGE:943362
8637	21605		1.06	1.1E-01	AW817918.1	EST_HUMAN	H. sapiens IL15 gene
8694	21662	35086	1.59	1.1E-01	AL134349.1	EST_HUMAN	PM1-ST0270-080200-001-009 ST0270 Homo sapiens cDNA
9170	22136	35562	1.82	1.1E-01	U02482.1	NT	DKFZp547P194.1 547 (synonym: hfbf1) Homo sapiens cDNA clone DKFZp547P194 5'
9263	22229	35660	0.96	1.1E-01	AI807474.1	EST_HUMAN	Pedococcus acidilactici H plasmid pSMB74 pedocin ACh production (pap) gene cluster papA, papB, papC and papD genes, complete cds
9362	22327	35756	0.96	1.1E-01	AF050081.1	NT	wf48c01.x1 Soares NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2358816 3' similar to contains Alu repetitive element
9398	22363	35794	2.27	1.1E-01	AA192183.1	EST_HUMAN	Homo sapiens C16orf3 large protein mRNA, complete cds
9398	22363	35795	2.27	1.1E-01	AA192183.1	EST_HUMAN	zp93b12.r1 Stralagene muscle 937209 Homo sapiens cDNA clone IMAGE:627743 5'
9490	22454	35894	0.77	1.1E-01	Y12727.1	NT	zp93b12.r1 Stralagene muscle 937209 Homo sapiens cDNA clone IMAGE:627743 5'
9520	22483	35929	2.1	1.1E-01	T72875.1	EST_HUMAN	P. furiosus partial dph5 gene and argF gene
9546	22509		0.62	1.1E-01	BE933260.1	EST_HUMAN	yd19h03.s1 Soares fetal liver spleen INFLS Homo sapiens cDNA clone IMAGE:108725 3' similar to gb:U81181 SODIUMPOTASSIUM-TRANSPORTING ATPASE BETA-2 (HUMAN);
9777	22718		0.89	1.1E-01	BE142305.1	EST_HUMAN	601438972F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3922048 5'
9853	22789		2.05	1.1E-01	BF085149.1	EST_HUMAN	CM3-HT0142-271099-028-g11 HT0142 Homo sapiens cDNA
10270	23195		0.68	1.1E-01	AL161543.2	NT	MR2-GN0027-040900-005-a08 GN0027 Homo sapiens cDNA
10476	23398		0.45	1.1E-01	BE315509.1	EST_HUMAN	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 43
10566	23488		1.01	1.1E-01	R80590.1	EST_HUMAN	601140231F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3049543 5'
10701	23623	37119	1.05	1.1E-01	U60528.1	NT	y06a09.s1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:147064 3'
11156	16103	29017	1.7	1.1E-01	F03265.1	EST_HUMAN	Ceratitis capitata yoyo retrotransposon gag-like, pol-like and env-like genes, complete cds
11267	24219		3.13	1.1E-01	AF169032.1	NT	HSC1RF022 normalized infant brain cDNA Homo sapiens cDNA clone c-1rf02 3'
11384	24331	37860	3.51	1.1E-01	R23708.1	EST_HUMAN	Carassius auratus activin beta A precursor, mRNA, complete cds
11392	24338	37868	1.54	1.1E-01	6981351	NT	y03f112.1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:131759 5' similar to contains Alu repetitive element/contains TAR1 repetitive element
11542	24483	38035	2.18	1.1E-01	Z11910.1	NT	Rattus norvegicus Phosphoruclease, liver, B-type (Pfk), mRNA
11542	24483	38036	2.18	1.1E-01	Z11910.1	NT	Z. mobilis tgi and lig genes encoding RNA guanine transglycosylase and DNA ligase
11636	24573	38137	3.66	1.1E-01	P17437	SWISSPROT	Z. mobilis tgi and lig genes encoding RNA guanine transglycosylase and DNA ligase

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Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1260	25084		2.03	1.1E-01	AA192153.1	EST_HUMAN	zp93b12.r1 Stratagene muscle 937209 Homo sapiens cDNA clone IMAGE:627743 5'
1279	25161		3.68	1.1E-01	BE767023.1	EST_HUMAN	RC2-NT0112-120600-014-f03 NT0112 Homo sapiens cDNA
1285	26732		2.18	1.1E-01	BE974596.1	EST_HUMAN	601680561R2 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:3950804 3'
1308	25580	31698	1.69	1.1E-01	BF239763.1	EST_HUMAN	601906350F1 NIH_MGC_54 Homo sapiens cDNA clone IMAGE:4134085 5'
1309	25912		1.32	1.1E-01	P14400	SWISSPROT	ELECTROMOTOR NEURON-ASSOCIATED PROTEIN 1
1206	14245		2.05	1.0E-01	O62855	SWISSPROT	DEOXYRIBONUCLEASE II PRECURSOR (DNASE II) (ACID DNASE) (LYSOSOMAL DNASE II)
1277	14312	27273	1.95	1.0E-01	A1985499.1	EST_HUMAN	ws08401.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2496577 3' similar to contains MER7.13
1393	14427	27396	2.25	1.0E-01	AL161504.2	NT	MER7 repetitive element ;
2497	15500	28526	1.16	1.0E-01	AW451365.1	EST_HUMAN	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 16
3524	16570	29483	1.32	1.0E-01	BF033991.1	EST_HUMAN	U1-H-B13-alc-d-07-0-U1.s1 NCI_CGAP_Sub5 Homo sapiens cDNA clone IMAGE:2736420 3'
3732	16774	29686	0.68	1.0E-01	BF239818.1	EST_HUMAN	601456301F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3858849 5'
3849	16889	29792	2.49	1.0E-01	AF297061.1	NT	601906489F1 NIH_MGC_54 Homo sapiens cDNA clone IMAGE:4134071 5'
3849	16889	29793	2.49	1.0E-01	AF297061.1	NT	Escherichia coli enterotoxin EspC (espC) gene, complete cds; and unknown genes
3976	17016	29930	2.66	1.0E-01	BF365703.1	EST_HUMAN	Escherichia coli enterotoxin EspC (espC) gene, complete cds; and unknown genes
4595	17607	30655	0.86	1.0E-01	AF792349.1	EST_HUMAN	QV2-NT0048-160800-316-e05 NT0048 Homo sapiens cDNA
4741	17761	30655	1.32	1.0E-01	U50450.1	NT	an32e04.y6 Geesler Wilms tumor Homo sapiens cDNA clone IMAGE:1700358 5'
4957	17972	30863	2.34	1.0E-01	AW952344.1	EST_HUMAN	Drosophila melanogaster tyrosine kinase p45 isoform (ter) mRNA, complete cds
5267	18274	31138	0.87	1.0E-01	AV721471.1	EST_HUMAN	EST364414 MAGE resequences, MAGEB Homo sapiens cDNA
5273	18278		1.04	1.0E-01	AV763960.1	EST_HUMAN	AV721471 HTB Homo sapiens cDNA clone HTBBQE10 5'
5394	18497		8.1	1.0E-01	W86490.1	EST_HUMAN	AV763960 MDS Homo sapiens cDNA clone MDSBQB11 5'
5492	18592		0.59	1.0E-01	X54015.1	NT	zh62h04.s1 Scores_fetal_liver_spleen_1NF1L_S1 Homo sapiens cDNA clone IMAGE:416695 3'
5980	18065		0.87	1.0E-01	AK024472.1	NT	Xcampesris genes for sensor and regulator protein
6140	19216	32445	12.15	1.0E-01	AF274875.1	NT	Homo sapiens mRNA for FLJ00085 protein, partial cds
6469	19334	32782	0.9	1.0E-01	AA481879.1	EST_HUMAN	Homo sapiens growth factor receptor-bound protein 7 (GRB7) gene, complete cds
6483	19548	32797	0.65	1.0E-01	AA406039.1	EST_HUMAN	z441g10.s1 Scores ovary tumor NbHOT Homo sapiens cDNA clone IMAGE:756258 3' similar to contains L1.13 L1 repetitive element ;
7220	20242		1.82	1.0E-01	R23821.1	EST_HUMAN	z487c12.s1 Scores_testis_NHT Homo sapiens cDNA clone IMAGE:743062 3'
8009	20947		2.16	1.0E-01	Y12488.1	NT	yh34h06.r1 Scores_placenta Nb2HP Homo sapiens cDNA clone IMAGE:131675 5' similar to contains Alu repetitive element;
8108	21045	34444	0.65	1.0E-01	AJ011400.1	NT	M.musculus whn gene
8108	21045	34445	0.65	1.0E-01	AJ011400.1	NT	Bos taurus mRNA for b17.2 subunit of NADH:ubiquinone oxidoreductase complex (complex I)
8265	21234	34645	0.63	1.0E-01	AA961091.1	EST_HUMAN	Bos taurus mRNA for b17.2 subunit of NADH:ubiquinone oxidoreductase complex (complex I)
							al32g01.1 Scores_testis_NHT Homo sapiens cDNA clone IMAGE:1407698 3' similar to gb:M34182 CAMP-DEPENDENT PROTEIN KINASE, GAMMA-CATALYTIC SUBUNIT (HUMAN);

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8287	21266	34665	0.45	1.0E-01	AF280225.1	NT	Homo sapiens TESTIN 2 and TESTIN 3 genes, complete cds, alternatively spliced
8287	21266	34666	0.45	1.0E-01	AF280225.1	NT	Homo sapiens TESTIN 2 and TESTIN 3 genes, complete cds, alternatively spliced
8506	21474		0.68	1.0E-01	4758365	NT	Homo sapiens fibroblast growth factor 13 (FGF13) mRNA
8837	21804		0.94	1.0E-01	AW189797.1	EST_HUMAN	xi09b01.x1 NCL CGAP U14 Homo sapiens cDNA clone IMAGE:2675689 3' similar to gb:X17206 40S
9540	22503	35952	1.19	1.0E-01	AF102855.2	NT	RIBOSOMAL PROTEIN S4 (HUMAN); contains TAR1.3 TAR1 repetitive element ;
9852	22788	36241	0.54	1.0E-01	R44993.1	EST_HUMAN	Rattus norvegicus synaptic SAPAP-interacting protein Synappon mRNA, complete cds
9865	22801		2.05	1.0E-01	M76729.1	NT	Y933h04.s1 Soares Infant brain 1N1B Homo sapiens cDNA clone IMAGE:34549 3'
9908	22728		2.65	1.0E-01	AE001501.1	NT	Human pro-alpha-1 (V) collagen mRNA, complete cds
9922	22808	36259	0.61	1.0E-01	W01955.1	EST_HUMAN	Helicobacter pylori, strain J99, section 62 of 132 of the complete genome
10180	23105	36386	1.63	1.0E-01	BF240154.1	EST_HUMAN	z666c10.s1 Soares_fetal heart_NbHH19W Homo sapiens cDNA clone IMAGE:327282 3'
10295	23220	36703	9.1	1.0E-01	AB046799.1	NT	z666c10.s1 Soares_fetal heart_NbHH19W Homo sapiens cDNA clone IMAGE:4133487 5'
10295	23220	36704	9.1	1.0E-01	AB046799.1	NT	Homo sapiens mRNA for KIAA1579 protein, partial cds
10502	23424		0.95	1.0E-01	AW957425.1	EST_HUMAN	Homo sapiens mRNA for KIAA1579 protein, partial cds
10507	23428	36928	0.55	1.0E-01	T61952.1	EST_HUMAN	EST1369615 MAGE resequences, MAGE Homo sapiens cDNA
10604	23616	37110	0.99	1.0E-01	BE792750.1	EST_HUMAN	Y929a06.s1 Stratagene fetal spleen (#937205) Homo sapiens cDNA clone IMAGE:72562 3' similar to
11018	23983		1.65	1.0E-01	AU159127.1	EST_HUMAN	contains Alu repetitive element
11370	24317	37844	2.25	1.0E-01	BF242946.1	EST_HUMAN	601584604F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3939086 5'
11370	24317	37845	2.25	1.0E-01	BF242946.1	EST_HUMAN	AU159127 THYR01 Homo sapiens cDNA clone THYR01000895 3'
11728	24614	38191	3.16	1.0E-01	BE790543.1	EST_HUMAN	601877703F1 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:4106089 5'
12365	25481		4.11	1.0E-01	BE537719.1	EST_HUMAN	601877703F1 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:4106089 5'
12588	25292		2.16	1.0E-01	7662165	NT	601582559F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3936734 5'
12604	25305		2.58	1.0E-01	X00854.1	NT	601065554F1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3451833 5'
12796	25425		1.45	1.0E-01	AA737961.1	EST_HUMAN	Homo sapiens KIAA0514 gene product (KIAA0514), mRNA
12895	25481		4.47	1.0E-01	BE537719.1	EST_HUMAN	Drosophila melanogaster ftz gene
12943	25522		1.32	1.0E-01	BE158905.1	EST_HUMAN	rx11c08.s1 NCL CGAP_GC3 Homo sapiens cDNA clone IMAGE:1255790 3'
12959	25891		6.14	1.0E-01	U66834.1	NT	601065554F1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3451833 5'
13016	26566		7.59	1.0E-01	AP001507.1	NT	QV4-HT0401-211299-064-g03 HT0401 Homo sapiens cDNA
2789	15781	28797	1.74	9.9E-02	AF274008.1	NT	Saccharomyces cerevisiae suppressor of ABF1 (SAB2) gene, complete cds
2798	15790	28808	1.71	9.8E-02	BE545554.1	EST_HUMAN	Bacillus halodurans genomic DNA, section 11/4
2798	15790	28809	1.71	9.9E-02	BE545554.1	EST_HUMAN	Drosophila melanogaster cAMP-dependent protein kinase type II regulatory subunit (pka-RII) mRNA,
3280	16334	29254	1.48	9.9E-02	AF099810.1	NT	complete cds
							601070219F1 NIH_MGC_12 Homo sapiens cDNA clone IMAGE:3456365 5'
							601070219F1 NIH_MGC_12 Homo sapiens cDNA clone IMAGE:3456365 5'
							Homo sapiens neurexin III-alpha gene, partial cds

Table 4
Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3974	17014	29928	0.67	9.9E-02	AB21637.1	EST_HUMAN	zu45c03.x5 Soares ovary tumor NihHOT Homo sapiens cDNA clone IMAGE:740932 3'
4707	17728	30622	1.02	9.9E-02	BE674249.1	EST_HUMAN	7d77c12.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3278998 3'
7044	20066	33373	2.59	9.9E-02	BE613498.1	EST_HUMAN	601504252F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3906084 5'
7163	18394	31239	7.77	9.9E-02	D83710.1	NT	Aspergillus terreus BSD mRNA for blasticidin S deaminase, complete cds
8247	21216	34624	0.65	9.9E-02	AW103088.1	EST_HUMAN	xx43c09.x1 NCI_CGAP_Ov23 Homo sapiens cDNA clone IMAGE:2596528 3' similar to contains Alu repetitive element; contains element MIR MIR repetitive element ;
8247	21216	34625	0.65	9.9E-02	AW103088.1	EST_HUMAN	xx43c09.x1 NCI_CGAP_Ov23 Homo sapiens cDNA clone IMAGE:2596528 3' similar to contains Alu repetitive element; contains element MIR MIR repetitive element ;
9612	22616	36068	1.23	9.9E-02	8755111	NT	Mus musculus phospholipid transfer protein (Pltp), mRNA
665	13635		1.88	9.8E-02	X56338.1	NT	O sativa RAMy3C gene for alpha-amylase
3160	16216	29130	4.26	9.8E-02	AF194274.1	NT	Daucus carota leucoanthocyanidin dioxygenase 2 (LDOX) mRNA, LDOX-2 allele, complete cds
4251	17280	30160	6.93	9.8E-02	AF257329.1	NT	Leptospira maculans beta-tubulin mRNA, complete cds
4251	17280	30161	6.93	9.8E-02	AF257329.1	NT	Leptospira maculans beta-tubulin mRNA, complete cds
7723	20879		0.94	9.8E-02	X54133.1	NT	Human HPTP delta mRNA for protein tyrosine phosphatase delta
9609	22613		1.21	9.8E-02	IM61943.1	NT	Human laminin B1 chain gene, exon 26
11788	23943	37465	1.83	9.8E-02	BF037421.1	EST_HUMAN	601400793F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3864287 5'
12330	25131		1.84	9.8E-02	8393751	NT	Rattus norvegicus microtubule-associated protein tau (Mapt), mRNA
1352	14387	27357	1.75	9.7E-02	AB005808.1	NT	Aloe arborescens mRNA for NADP-malic enzyme, complete cds
1589	14821		1.33	9.7E-02	4503710	NT	Homo sapiens fibroblast growth factor receptor 3 (achondroplasia, thanatophoric dwarfism) (FGFR3) mRNA
2270	15283	28309	2.78	9.7E-02	BE188660.1	EST_HUMAN	QV1-HT0516-070300-085-s04 HT0516 Homo sapiens cDNA
4008	17047		4.89	9.7E-02	Q99795	SWISSPROT	CELL SURFACE A33 ANTIGEN PRECURSOR (GLYCOPROTEIN A33)
5418	18521	31398	0.88	9.7E-02	AF099189.1	NT	Caulobacter crescentus thymidylate kinase (tnk) and DNA polymerase III delta prime subunit (dnaC) genes, complete cds
5418	18521	31399	0.88	9.7E-02	AF099189.1	NT	Caulobacter crescentus thymidylate kinase (tnk) and DNA polymerase III delta prime subunit (dnaC) genes, complete cds
6130	19207	32432	1.48	9.7E-02	AW964476.1	EST_HUMAN	EST366546 MAGE resequences, MAGE Homo sapiens cDNA
7517	20482	33843	3.36	9.7E-02	Z99119.1	NT	Bacillus subtilis complete genome (section 16 of 21); from 2897771 to 3213410
8315	21284	34697	1.09	9.7E-02	N22798.1	EST_HUMAN	yw41c03.s1 Weizmann Olfactory Epithelium Homo sapiens cDNA clone IMAGE:254788 3'
8315	21284	34698	1.09	9.7E-02	N22798.1	EST_HUMAN	yw41c03.s1 Weizmann Olfactory Epithelium Homo sapiens cDNA clone IMAGE:254788 3'
9201	22167	35597	1.52	9.7E-02	A1953984.1	EST_HUMAN	PEPTIDYL-PROLYL CIS-TRANS ISOMERASE A (HUMAN);
11528	24470		2.01	9.7E-02	U58337.1	NT	Mus musculus ligatin (Lgtn) mRNA, partial cds
2032	16051	28066	1.27	9.6E-02	A1080721.1	EST_HUMAN	ca7d11.x1 Soares_NihHMPu_S1 Homo sapiens cDNA clone IMAGE:1678485 3'

Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2032	15051	28067	1.27	9.6E-02	AI080721.1	EST_HUMAN	oz47d11.x1 Soares_NHMPu_S1 Homo sapiens cDNA clone IMAGE:1678485 3'
4372	17399	30279	6.7	9.6E-02	Z32886.2	NT	Proteus mirabilis fimbrial operon, strain H4320
5037	18050	30930	1.16	9.6E-02	AW866230.1	EST_HUMAN	EST378303 IMAGE resequences, MAGI Homo sapiens cDNA
6225	19299		2.63	9.6E-02	BE910039.1	EST_HUMAN	601468038F1 NIH_MGC_70 Homo sapiens cDNA clone IMAGE:3900765 5'
8719	21687		0.65	9.6E-02	AU137084.1	EST_HUMAN	AU137084 PLACET1 Homo sapiens cDNA clone PLACE1005740 5'
9902	22654	36315	1.35	9.6E-02	AV887898.1	EST_HUMAN	AV687898 GKG Homo sapiens cDNA clone GKCAAH02 5'
10231	23156		1.29	9.6E-02	BE894896.1	EST_HUMAN	601434030F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3918363 5'
10399	23321	36805	1.27	9.6E-02	AJ243211.1	NT	Homo sapiens DMBT1 candidate tumour suppressor gene, exons 1 to 55
10398	23321	36806	1.27	9.6E-02	AJ243211.1	NT	Homo sapiens DMBT1 candidate tumour suppressor gene, exons 1 to 55
10479	23401	36898	0.44	9.6E-02	BF677270.1	EST_HUMAN	60206769F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4250969 5'
10511	23433	36930	1.37	9.6E-02	AB013985.1	NT	Anthrax toxin Tansposon Tam3 pseudogene for transposase (in S-5 copy)
10511	23433	36931	1.37	9.6E-02	AB013985.1	NT	Anthrax toxin Tansposon Tam3 pseudogene for transposase (in S-5 copy)
10621	23543	37043	3.3	9.6E-02	P08174	SWISSPROT	COMPLEMENT DECA-ACCELERATING FACTOR PRECURSOR (CD55)
11094	24054	37577	5.31	9.6E-02	Z79702.1	NT	Mycobacterium tuberculosis H37Rv complete genome, segment 102/162
12028	24904	38498	1.53	9.6E-02	AA623755.1	EST_HUMAN	zu91g01.s1 Soares_infant brain 1N1B Homo sapiens cDNA clone IMAGE:745392 3'
12993	25515		1.81	9.6E-02	H14599.1	EST_HUMAN	ym19h03.s1 Soares_infant brain 1N1B Homo sapiens cDNA clone IMAGE:48653 3'
12995	25553	31719	1.51	9.6E-02	BE728219.1	EST_HUMAN	601563356F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3832908 5'
4128	17161	30050	2.66	9.5E-02	AW992395.1	EST_HUMAN	CM2-BN0023-050200-087-f12 BN0023 Homo sapiens cDNA
5748	18842	32025	0.81	9.5E-02	P51854	SWISSPROT	TRANSKETOLASE 2 (TK 2) (TRANSKETOLASE RELATED PROTEIN)
7294	20266	33601	0.51	9.5E-02	AA780728.1	EST_HUMAN	ac68a09.s1 Stragene fetal retina 937202 Homo sapiens cDNA clone IMAGE:867736 3'
7522	20487	33849	4.14	9.5E-02	AB003473.1	NT	Timersurus flaviviridis DNA for phospholipase A2 inhibitor, complete cds
7818	20767	34144	7.16	9.5E-02	AL161538.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 38
7863	18842	32025	0.89	9.5E-02	P51854	SWISSPROT	TRANSKETOLASE 2 (TK 2) (TRANSKETOLASE RELATED PROTEIN)
8212	21181	34591	2.85	9.5E-02	BF035861.1	EST_HUMAN	601453642F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3857243 5'
8212	21181	34592	2.85	9.5E-02	BF035861.1	EST_HUMAN	601453642F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3857243 5'
11039	24003	37528	2.31	9.5E-02	BF035861.1	EST_HUMAN	601453642F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3857243 5'
11039	24003	37529	2.31	9.5E-02	BF035861.1	EST_HUMAN	601453642F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3857243 5'
1890	14876	27871	4.07	9.4E-02	BF671083.1	EST_HUMAN	602150882F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4291917 5'
3894	16934	29844	4.91	9.4E-02	Z33059.1	NT	M. capricolum DNA for CONTIG MC073
5240	18248		0.96	9.4E-02	X88106.1	NT	Lactobacillus bacteriophage phi17e complete genomic DNA
6450	19515	32766	1.21	9.4E-02	AF097363.1	NT	Triticum aestivum heat shock protein 101 (Hsp101a) mRNA, complete cds
7851	20797	34173	0.54	9.4E-02	L78833.1	NT	Human BRCA1, Rho7 and val genes, complete cds, and ipf35 gene, partial cds
8947	21913		2.5	9.4E-02	Z46863.1	NT	Acinetobacter sp. cyoD, cobQ, sodM, lysS, rubA, rubB, estB, oxyR, ppk, mtgA, ORF2 and ORF3 genes

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Table 4

Single Exon Probes Expressed In Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
11280	20797	34173	2.22	9.4E-02	L78833.1	NT	Human BRCA1, Rho7 and vail genes, complete cds, and ipf35 gene, partial cds
12212	25826		10.73	9.4E-02	U31815.1	NT	Rattus norvegicus calcium channel alpha-1C subunit (ROB2) mRNA, partial cds
13087	25817	31682	1.37	9.4E-02	U27689.1	NT	Human pephBGT-1 beta1ne-GABA transporter mRNA, complete cds
3002	16060		1.71	9.3E-02	4809280	NT	Homo sapiens BAI1-associated protein 3 (BAIAP3) mRNA
3041	16099		7.39	9.3E-02	6912525	NT	Homo sapiens nasopharyngeal epithelium specific protein 1 (NESG1), mRNA
3270	16324	29247	2.01	9.3E-02	BF575511.1	EST_HUMAN	602133086F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4288269 5'
4179	17210	30096	3.73	9.3E-02	BE391943.1	EST_HUMAN	601286082F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3607653 5'
4179	17210	30097	3.73	9.3E-02	BE391943.1	EST_HUMAN	601286082F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3607653 5'
4766	17786		2.29	9.3E-02	AV732224.1	EST_HUMAN	AV732224 HTF Homo sapiens cDNA clone HTFAUA06 5'
5745	18839		0.66	9.3E-02	AP001507.1	NT	Bacillus halodurans genomic DNA, section 1/14
8153	21091	34490	0.59	9.3E-02	AL163210.2	NT	Homo sapiens chromosome 21 segment HS21C010
8591	21559	34975	0.6	9.3E-02	AW568007.1	EST_HUMAN	EST169 Human Fetal Brain MATCHMAKER cDNA Library Homo sapiens cDNA
9480	22444		0.42	9.3E-02	AL113179.1	NT	Botrytis cinerea strain T4 cDNA library under conditions of nitrogen deprivation
10088	22995	36464	2.32	9.3E-02	BE962631.2	EST_HUMAN	601655988R1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:38555981 3'
10551	23473	36967	3.65	9.3E-02	Q15034	SWISSPROT	HYPOTHETICAL PROTEIN KIAA0032
10551	23473	36968	3.65	9.3E-02	Q15034	SWISSPROT	HYPOTHETICAL PROTEIN KIAA0032
10683	23605		3.59	9.3E-02	AW206117.1	EST_HUMAN	U1H-B11-efx-h-05-0-U1 st NCL_CGAP_Sub3 Homo sapiens cDNA clone IMAGE:2723553 3'
12482	25750		2.55	9.3E-02	AJ249850.1	NT	Photobacterium damsela subsp. damsela partial gyrB gene for DNA gyrase B subunit
12831	25778		9.12	9.3E-02	AW468850.1	EST_HUMAN	hd28h12.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2910887 3'
							Mus musculus major histocompatibility locus class II region; Fas-binding protein Daxx (DAXX) gene, partial cds; Bing1 (BING1), tapasin (tapasin), RalGDS-like factor (RLF), KE2 (KE2), BING4 (BING4), beta1, 3-galactosyl transferase (beta1,3-galactosyl tr>
13040	25824		2.24	9.3E-02	AF100956.1	NT	Molluscum contagiosum virus subtype 1, complete genome
231	13331	26252	7.81	9.2E-02	U60315.1	NT	Molluscum contagiosum virus subtype 1, complete genome
231	13331	26253	7.81	9.2E-02	U60315.1	NT	Molluscum contagiosum virus subtype 1, complete genome
231	13331	26254	7.81	9.2E-02	U60315.1	NT	Molluscum contagiosum virus subtype 1, complete genome
2236	15250		2.72	9.2E-02	R54156.1	EST_HUMAN	y998107.r1 Soares Infant brain 1N1B Homo sapiens cDNA clone IMAGE:41618 5'
3194	16249	29167	3.72	9.2E-02	Q28631	SWISSPROT	MAJOR EPIDIDYMYM-SPECIFIC PROTEIN E4 (EPIDIDYMAL PROTEIN BE-20)
3316	16369	29289	0.99	9.2E-02	AA534354.1	EST_HUMAN	nt79e01.st NCL_CGAP_C03 Homo sapiens cDNA clone IMAGE:926136 3'
3599	16944		1.27	9.2E-02	6755215	NT	Mus musculus pre T-cell antigen receptor alpha (Ptra), mRNA
4266	17295		1.24	9.2E-02	U92048.1	NT	Human herpesvirus 1 strain KOS-63, latency-associated transcript, promoter region
4337	17364		0.94	9.2E-02	BE299722.1	EST_HUMAN	600944365F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:2960176 5'
4668	17689	30575	1.4	9.2E-02	X96402.1	NT	G gallus Mia-OK gene
8342	21311	34725	1.87	9.2E-02	T49920.1	EST_HUMAN	y99c09.r1 Stragagene placenta (#637225) Homo sapiens cDNA clone IMAGE:69803 5' similar to similar to gb:X56009 GUANINE NUCLEOTIDE-BINDING PROTEIN G(S), ALPHA SUBUNIT (HUMAN)

Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8517	21485	34899	2.19	9.2E-02	X95256.1	NT	H.vulgare xylase isomerase gene
12002	24879	38475	1.74	9.2E-02	AF026522.3	NT	Mesocricetus auratus oviductin precursor (OVI) gene, complete cds
13019	25986		1.31	9.2E-02	11466872	NT	Podospora anserina mitochondrion, complete genome
423	13118	26017	7.62	9.1E-02	X77865.1	NT	O. cuniculus k12 keratin gene
3684	16727		0.96	9.1E-02	AW372569.1	EST_HUMAN	PM2-BT0349-181299-001-402 BT0349 Homo sapiens cDNA
4510	17535	30419	1.51	9.1E-02	AL161554.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 54
5304	18307		0.98	9.1E-02	AB010896.1	NT	Clona intestinalis endostyle-specific mRNA, complete cds
5819	18909	32093	1.27	9.1E-02	AF128756.1	NT	Homo sapiens MSH55 gene, partial cds; and CLIC1, DDAH, G6b, G6c, G5b, G6d, G6e, G6f, BAT5, G5b, CSK2B, BAT4, G4, Apo M, BAT3, BAT2, AIF-1, 1C7, LST-1, LTB, TNF, and LTA genes, complete cds
7528	26000		0.52	9.1E-02	AF029308.1	NT	Homo sapiens chromosome 9 duplication of the T cell receptor beta locus and tryptophan gene families
7616	20576	33939	12.92	9.1E-02	AW160658.1	EST_HUMAN	au/4a05.y1 Schneider fetal brain 00004 Homo sapiens cDNA clone IMAGE:2781968 5'
7937	20879	34269	0.74	9.1E-02	AP000081.1	NT	Aeropyrum pernix genomic DNA, section 4/7
7977	20916	34307	0.87	9.1E-02	U59073.1	NT	Mus musculus thymoprotein zeta mRNA, complete cds
9276	22242	35671	0.95	9.1E-02	Y14379.1	NT	Homo sapiens gamma adducin gene, exon 9
10793	23714		1.84	9.1E-02	T02984.1	EST_HUMAN	FB19F10 Fetal brain, Stragene Homo sapiens cDNA clone FB19F10 3'end
10823	23744	37245	1.24	9.1E-02	S74059.1	NT	Tg616=Cyl actin [Tripneustes gratilla=sea urchins, embryos, Genomic, 5275 nt]
10852	23772	37271	0.8	9.1E-02	Y11187.1	NT	A.thaliana RH1, TC1, G14587-5, G14587-6, and PRL1 genes
12151	25009		3.53	9.1E-02	9633494	NT	Bacteriophage Mu, complete genome
12993	25919		2.15	9.1E-02	AA179901.1	EST_HUMAN	zp38h12.s1 Stragene muscle 937209 Homo sapiens cDNA clone IMAGE:611783 3' similar to
12468	25217		1.82	9.1E-02	AF052695.1	NT	SW:TRT3_HUMAN P45378 TROPONIN T, FAST SKELETAL MUSCLE, ISOFORM BETA, ;
12916	25771		1.78	9.1E-02	AJ291390.1	NT	Rattus norvegicus cell cycle protein p55ODC gene, complete cds
						NT	Homo sapiens partial MUC3B gene for MUC3B much, exons 1-11
							FOLATE RECEPTOR ALPHA PRECURSOR (FR-ALPHA) (FOLATE RECEPTOR 1) (FOLATE RECEPTOR, ADULT) (ADULT FOLATE-BINDING PROTEIN) (FBP) (OVARIAN TUMOR-ASSOCIATED ANTIGEN MOV18) (KB CELLS FBP)
746	13807	26747	6.38	9.0E-02	P15328	SWISSPROT	ANTIGEN MOV18 (KB CELLS FBP)
							hva9g10.x1 NC1_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3175842 3' similar to contains Alu repetitive element
1640	14672	27645	6.7	9.0E-02	BE220482.1	EST_HUMAN	HIV-1 p8c095-06 from USA envelope glycoprotein (env) gene, partial cds
2815	15807	28826	6.5	9.0E-02	AF138522.1	NT	HIV-1 p8c095-06 from USA envelope glycoprotein (env) gene, partial cds
2815	15807	28827	6.5	9.0E-02	AF138522.1	NT	Dicystellum discoidium spore coat structural protein SP65 (cotE) gene, complete cds
3347	16398	29321	1.11	9.0E-02	AF279135.1	NT	Corticosteroid-binding globulin [Salimiri sclerous=squirrel monkeys, liver, mRNA, 1474 nt]
4328	17356	30243	0.83	9.0E-02	S68757.1	NT	Corticosteroid-binding globulin [Salimiri sclerous=squirrel monkeys, liver, mRNA, 1474 nt]
4328	17356	30244	0.83	9.0E-02	S68757.1	NT	Corticosteroid-binding globulin [Salimiri sclerous=squirrel monkeys, liver, mRNA, 1474 nt]

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Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4448	17474	30363	1.25	9.0E-02	P55268	SWISSPROT	LAMININ BETA-2 CHAIN PRECURSOR (S-LAMININ)
4695	17718	30611	2.37	9.0E-02	X65740.2	NT	Plasmodium falciparum P-type ATPase 3 gene
5281	18269	31137	0.93	9.0E-02	Q24697	SWISSPROT	REGULATORY PROTEIN ZESTIE
6110	19189	32409	14.12	9.0E-02	W66037.1	EST_HUMAN	zaf8a12.1 Soares_fetal_lung_NbHL19W Homo sapiens cDNA clone IMAGE:297894 5' similar to PIR:S52171 S52171 small G protein - human ;
6880	19932		1.14	9.0E-02	BF062851.1	EST_HUMAN	7h63d03.x1 NCL_CGAP_Cot16 Homo sapiens cDNA clone IMAGE:3320845 3' similar to contains Alu repetitive element;
6931	20155	33473	0.86	9.0E-02	R62805.1	EST_HUMAN	y11b08.s1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:138903 3'
12762	25404		2.03	9.0E-02	AF022236.1	NT	Escherichia coli strain E2348/89 pathogenicity island, rOrf1 (rOrf1), rOrf2 (rOrf2), EscR (escR), EscS (escS), EscT (escT), EscU (escU), CesD (cesD), EscC (escC), EscJ (escJ), SepZ (sepZ), EscV (escV), EscN (escN), SepQ (sepQ), Tir (tir), OrfU (orfU), >
1432	14466	27442	2.04	8.9E-02	BF701593.1	EST_HUMAN	602129030F2 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4285951 5'
1432	14466	27443	2.04	8.9E-02	BF701593.1	EST_HUMAN	602129030F2 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4285951 5'
2396	15403	28429	1.1	8.9E-02	BE15372.1	EST_HUMAN	PM0-HT0339-251199-003-401 HT0339 Homo sapiens cDNA
4227	17256		2	8.9E-02	AF286055.1	NT	Atrichum angustatum AtranFic2 protein (AtranFic2) gene, partial cds
5950	19038	32230	2.84	8.9E-02	AW452122.1	EST_HUMAN	UI-H-B13-alc-f-08-0-UJ.s1 NCL_CGAP_Sub55 Homo sapiens cDNA clone IMAGE:3068294 3'
5950	19038	32231	2.84	8.9E-02	AW452122.1	EST_HUMAN	UI-H-B13-alc-f-08-0-UJ.s1 NCL_CGAP_Sub55 Homo sapiens cDNA clone IMAGE:3068294 3'
5968	19051	32252	3.5	8.9E-02		NT	Homo sapiens similar to endoglycan (H. sapiens) (LOC83107), mRNA
7399	20367	33720	1.49	8.9E-02	P47259	SWISSPROT	FOLD BIFUNCTIONAL PROTEIN [INCLUDES: METHYLENETETRAHYDROFOLATE DEHYDROGENASE; METHENYLtetrahydrofolate cyclohydrolase]
7807	20757		2.02	8.9E-02	Z78021.1	NT	H. sapiens flow-sorted chromosome 8 HindIII fragment, SC6pA20F8
8385	21354	34762	0.77	8.9E-02	P28475	SWISSPROT	NITRIC-OXIDE SYNTHASE, BRAIN (NOS, TYPE I) (NEURONAL NOS) (N-NOS) (NNOS) (CONSTITUTIVE NOS) (NC-NOS) (BNOS)
8468	21437	34855	0.7	8.9E-02	BF701665.1	EST_HUMAN	602129111F2 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4285827 5'
8468	21437	34856	0.7	8.9E-02	BF701665.1	EST_HUMAN	602129111F2 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4285827 5'
8945	21911	35336	5.01	8.9E-02	AA309319.1	EST_HUMAN	EST180187 Liver, hepatocellular carcinoma Homo sapiens cDNA 5' end
9978	22905	36399	0.62	8.9E-02	A1285627.1	EST_HUMAN	qu55c05.x1 NCL_CGAP_Lym9 Homo sapiens cDNA clone IMAGE:1988680 3' similar to contains MER10.b1 MER10 repetitive element;
9978	22905	36370	0.62	8.9E-02	A1285627.1	EST_HUMAN	qu55c05.x1 NCL_CGAP_Lym9 Homo sapiens cDNA clone IMAGE:1988680 3' similar to contains MER10.b1 MER10 repetitive element;
10090	23016	36492	0.87	8.9E-02	AA339356.1	EST_HUMAN	EST44454 Fetal brain 1 Homo sapiens cDNA 5' end
12150	25743		1.3	8.9E-02	P30143	SWISSPROT	HYPOTHEICAL 51.7 KD PROTEIN IN THRC-TALB INTERGENIC REGION (ORF8)
12211	25776		1.91	8.9E-02	P19524	SWISSPROT	MYOSIN-2 ISOFORM
12367	25154		9.08	8.9E-02	BF699918.1	EST_HUMAN	602123682F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4286180 5'

Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
12530	25258		1.81	8.9E-02	6680220	NT	Mus musculus hippocampus abundant gene transcript 1 (Hlat1), mRNA
12571	25282		1.5	8.9E-02	U29895.1	NT	Human 4-hydroxyphenylpyruvate-dioxygenase gene, complete cds
1374	14408	27378	1.25	8.8E-02	Q27474	SWISSPROT	PROBABLE DNA LIGASE (POLYDEOXYRIBONUCLEOTIDE SYNTHASE (ATP))
3921	16961	29874	1.03	8.8E-02	AA299128.1	EST_HUMAN	EST11595 Uterus Homo sapiens cDNA 5' end
							TRANSCRIPTION INITIATION FACTOR TFIIID 135 KDA SUBUNIT (TAFII135) (TAFII130)
4065	17101		3.7	8.8E-02	O00268	SWISSPROT	Homo sapiens chromogranin A (parathyroid secretory protein 1) (CHGA) mRNA
4267	17298		1.26	8.8E-02	4502804	NT	Homo sapiens paired box gene 6 (enitidia, keratilis) (PAX6), isoform b, mRNA
4331	17359		2.3	8.8E-02	4590423	NT	Sheep mRNA for angiotensinogen, complete cds
7792	20744		0.86	8.8E-02	D17620.1	NT	zn99a05.s1 Stratagene colon (#937204) Homo sapiens cDNA clone IMAGE:566288 3'
9339	22304	35732	1.32	8.8E-02	AA151872.1	EST_HUMAN	601191770F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3535648 5'
11453	24396	37941	3.43	8.8E-02	BE284455.1	EST_HUMAN	601191770F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3535648 5'
11453	24396	37942	3.43	8.8E-02	BE284455.1	EST_HUMAN	601191770F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3535648 5'
11593	24531	38088	5.78	8.8E-02	AL040129.1	EST_HUMAN	DKFZp434D13.1_r1_434 (synonym: htes3) Homo sapiens cDNA clone DKFZp434D13.13 5'
12441	25204	31827	2.4	8.8E-02	Z71561.1	NT	S. cerevisiae chromosome XIV reading frame ORF YNL285w
1654	14686	27661	1.55	8.7E-02	AI167281.1	EST_HUMAN	ox65b01.s1 Soares_NIHMPu_S1 Homo sapiens cDNA clone IMAGE:1661161 3'
3707	16750	29665	3.84	8.7E-02	U82695.2	NT	Homo sapiens zinc finger protein 92 (ZFP92), expressed-Xq28STS protein (XQ28ORF), and biglycan (BGN) genes, complete cds; and plasma membrane calcium ATPase isoform 3 (PMCA3) gene, partial cds
3707	16750	29666	3.84	8.7E-02	U82695.2	NT	Homo sapiens zinc finger protein 92 (ZFP92), expressed-Xq28STS protein (XQ28ORF), and biglycan (BGN) genes, complete cds; and plasma membrane calcium ATPase isoform 3 (PMCA3) gene, partial cds
4736	17756	30850	1.2	8.7E-02	AF176636.1	NT	Mus musculus JNK interacting protein-3a (Jip3) mRNA, complete cds
5138	18147		1.02	8.7E-02	AE000895.1	NT	Methanobacterium thermoautotrophicum from bases 1176181 to 1189406 (section 101 of 148) of the complete genome
5166	18175	31053	0.97	8.7E-02	6563384	NT	Homo sapiens protein kinase C, nu (PRKCN), mRNA
5387	18490	31365	6.04	8.7E-02	AA286875.1	EST_HUMAN	zs55g08.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:701438 3'
5387	18490	31366	6.04	8.7E-02	AA286875.1	EST_HUMAN	zs55g08.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:701438 3'
7022	20147	33466	0.81	8.7E-02	AJ271885.2	NT	Mus musculus partial Kcnq1 gene for potassium channel protein, exons 10-14
7022	20147	33467	0.81	8.7E-02	AJ271885.2	NT	Mus musculus partial Kcnq1 gene for potassium channel protein, exons 10-14
7243	19978	33275	0.63	8.7E-02	AF281342.1	NT	Oncorhynchus mykiss TAT-binding protein:1 mRNA, partial cds
8860	21827	35250	0.71	8.7E-02	AE004787.1	NT	Pseudomonas aeruginosa PAO1, section 348 of 529 of the complete genome
8860	21827	35251	0.71	8.7E-02	AE004787.1	NT	Pseudomonas aeruginosa PAO1, section 348 of 529 of the complete genome
11067	24030		2.15	8.7E-02	L04758.1	NT	Oryzias latipes cytochrome P-450 (CYP4A4) gene, 5' end
11641	24578	38144	1.79	8.7E-02	AJ007763.1	NT	Glucobacter oxydans tRNA-ile and tRNA-Ala genes

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Table 4
Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
12123	24992	38593	1.89	8.7E-02	Z74060.1	NT	S.cerevisiae chromosome IV reading frame ORF YDL012c
12123	24992	38594	1.89	8.7E-02	Z74060.1	NT	S.cerevisiae chromosome IV reading frame ORF YDL012c
12428	25198		1.8	8.7E-02	X17116.1	NT	Human DNA for immunoglobulin alpha heavy chain from a case of alpha heavy chain disease
1257	14292	27256	6.2	8.6E-02	AJ271736.1	NT	Homo sapiens Xq pseudautosomal region; segment 2/2
2256	15270	28285	1.96	8.6E-02	BE408667.1	EST_HUMAN	601304016F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3638643 5'
3202	16257	29176	4.47	8.6E-02	L05468.1	NT	Trichomonas vaginalis beta-tubulin (tub1) gene, complete cds
3658	16701		4.37	8.6E-02	AF153362.1	NT	Dictyostelium discoideum adenyl cyclase (acrA) gene, complete cds
3793	16834		0.66	8.6E-02	U29187.1	NT	Mus musculus long incubation prion protein (Prnpb) and prion-like protein (Prnd) genes, complete cds
4512	17537	30421	0.67	8.6E-02	U68179.1	NT	Oryctolagus cuniculus galectin-3 gene, untranslated exon and 5' flanking region
5170	18179		1.09	8.6E-02	L13419.1	NT	Chromatium vinosum tetraheme cytochrome c gene, 3' end, bacterial ankyrin homologue, flavocytochrome c
5276	18282		1.09	8.6E-02	AB011163.1	NT	heme subunit fccA (complete cds), and flavin subunit, fccB (3' end)
6213	19287	32520	4.24	8.6E-02	Y10826.1	NT	Homo sapiens mRNA for KIAA0501 protein, partial cds
6510	19574	32828	1.48	8.6E-02	J00440.1	NT	Homo sapiens LON1b gene
6510	19574	32829	1.48	8.6E-02	J00440.1	NT	Mouse germline IgM chain gene, D region; D-q52, mu switch region (part a)
7834	20781	34159	1.01	8.6E-02	P14616	SWISSPROT	Mouse germline IgM chain gene, D region; D-q52, mu switch region (part a)
8262	21231	34641	1.33	8.6E-02	5730066	NT	INSULIN RECEPTOR-RELATED PROTEIN PRECURSOR (IRR) (IR-RELATED RECEPTOR)
8405	21374	34782	0.66	8.6E-02	5730066	NT	Homo sapiens Smf2-related CBP activator protein (SRCAP) mRNA
8469	21438	36495	0.81	8.6E-02	U60168.1	NT	Homo sapiens Smf2-related CBP activator protein (SRCAP) mRNA
10094	23020	36495	1.04	8.6E-02	AF11170.3	NT	Homo sapiens hypothetical protein FLJ11006 (FLJ11006), mRNA
10131	23057	36933	1.57	8.6E-02	AW682163.1	EST_HUMAN	Dictyostelium discoideum proteasome subunit C2 homolog PrtC (prtC) gene, complete cds
10513	23435	36933	0.97	8.6E-02	AF026504.1	NT	Homo sapiens 14q32. Jagged2 gene, complete cds; and unknown gene
11579	24517	38072	2.47	8.6E-02	BF305606.1	EST_HUMAN	h20c08.x1 NCI_CGAP_GU1 Homo sapiens cDNA clone IMAGE:2872846 3'
11579	24517	38073	2.47	8.6E-02	BF305606.1	EST_HUMAN	Rattus norvegicus SPA-1 like protein p1284 mRNA, complete cds
11767	23922	37441	9.23	8.6E-02	AE001073.1	NT	601893437F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4139216 5'
11901	24782	38370	1.57	8.6E-02	AF283660.1	NT	601893437F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4139216 5'
2406	15413	28437	2.86	8.5E-02	AE000652.1	NT	Archaeoglobus fulgidus section 34 of 172 of the complete genome
5752	18846	32028	0.71	8.5E-02	AA985491.1	EST_HUMAN	Bacillus stearothermophilus BstFI methylase (Fim) and BstFI restriction endonuclease (FIR) genes, complete cds
5793	18885		1.92	8.5E-02	P08089	SWISSPROT	Helicobacter pylori 26695 section 130 of 134 of the complete genome
6127	19205	32428	6.34	8.5E-02	AF233885.1	NT	cg33b07.s1 NCI_CGAP_Kid6 Homo sapiens cDNA clone IMAGE:1592917 3' similar to dbK01144 HLA CLASS II HISTOCOMPATIBILITY ANTIGEN, GAMMA CHAIN PRECURSOR (HUMAN); M PROTEIN, SEROTYPE 6 PRECURSOR
							Mus musculus phospholipase C-like protein mRNA, partial cds

Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8953	21919	35345	1.92	8.5E-02	6754779	NT	Mus myosin XV (Myo15), mRNA
10196	23121	36607	3.17	8.5E-02	BE833054.1	EST_HUMAN	RC4-OT0037-200700-014-e05 OT0037 Homo sapiens cDNA
10196	23121	36608	3.17	8.5E-02	BE833054.1	EST_HUMAN	RC4-OT0037-200700-014-e05 OT0037 Homo sapiens cDNA
10338	23282	36742	0.44	8.5E-02	A1140618.1	EST_HUMAN	q05g05.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1738136 3'
10728	23650	37143	0.56	8.5E-02	X76731.1	NT	V. ammodontes gene for ammodontin C
10851	23771	37270	1	8.5E-02	11418108	NT	Homo sapiens chromosome 22 open reading frame 5 (C22ORF5), mRNA
11490	24433		8.1	8.5E-02	AF155510.1	NT	Homo sapiens heparanase precursor, mRNA, complete cds
11507	24439	37989	4.05	8.5E-02	AB001562.1	NT	Streptococcus mutans gene for glucose-1-phosphate uridylyltransferase, complete cds
12985	25547		5.18	8.5E-02	AA382834.1	EST_HUMAN	EST72736 Ovary II Homo sapiens cDNA 5' end
2875	15901	28690	3.66	8.4E-02	W69330.1	EST_HUMAN	zd44e11.1 Soares_fetal_heart_NH-H19W Homo sapiens cDNA 5' end
4381	17409	30290	1.02	8.4E-02	AF257213.1	NT	Cavia porcellus glycoprotein alpha-subunit mRNA, complete cds
4381	17409	30291	1.02	8.4E-02	AF257213.1	NT	Cavia porcellus glycoprotein alpha-subunit mRNA, complete cds
5235	18243	31115	0.98	8.4E-02	5453817	NT	Homo sapiens nucleobindin 1 (NUCB1), mRNA
5385	18488	31363	8.74	8.4E-02	BE267153.1	EST_HUMAN	601190436F1 NIH_MGC 7 Homo sapiens cDNA clone IMAGE:3534393 5'
6847	19900	33194	1.86	8.4E-02	AK024458.1	NT	Homo sapiens mRNA for FLJ00050 protein, partial cds
8363	21332	34744	7.84	8.4E-02	BE095074.1	EST_HUMAN	CM3-BT0790-260400-162-d05 B T0790 Homo sapiens cDNA
9194	22160	35588	1.02	8.4E-02	AF218890.1	NT	Homo sapiens attractin precursor (ATRIN) gene, exon 2
10727	23649	37142	1.9	8.4E-02	A1735184.1	EST_HUMAN	as88g10.x1 Barsstead colon HPLRB7 Homo sapiens cDNA clone IMAGE:2335842 3' similar to TR:O88312
12351	23146	31853	1.48	8.4E-02	R79408.1	EST_HUMAN	O88312 GOB-4.1
2027	15047	28060	0.97	8.3E-02	5835680	NT	y83h12.11 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:145895 5'
2027	15047	28061	0.97	8.3E-02	5835680	NT	lxodes hexagonus mitochondrion, complete genome
3606	16651	29568	6.11	8.3E-02	P75334	SWISSPROT	lxodes hexagonus mitochondrion, complete genome
3634	16677	29590	0.69	8.3E-02	A1436797.1	EST_HUMAN	HYPOTHETICAL LIPOPROTEIN MG309 HOMOLOG PRECURSOR
3634	16677	29591	0.66	8.3E-02	A1436797.1	EST_HUMAN	tr82g06.x1 Soares_NHMPu_S1 Homo sapiens cDNA clone IMAGE:2125210 3'
6389	19457	32702	0.78	8.3E-02	A1942338.1	EST_HUMAN	tr82g06.x1 Soares_NHMPu_S1 Homo sapiens cDNA clone IMAGE:2125210 3'
6502	19566	32818	2.54	8.3E-02	AF052683.1	NT	wo79f11.x1 NCL_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2461581 3'
8313	21282	34694	3.61	8.3E-02	AF195787.1	NT	Homo sapiens protocadherin 43 gene, exon 1
8346	21315		1.19	8.3E-02	AA865285.1	EST_HUMAN	Rattus norvegicus dystrophin-related protein 2 A-form splice variant (Dtp2) mRNA, complete cds
8642	21610		1.54	8.3E-02	AA867873.1	EST_HUMAN	cg88g08.s1 NCL_CGAP_Kids Homo sapiens cDNA clone IMAGE:1455422 3' similar to contains L1 L1 L1
9896	22849	36306	1.58	8.3E-02	AW583503.1	EST_HUMAN	replicative element 1
9909	22730		2.19	8.3E-02	AL161595.2	NT	cg81f10.s1 NCL_CGAP_Kid6 Homo sapiens cDNA clone IMAGE:1592779 3'
							tr80h10.x1 Human Pancreatic Islets Homo sapiens cDNA 3' similar to TR:Q15332 Q15332 GAMMA
							SUBUNIT OF SODIUM POTASSIUM ATPASE LIKE 1
							Arabidopsis thaliana DNA chromosome 4, contig fragment No. 91

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Table 4
Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10706	23628		0.6	8.3E-02	AF020408.1	NT	Dictyostellium discoideum DocA (dca) mRNA, complete cds
12444	25924		1.48	8.3E-02	BE958488.1	EST_HUMAN	601844770F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:3929993 5'
1379	14413		7.44	8.2E-02	Y08170.2	NT	Gallus gallus mRNA for OBCAM protein gamma isoform
1494	14527	27499	1.77	8.2E-02	AF167077.2	NT	Canis familiaris glutamate transporter (EAAT4) mRNA, complete cds
3089	16147		2.24	8.2E-02	AL163206.2	NT	Homo sapiens chromosome 21 segment HS21C006
3815	16855		1.61	8.2E-02	AL161498.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 10
4033	17071	29972	1.22	8.2E-02	AL163206.2	NT	Homo sapiens chromosome 21 segment HS21C006
4313	17342	30222	5.83	8.2E-02	P48960	SWISSPROT	LEUCOCYTE ANTIGEN CD97 PRECURSOR
4313	17342	30223	5.83	8.2E-02	P48960	SWISSPROT	LEUCOCYTE ANTIGEN CD97 PRECURSOR
4313	17342	30224	5.83	8.2E-02	P48960	SWISSPROT	LEUCOCYTE ANTIGEN CD97 PRECURSOR
5108	18118	30992	1.29	8.2E-02	AF240776.1	NT	Mus musculus pepsinogen F (Pepf) mRNA, complete cds
5118	18128	31004	4.13	8.2E-02	U76009.1	NT	Mus musculus zinc transporter (Znt-3) gene, complete cds
5300	18128	31004	0.95	8.2E-02	U76009.1	NT	Mus musculus zinc transporter (Znt-3) gene, complete cds
5408	18511	31389	1.47	8.2E-02	BE897030.1	EST_HUMAN	601439576F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3924523 5'
7221	20243	33577	2.84	8.2E-02	AF309655.1	NT	Bos taurus connective tissue growth factor precursor (CTGF) gene, complete cds
8005	20944		0.6	8.2E-02	AV743341.1	EST_HUMAN	AV743341 CB Homo sapiens cDNA clone CBLANF07 5'
9057	22023		0.45	8.2E-02	U29397.1	NT	Rattus norvegicus plasma membrane Ca2+ ATPase isoform 3 (PMCA3) gene, 5' flanking region
9124	22090	35518	2.76	8.2E-02	AW875126.1	EST_HUMAN	RC2-PT0004-031299-011-005 PT0004 Homo sapiens cDNA
9658	22885	36346	5.43	8.2E-02	X04197.1	NT	Beet necrotic yellow vein virus RNA-2
10121	23047	36526	2.38	8.2E-02	BE254318.1	EST_HUMAN	601115055F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3355506 5'
12450	25209	31831	6.88	8.2E-02	AE002246.2	NT	Chlamydia pneumoniae AR39, section 73 of 94 of the complete genome
12835	25710		5.74	8.2E-02	AF275366.1	NT	Mus musculus epidermal growth factor receptor (Egfr) gene, exons 5 through 28, and complete cds, alternatively spliced
1493	14526	27498	1.05	8.1E-02	AB017138.1	NT	Pseudomonas putida malonate decarboxylase gene cluster (mdcA, mdcB, mdcC, mdcD, mdcE, mdcG, mdcH, mdcI, and mdcM genes), complete cds
5848	18938	32123	1.05	8.1E-02	AE004006.1	NT	Xylella fastidiosa, section 152 of 229 of the complete genome
6516	19579	32836	1.38	8.1E-02	T11532.1	EST_HUMAN	A1484F Heart Homo sapiens cDNA clone A1484
7403	20371		0.81	8.1E-02	AL163279.2	NT	Homo sapiens chromosome 21 segment HS21C079
7836	20782		0.9	8.1E-02	AI692681.1	EST_HUMAN	wd86108.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:2338503 3'
8663	21651	35072	0.53	8.1E-02	11426974	NT	Homo sapiens hypothetical protein FLJ10060 (FLJ10060), mRNA
8663	21661	35073	0.53	8.1E-02	11426974	NT	Homo sapiens hypothetical protein FLJ10060 (FLJ10060), mRNA
10272	23197		1.58	8.1E-02	AY005150.1	NT	Homo sapiens extracellular glycoprotein lactin precursor, gene, complete cds
11827	24710	38294	1.53	8.1E-02	AL163202.2	NT	Homo sapiens chromosome 21 segment HS21C002
6	16530	26026	4.82	8.0E-02	AW954653.1	EST_HUMAN	EST386723 MAGC resequences, MAGC Homo sapiens cDNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1709	18875	27722	13.63	8.0E-02	D26535.1	NT	Human gene for dihydrolipoamide succinyltransferase, complete cds (exon 1-15)
1709	18875	27723	13.63	8.0E-02	D26535.1	NT	Human gene for dihydrolipoamide succinyltransferase, complete cds (exon 1-15)
1919	14943	27939	4.07	8.0E-02	BE067219.1	EST_HUMAN	PM3-BT0347-170200-001-b08 BT0347 Homo sapiens cDNA
2384	15392	28417	1.05	8.0E-02	D90915.1	NT	Synechocystis sp. PCC8803 complete genome, 17/27, 2137259-2267259
2384	15392	28418	1.05	8.0E-02	D90915.1	NT	Synechocystis sp. PCC8803 complete genome, 17/27, 2137259-2267259
2478	15482		4.89	8.0E-02	BF248744.1	EST_HUMAN	601855548F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4075619 5'
2831	14137	27098	0.99	8.0E-02	M23449.1	NT	Dictyosellum discoideum cyclic nucleotide phosphodiesterase gene, complete cds
2811	15969	28892	0.76	8.0E-02	AL44507.1	NT	Thermoplasma acidophilum complete genome; segment 5/5
3830	16870	29772	6.64	8.0E-02	AW966118.1	EST_HUMAN	EST378191 MAGC resequences, MAG1 Homo sapiens cDNA
4810	17827	30724	1.7	8.0E-02	AI434202.1	EST_HUMAN	h31g02.x1 NCL_CGAP_Gas4 Homo sapiens cDNA clone IMAGE:213214 3'
4818	17835	30733	0.99	8.0E-02	AF116556.1	NT	Arabidopsis thaliana putative transcription factor (HUA2) mRNA, complete cds
4852	17869		7.57	8.0E-02	X72794.1	NT	M. musculus gene for gelatinase B
5832	18922	32105	0.71	8.0E-02	AW951139.1	EST_HUMAN	EST383209 MAGC resequences, MAGA Homo sapiens cDNA
5993	19077	32274	3.28	8.0E-02	AF275949.1	NT	Homo sapiens ABCA1 (ABCA1) gene, complete cds
7386	19077	32274	1.44	8.0E-02	AF275949.1	NT	Homo sapiens ABCA1 (ABCA1) gene, complete cds
8465	21434	34851	3.74	8.0E-02	AL114993.1	NT	Botrytis cinerea strain T4 cDNA library under conditions of nitrogen deprivation
9744	22885	36139	1.21	8.0E-02	X74208.1	NT	H. sapiens AGT gene, intron 4
9744	22885	36140	1.21	8.0E-02	X74208.1	NT	H. sapiens AGT gene, intron 4
10519	23441		0.6	8.0E-02	AL163209.2	NT	Homo sapiens chromosome 21 segment HS21C009
11145	24105	37632	2.19	8.0E-02	AF217798.1	NT	Homo sapiens SCG10 like-protein, helicase-like protein NHL, M68, and ADP-ribosylation factor related protein 1 (ARFRP1) genes, complete cds
12483	25230	31798	6.54	8.0E-02	AJ005375.1	NT	Drosophila oreana hunchback region
13036	18342		2.06	8.0E-02	4503034	NT	Homo sapiens cAMP responsive element binding protein-like 2 (CREBL2) mRNA
2184	15189	28219	4.36	7.9E-02	BE250008.1	EST_HUMAN	600943191F1 NIH_MGC_15 Homo sapiens cDNA clone IMAGE:2959510 5'
2992	18050	28971	8.43	7.9E-02	AI582029.1	EST_HUMAN	ar98c08.x1 Barstead colon HPLRB7 Homo sapiens cDNA clone IMAGE:2173646 3' similar to gb:Z26876
3864	18903	29808	5.68	7.9E-02	6881044	NT	60S RIBOSOMAL PROTEIN L38 (HUMAN);
3864	18903	29809	5.68	7.9E-02	6881044	NT	Mus musculus colony stimulating factor 1 receptor (Csf1r), mRNA
4722	17866	30633	1.08	7.9E-02	BF348454.1	EST_HUMAN	Mus musculus colony stimulating factor 1 receptor (Csf1r), mRNA
4849	17866		1.49	7.9E-02	AB008019.1	NT	602019770F1 NCL_CGAP_Bm67 Homo sapiens cDNA clone IMAGE:4155401 5'
6855	19908		1.06	7.9E-02	BF368016.1	EST_HUMAN	Arabidopsis thaliana RXW24L mRNA, partial cds
8368	21335	34747	3.26	7.9E-02	U27832.1	NT	RO3-GN0042-310800-024-411 GN0042 Homo sapiens cDNA
10388	23310	36788	4.89	7.9E-02	AI081644.1	EST_HUMAN	Saccharomyces cerevisiae suppressor of Mif2 Sm4p (SMT4) gene, complete cds ou63605.st NCL_CGAP_Br2 Homo sapiens cDNA clone IMAGE:1632465 3' similar to WP: C37A2.2 CE08611;

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Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10388	23310	36789	4.89	7.9E-02	AI081644.1	EST_HUMAN	ou63b05.s1 NCI_CGAP_Br2 Homo sapiens cDNA clone IMAGE:1632465 3' similar to WP:C37A2.2 CE08611:
1215	14253	27210	1.69	7.8E-02	AI793275.1	EST_HUMAN	oo59d02.y5 NCI_CGAP_Lu5 Homo sapiens cDNA clone IMAGE:1570467 5' similar to contains L1.13 L1 repetitive element:
1215	14253	27211	1.69	7.8E-02	AI793275.1	EST_HUMAN	oo59d02.y5 NCI_CGAP_Lu5 Homo sapiens cDNA clone IMAGE:1570467 5' similar to contains L1.13 L1 repetitive element:
5123	16804		3.25	7.8E-02	BE260048.1	EST_HUMAN	600943055F1 NIH_MGC_15 Homo sapiens cDNA clone IMAGE:2959693 5'
7279	20013	33317	1.29	7.8E-02	U82695.2	NT	Homo sapiens zinc finger protein 92 (ZFP92), expressed-Xq28STS protein (XQ28ORF), and biglycan (BGN) genes, complete cds; and plasma membrane calcium ATPase isoform 3 (PMCA3) gene, partial cds
7279	20013	33318	1.29	7.8E-02	U82695.2	NT	Homo sapiens zinc finger protein 92 (ZFP92), expressed-Xq28STS protein (XQ28ORF), and biglycan (BGN) genes, complete cds; and plasma membrane calcium ATPase isoform 3 (PMCA3) gene, partial cds
9137	22103	35529	1.26	7.8E-02	BE897947.1	EST_HUMAN	60144039F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3925449 5'
9232	22198	35626	0.6	7.8E-02	X78344.1	NT	S.cerevisiae CAT8 gene
9408	22373	35808	0.66	7.8E-02	AF233437.1	NT	Homo sapiens FYVE domain-containing dual specificity protein phosphatase FYVE-DSP1b mRNA, complete cds
9408	22373	35809	0.66	7.8E-02	AF233437.1	NT	Homo sapiens FYVE domain-containing dual specificity protein phosphatase FYVE-DSP1b mRNA, complete cds
9716	22744	36195	1.23	7.8E-02	AA469354.1	EST_HUMAN	nc68b06.r1 NCI_CGAP_Prl Homo sapiens cDNA clone IMAGE:771731
10161	23086	36563	0.65	7.8E-02	Z98124.1	NT	Bacillus subtilis complete genome (section 21 of 21): from 3999281 to 4214814
12114	24984	38586	1.64	7.8E-02	BF025981.1	EST_HUMAN	601669979F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3953083 5'
1399	15667	27402	0.93	7.7E-02	AF181897.1	NT	Homo sapiens WRN (WRN) gene, complete cds
3600	16645		2.05	7.7E-02	AJ238093.1	NT	Homo sapiens partial AF-4 gene, exons 2 to 7 and Alu repeat elements
5622	18718	31877	0.61	7.7E-02	AF062636.1	NT	Gallus gallus collagen type XII alpha-1 (COL12A1) gene, promoter region and partial cds
8241	21210	34615	7.34	7.7E-02	AA402949.1	EST_HUMAN	zu53d11.r1 Soares ovary tumor N6HOT Homo sapiens cDNA clone IMAGE:741717 5' similar to TR:G1173905 G1173905 SPLICEOSOME ASSOCIATED PROTEIN. ;
10195	23120	36606	3.76	7.7E-02	P39080	SWISSPROT	PROBABLE SERINE/THREONINE-PROTEIN KINASE YBR059C
10490	23412	36909	0.76	7.7E-02	AJ318662.1	EST_HUMAN	ta80b08.x1 NCI_CGAP_HSC2 Homo sapiens cDNA clone IMAGE:2050359 3' similar to gb:Z26876 60S RIBOSOMAL PROTEIN L38 (HUMAN);
10490	23412	36910	0.76	7.7E-02	AJ318662.1	EST_HUMAN	RIBOSOMAL PROTEIN L38 (HUMAN);
11352	24302	37829	4.65	7.7E-02		NT	RIBOSOMAL PROTEIN L38 (HUMAN);
12671	25785		1.91	7.7E-02	11422757	NT	Homo sapiens KIAA0628 gene product (KIAA0628), mRNA
					11436859	NT	Homo sapiens interferon regulatory factor 7 (IRF7), mRNA

Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3398	16447	29373	2.43	7.6E-02	BE514432.1	EST_HUMAN	601316426F1 NIH_MGC_8 Homo sapiens cDNA clone IMAGE:3684903 5'
3419	16467	29387	1	7.6E-02	AA296447.1	EST_HUMAN	EST112214 Cerebellum II Homo sapiens cDNA 5' end similar to similar to protocadherin 43
6216	19290	32523	0.72	7.6E-02	AJ061275.1	EST_HUMAN	an25g02.x1 Gessler Wilms tumor Homo sapiens cDNA clone IMAGE:1699730 3'
6491	19556	32806	0.87	7.6E-02	BE379328.1	EST_HUMAN	601236402F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3608401 5'
9725	22753	36206	1.35	7.6E-02	AJ131016.1	NT	Homo sapiens SCL gene locus
10257	23182		1.42	7.6E-02	AL139078.2	NT	Campylobacter jejuni NCTC11168 complete genome, segment 5/6
10580	23502	36994	0.47	7.6E-02	BE708002.1	EST_HUMAN	RG1-HT0545-020800-017-d06 HT0545 Homo sapiens cDNA
10714	23636		0.56	7.6E-02	BE959638.2	EST_HUMAN	601654915R1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:3839810 3'
10852	23872	37384	0.67	7.6E-02	X92856.1	NT	L. esculentum mRNA for tissue phosphate translocator
10952	23872	37385	0.67	7.6E-02	X92856.1	NT	L. esculentum mRNA for tissue phosphate translocator
11986	24863	38459	1.9	7.6E-02	AW998645.1	EST_HUMAN	QV3-BN0046-150400-151-e04 BN0046 Homo sapiens cDNA
785	13845	26790	2.89	7.5E-02	5902093	NT	Homo sapiens solute carrier family 6 (neurotransmitter transporter, glycine), member 9 (SLC6A9), mRNA
785	13845	26791	2.89	7.5E-02	5902093	NT	Homo sapiens solute carrier family 6 (neurotransmitter transporter, glycine), member 9 (SLC6A9), mRNA
1935	14859	27955	0.93	7.5E-02	AL163278.2	NT	Homo sapiens chromosome 21 segment HS21C078
4536	17559	30447	0.63	7.5E-02	AB015981.1	NT	Homo sapiens IL-18 gene for interleukin-18, intron 1 and exon 2
5952	19037	32233	0.71	7.5E-02	AJ948714.1	EST_HUMAN	wq24h09.x1 NCI_CGAP_K1811 Homo sapiens cDNA clone IMAGE:2472257 3'
8681	21649	35071	1.01	7.5E-02	AJ884387.1	EST_HUMAN	w52b02.x1 NCI_CGAP_Bm25 Homo sapiens cDNA clone IMAGE:2428491 3' similar to gb:M14328 ALPHA ENOLASE (HUMAN);
8852	21819	35239	1.29	7.5E-02	AU116913.1	EST_HUMAN	AU116913 HEMBA1 Homo sapiens cDNA clone HEMBA1000264 5'
10392	23314		0.45	7.5E-02	BF221730.1	EST_HUMAN	7c81c05.x1 NCI_CGAP_Fr28 Homo sapiens cDNA clone IMAGE:3578504 3' similar to contains element
10859	23779	37279	0.9	7.5E-02	BF206809.1	EST_HUMAN	MER27 repetitive element;
10953	23873	37386	0.66	7.5E-02	X79480.1	NT	601870205F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4100449 5'
478	13550	26478	1.24	7.4E-02	AW838547.1	EST_HUMAN	C.fiml DSM 20113 16S rDNA
1456	14489		1.08	7.4E-02	AF030027.1	NT	RC5-L T0054-260100-011-H09 L T0054 Homo sapiens cDNA
2585	15586		0.99	7.4E-02	6755059	EST	Equine herpesvirus 4 strain NS80567, complete genome
3608	16653	29571	0.78	7.4E-02	AJ807385.1	EST_HUMAN	Mus musculus paired-like homeodomain transcription factor 1 (Pitx1), mRNA
4733	17753	30646	1.09	7.4E-02	L78810.1	NT	wf43h01.x1 Soares NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2355385 3'
4833	17850	30750	3.24	7.4E-02	6978442	NT	Homo sapiens ADP/ATP carrier protein (ANT-2) gene, complete cds
4979	17994	30883	2.52	7.4E-02	6678492	NT	Rattus norvegicus Activin receptor like kinase 1 (Acvrl1), mRNA
6643	19701		1.8	7.4E-02	R17477.1	EST_HUMAN	Mus musculus ubiquitin c-terminal hydrolase related polypeptide (Uchlp), mRNA
7707	20664	34031	0.79	7.4E-02	AA605132.1	EST_HUMAN	Y014q06.r1 Soares infant brain 1N1B Homo sapiens cDNA clone IMAGE:32339 5'
							no71d02.s1 NCI_CGAP_AA1 Homo sapiens cDNA clone IMAGE:112259 3'

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8233	21202	34608	1.2	7.4E-02	BE880112.1	EST_HUMAN	601493366F1 NIH_MGC_69 Homo sapiens cDNA clone IMAGE:3895264 5'
8846	21813	35233	1.01	7.4E-02	U56089.1	NT	Human periodic typtophan protein 2 (PWP2) gene, exons 15 to 21, and complete cds
9521	22484	35930	1.02	7.4E-02	AW629605.1	EST_HUMAN	O15127 SECRETORY CARRIER-ASSOCIATED MEMBRANE PROTEIN 2 ;
9521	22484	35931	1.02	7.4E-02	AW629605.1	EST_HUMAN	hh67d11.y1 NCI_CGAP_GU1 Homo sapiens cDNA clone IMAGE:2967861 5' similar to SW:SCA2_HUMAN
9794	21117	34516	0.48	7.4E-02	AI672939.1	EST_HUMAN	hh67d11.y1 NCI_CGAP_GU1 Homo sapiens cDNA clone IMAGE:2967861 5' similar to SW:SCA2_HUMAN
9794	21117	34517	0.48	7.4E-02	AI672939.1	EST_HUMAN	hh67d11.y1 NCI_CGAP_GU1 Homo sapiens cDNA clone IMAGE:2967861 5' similar to SW:SCA2_HUMAN
10173	23098	36578	1.07	7.4E-02	U62293.1	NT	Human LIM-kinase1 and alternatively spliced LIM-kinase1 (LIMK1) gene, complete cds
10301	23226	36708	0.53	7.4E-02	BF512678.1	EST_HUMAN	UHH-BW1-arn9-g-06-0-U1.s1 NCI_CGAP_Sub7 Homo sapiens cDNA clone IMAGE:3069898 3'
12408	25181		1.47	7.4E-02	11525893	NT	Homo sapiens histone deacetylase 5 (NY-CO-9), mRNA
12665	25903		2.51	7.4E-02	AW378491.1	EST_HUMAN	CM4-HT0243-081199-037-d11 HT0243 Homo sapiens cDNA
469	13542	26468	1.3	7.3E-02	BE964961.2	EST_HUMAN	601658738R1 NIH_MGC_69 Homo sapiens cDNA clone IMAGE:3886209 3'
489	13542	26469	1.3	7.3E-02	BE964961.2	EST_HUMAN	601658738R1 NIH_MGC_69 Homo sapiens cDNA clone IMAGE:3886209 3'
885	13748	26674	5.48	7.3E-02	AE001789.1	NT	Thermotoga maritima section 101 of 138 of the complete genome
1477	18689	27486	3.94	7.3E-02	AW900281.1	EST_HUMAN	CM0-NN1004-130300-284-g08 NN1004 Homo sapiens cDNA
1862	15879		15.78	7.3E-02	AL163302.2	NT	Homo sapiens chromosome 21 segment HS21G102
3785	18826		0.72	7.3E-02	U66059.1	NT	Human gemline T-cell receptor beta chain Dopamine-beta-hydroxylase-like, TRY1, TRY2, TRY3, TCRBV27S1P, TCRBV22S1A2N1T, TCRBV9S1A1T, TCRBV7S1A1N2T, TCRBV5S1A1T, TCRBV13S3, TCRBV6S7P, TCRBV7S3A2T, TCRBV13S2A1T, TCRBV9S2A2PT, TCRBV7S2A1N4T, TCRBV19S9V13S>
6032	18046		1.06	7.3E-02	U12283.1	NT	Mus musculus transcription factor USF2 (USF2) gene, exons 8-10 and complete cds
6595	19655	32927	1.04	7.3E-02	AA779977.1	EST_HUMAN	zj24a02.s1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:451178 3' similar to gbL02426 26S PROTEASE SUBUNIT 4 (HUMAN);
7708	20663	34029	2.47	7.3E-02	P05143	SWISSPROT	PROLINE-RICH PROTEIN MP-3
7708	20663	34030	2.47	7.3E-02	P05143	SWISSPROT	PROLINE-RICH PROTEIN MP-3
8508	21479		1.2	7.3E-02	7662107	NT	Homo sapiens KIAA0424 protein (KIAA0424), mRNA
9565	22527		1.39	7.3E-02	AB011090.1	NT	Homo sapiens mRNA for KIAA0518 protein, partial cds
11552	19655	32927	1.89	7.3E-02	AA779977.1	EST_HUMAN	zj24a02.s1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:451178 3' similar to gbL02426 26S PROTEASE SUBUNIT 4 (HUMAN);
12025	25510		1.33	7.3E-02	Z73597.1	NT	S.cerevisiae chromosome XVI reading frame ORF YFL241c
120	13229	26156	0.7	7.2E-02	AE000892.1	NT	Methanobacterium thermoautotrophicum from bases 1029155 to 1039934 (section 88 of 148) of the complete genome

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
120	13229	26157	0.7	7.2E-02	AE000882.1	NT	Methanobacterium thermoautotrophicum from bases 1029155 to 1039934 (section 88 of 148) of the complete genome
1472	14505	27478	2.77	7.2E-02	AL163301.2	NT	Homo sapiens chromosome 21 segment HS21C101
1472	14505	27479	2.77	7.2E-02	AL163301.2	NT	Homo sapiens chromosome 21 segment HS21C101
2556	15558		2.98	7.2E-02	U14794.1	NT	Human immunodeficiency virus type 1 isolate 28 reverse transcriptase (pol) gene, internal fragment, partial cds
3900	16940	29851	0.74	7.2E-02	AW298322.1	EST_HUMAN	UIH-BWO-aj-a-05-0-J1.s1 NC1_CGAP_Sub8 Homo sapiens cDNA clone IMAGE:2732049 3'
4373	17400	30280	4.57	7.2E-02	BF572307.1	EST_HUMAN	602077757F1 NIH_MGC_92 Homo sapiens cDNA clone IMAGE:4251950 5'
5360	18485	31336	2.81	7.2E-02	U67531.1	NT	Methanococcus jannaschii section 73 of 150 of the complete genome
5361	18486	31337	9.14	7.2E-02	P11120	SWISSPROT	CALMODULIN
6239	19312		0.73	7.2E-02	BF217596.1	EST_HUMAN	601883905F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4086224 5'
7374	20344	33696	1.76	7.2E-02	BF216086.1	EST_HUMAN	601883558F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4095710 5'
7391	20360	33712	0.6	7.2E-02	AF221126.1	NT	Streptococcus pneumoniae putative response regulator (zmpR), putative histidine kinase (zmpS), and putative zinc metalloprotease (zmpB) genes, complete cds
7417	20384		1.74	7.2E-02	5834897	NT	Strongylocentrotus purpuratus mitochondrion, complete genome
8529	21497	34912	0.69	7.2E-02	P05143	SWISSPROT	PROLINE-RICH PROTEIN MP-3
8529	21497	34913	0.69	7.2E-02	P05143	SWISSPROT	PROLINE-RICH PROTEIN MP-3
9419	22384		0.62	7.2E-02	Y17217.1	NT	Lactococcus lactis cspE gene
9634	22861		0.63	7.2E-02	X16349.1	NT	Human gene for sex hormone-binding globulin (SHBG)
9970	22897	36360	1.98	7.2E-02	AV712452.1	EST_HUMAN	AV712452 DCA Homo sapiens cDNA clone DCAUAG01 5'
10117	23043	36523	3.63	7.2E-02	L14561.1	NT	Homo sapiens plasma membrane calcium ATPase isoform 1 (ATP2B1) gene, alternative splice products, partial cds
10274	23199	36683	1.17	7.2E-02	BF125369.1	EST_HUMAN	601763523F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:4028436 5'
10362	23285	36762	2.29	7.2E-02	AW873187.1	EST_HUMAN	h24f11.x1 NC1_CGAP_Adr1 Homo sapiens cDNA clone IMAGE:3120333 3' similar to TR:Q9Z340 Q9Z340
10552	23474	36869	0.54	7.2E-02	AA768204.1	EST_HUMAN	ATYPICAL PKC SPECIFIC BINDING PROTEIN. ;
						EST_HUMAN	ca62c07.s1 NC1_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1316844 3'
10717	23639	37132	2.17	7.2E-02	U82895.2	NT	Homo sapiens zinc finger protein 92 (ZFP92), expressed-Xq28STS protein (XQ28ORF), and biglycan (BGN) genes, complete cds; and plasma membrane calcium ATPase isoform 3 (PMCA3) gene, partial cds
10840	23760	37260	5.41	7.2E-02	BE565003.1	EST_HUMAN	601343926F1 NIH_MGC_53 Homo sapiens cDNA clone IMAGE:3685951 5'
10864	23784		3.24	7.2E-02	BE539214.1	EST_HUMAN	601065104F1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3451559 5'
11258	24210	37733	4.17	7.2E-02	AF049874.1	NT	Rattus norvegicus bHLH transcription factor Mist1 (Mist1) gene, complete cds
12311	25119	31842	1.58	7.2E-02	AA773896.1	EST_HUMAN	af61a04.r1 Soares_NHMPu_S1 Homo sapiens cDNA clone IMAGE:1048398 5'
12350	25145		5.13	7.2E-02	AJ230796.1	EST_HUMAN	AJ230796 Homo sapiens library (Seranski P) Homo sapiens cDNA clone PS13D5 3'

Table 4

Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
12469	25218		3.99	7.2E-02	U82828.1	NT	Homo sapiens alaxia telangiectasia (ATM) gene, complete cds
12484	25754		8.41	7.2E-02	AW900982.1	EST_HUMAN	CMA4-NN1009-200300-118-c11 NN1009 Homo sapiens cDNA
12880	25933		1.45	7.2E-02	AF020438.1	NT	Homo sapiens ATP-citrate lyase gene, intron 3
12864	25533		1.85	7.2E-02	AA401779.1	EST_HUMAN	z557c12.r1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:726454 5'
1920	14944	27940	1.83	7.1E-02	L02280.1	NT	Human immunodeficiency virus type 1 (D9) proviral structural capsid protein (gag) gene; partial cds
2300	15312	28332	6.39	7.1E-02	BF208802.1	EST_HUMAN	601872281F1 NIH_MGC_53 Homo sapiens cDNA clone IMAGE:4092831 5'
8239	21208	34812	0.87	7.1E-02	AI125284.1	EST_HUMAN	q82a10.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1736922 3'
12163	25038		6.33	7.1E-02	BE304784.1	EST_HUMAN	601143974F1 NIH_MGC_15 Homo sapiens cDNA clone IMAGE:3051234 5'
529	13600	26518	1.42	7.0E-02	Q07092	SWISSPROT	COLLAGEN ALPHA 1(XVI) CHAIN PRECURSOR
1498	14532		1.82	7.0E-02	X96877.1	NT	M. artellia Mcut-1 gene
1776	14805	27791	1.18	7.0E-02	AA056343.1	EST_HUMAN	z56f04.s1 Stratigene colon (#937204) Homo sapiens cDNA clone IMAGE:5095599 3'
3042	16100	29015	1.76	7.0E-02	AW138152.1	EST_HUMAN	UI-H-B11-acy-c-07-UJ.st NCL_OGAP_Sub3 Homo sapiens cDNA clone IMAGE:2716020 3'
3913	16953	29884	0.96	7.0E-02	AA815438.1	EST_HUMAN	ai65a12.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:5095599 3'
4074	17110	30004	1.05	7.0E-02	BE070284.1	EST_HUMAN	RIBOSOMAL PROTEIN L32 (HUMAN);
4184	17195		1.24	7.0E-02	AW792862.1	EST_HUMAN	QV4-BT0407-280100-090-e10 BT0407 Homo sapiens cDNA
4242	17271	30156	1.28	7.0E-02	AF077821.1	NT	GM0-JM0001-060300-270-e12 UM0001 Homo sapiens cDNA
4966	17981	30871	8.41	7.0E-02	BF381987.1	EST_HUMAN	Caris familiaris Inducible nitric oxide synthase mRNA, complete cds
5481	18553		1.03	7.0E-02	Y09143.2	NT	601816291F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4050071 5'
7630	20590	33953	0.9	7.0E-02	AV689285.1	EST_HUMAN	Lumbricus rubellus mRNA for cyclophilin B
7804	20808	34186	0.8	7.0E-02	Y19187.1	NT	AV689285 GKC Homo sapiens cDNA clone GKCCAE08 5'
9454	22418	35858	1.2	7.0E-02	K02901.1	NT	Gallus gallus mRNA for partial azonin, XL spliced variant (azc gene)
9956	22883	36345	1.21	7.0E-02	K02901.1	NT	African swine fever virus, complete genome
10312	23238	36718	0.78	7.0E-02	U27268.1	NT	Rat Ig germ-line epsilon H-chain gene C-region, 3' end
11700	24665	38242	2.23	7.0E-02	AA724295.1	EST_HUMAN	Human myosin binding protein H (MyBP-H) gene, complete cds
12939	25519	31710	1.68	7.0E-02	11421638	NT	ah99a05.s1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1327184 3' similar to gb:L14837
515	13588	26504	11.2	6.9E-02	AL163210.2	NT	TIGHT JUNCTION PROTEIN ZO-1 (HUMAN);
515	13586	26505	11.2	6.9E-02	AL163210.2	NT	Homo sapiens hypothetical protein FLJ20116 (FLJ20116), mRNA
1336	14370		1.68	6.9E-02	4507968	NT	Homo sapiens chromosome 21 segment HS21C010
3807	16847	29754	1.37	6.9E-02	Q06364	SWISSPROT	Homo sapiens regulator of Gz-selective protein signaling (ZGAP1) mRNA, and translated products
3807	16847	29755	1.37	6.9E-02	Q06364	SWISSPROT	26S PROTEASOME REGULATORY SUBUNIT S3 (NUCLEAR ANTIGEN 21D7)

Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5151	18161	31041	0.97	6.9E-02	AA670289.1	EST_HUMAN	af25608.s1 Soares_tetral_fetus_Nb2HF8_9w Homo sapiens cDNA clone IMAGE:1032710 3'
6026	19109		0.57	6.9E-02	AF161364.1	NT	Homo sapiens HSPC101 mRNA, partial cds
7876	20820		0.67	6.9E-02	AF164987.1	NT	Canine distemper virus strain A7517, complete genome
8387	21356		1.18	6.9E-02	U12022.1	NT	Human calmodulin (CALM1) gene, exons 2,3,4,5 and 6, and complete cds
8899	21855	35287	1.08	6.9E-02	BE597435.1	EST_HUMAN	601340661F1 NIH_MGC_53 Homo sapiens cDNA clone IMAGE:3683030 5'
8899	21855	35288	1.08	6.9E-02	BE597435.1	EST_HUMAN	601340661F1 NIH_MGC_53 Homo sapiens cDNA clone IMAGE:3683030 5'
9475	22439	35879	0.55	6.9E-02	U22967.1	NT	Barbarie duck parvovirus REP protein (rep) and three capsid protein VP (vp) genes, complete cds
12343	25141		2.17	6.9E-02	X74315.1	NT	X.laevis XFD2 mRNA for fork head protein
12519	25250		1.75	6.9E-02	P44821	SWISSPROT	PROTEIN TRANSPORT PROTEIN HOFH HOMOLOG
13112	25631	31648	3.69	6.9E-02	BF352899.1	EST_HUMAN	IL3-HT0619-110700-210-C04 HT0619 Homo sapiens cDNA
1899	14924	27918	1.18	6.8E-02	AA496759.1	EST_HUMAN	ae30702.r1 Gessler Wilms tumor Homo sapiens cDNA clone IMAGE:897339 5' similar to gb:M22382
1899	14924	27918	1.18	6.8E-02	AA496759.1	EST_HUMAN	ae30702.r1 Gessler Wilms tumor Homo sapiens cDNA clone IMAGE:897339 5' similar to gb:M22382
1922	14946	27942	4.7	6.8E-02	AF156673.1	NT	MITOCHONDRIAL MATRIX PROTEIN P1 PRECURSOR (HUMAN);
3117	16174	29084	1.05	6.8E-02	AA781996.1	EST_HUMAN	MITOCHONDRIAL MATRIX PROTEIN P1 PRECURSOR (HUMAN);
3117	16174	29085	1.05	6.8E-02	AA781996.1	EST_HUMAN	Homo sapiens putative hepatic transcription factor (WBSR14) gene, complete cds
3117	16174	29086	1.05	6.8E-02	AA781996.1	EST_HUMAN	ai75a06.s1 Soares_testis_NHT Homo sapiens cDNA clone 1376626 3'
4583	17805		0.71	6.8E-02	BE141076.1	EST_HUMAN	ai75a06.s1 Soares_testis_NHT Homo sapiens cDNA clone 1376626 3'
5283	18289		0.76	6.8E-02	T03013.1	EST_HUMAN	MRO-HT0069-071099-001-c05 HT0069 Homo sapiens cDNA
6776	19831		0.66	6.8E-02	P20792	SWISSPROT	FB20A6 Fetal brain, Stralagene Homo sapiens cDNA clone FB20A6 3'end
7084	20018		1.05	6.8E-02	BE061890.1	EST_HUMAN	CELL-SURFACE RECEPTOR DAF-1 PRECURSOR
7497	20462	33922	7.18	6.8E-02	AL163288.2	NT	RC1-BT0254-090300-017-d09 BT0254 Homo sapiens cDNA
7948	20889	34280	0.64	6.8E-02	U16856.1	NT	Homo sapiens chromosome 21 segment HS21C068
8631	21599	35020	5.44	6.8E-02	AJ248287.1	NT	Dicystellum discoidium myosin heavy chain kinase A (MHCK A) mRNA, complete cds
8631	21599	35021	5.44	6.8E-02	AJ248287.1	NT	Pyrococcus abyssi complete genome; segment 5/6
12140	25949		3.73	6.8E-02	T03214.1	EST_HUMAN	Pyrococcus abyssi complete genome; segment 5/6
12274	25094		2.52	6.8E-02	AA758014.1	EST_HUMAN	FB4A8 Fetal brain, Stralagene Homo sapiens cDNA clone FB4A8 3' end similar to LINE-1
12832	25449		1.68	6.8E-02	AW975839.1	EST_HUMAN	ae6705.s1 Soares_testis_NHT Homo sapiens cDNA clone 1320705 3'
12894	25480		2.35	6.8E-02	9910585	NT	EST1387948 MAGE resequences, MAGN Homo sapiens cDNA
1531	14564		1.93	6.7E-02	AF115536.1	NT	Mus musculus latent TGF beta binding protein (Tgfb), mRNA
1910	14934	27930	1.99	6.7E-02	AJ220286.1	EST_HUMAN	Oncorhynchus mykiss TAP1 protein (OnmyTAP1) mRNA, OnmyTAP1*01 allele, complete cds
3730	16772	29883	4.34	6.7E-02	P17278	SWISSPROT	iqg79e04.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1841408 3'
8183	21153	34560	1.01	6.7E-02	X62995.1	NT	HOMEBOX PROTEIN HOXD4 (HOXD4)
							H.sapiens DNA for cGMP phosphodiesterase (exons 4-22)

Table 4

Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8183	21153	34561	1.01	6.7E-02	X62696.1	NT	H. sapiens DNA for cGMP phosphodiesterase (exons 4-22)
8781	21748	35170	0.45	6.7E-02	AW082688.1	EST_HUMAN	xb61c11.x1 Soares_NFL_T_QBC_S1 Homo sapiens cDNA clone IMAGE:2580788 3'
9859	22886	36347	0.73	6.7E-02	AW137359.1	EST_HUMAN	UI-H-B11-acr-g-01-Q-U1.s1 NCL_CGAP_Sub3 Homo sapiens cDNA clone IMAGE:2715433 3'
9859	22886	36348	0.73	6.7E-02	AW137359.1	EST_HUMAN	UI-H-B11-acr-g-01-Q-U1.s1 NCL_CGAP_Sub3 Homo sapiens cDNA clone IMAGE:2715433 3'
1371	14406	27376	0.9	6.6E-02	AF245116.1	NT	Drosophila melanogaster cactin mRNA, complete cds
2192	15207	28226	2.66	6.6E-02	AL289241.1	NT	Mus musculus Capn12 gene for calpain 12, exons 1-21, three alternative transcripts
3477	16523	29447	11.07	6.6E-02	R64306.1	EST_HUMAN	yt18b10.s1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:139579 3'
3491	16537	29462	2.1	6.6E-02	7108357	NT	Homo sapiens mesothelin (MSLN), transcript variant 1, mRNA
3491	16537	29463	2.1	6.6E-02	7108357	NT	Homo sapiens mesothelin (MSLN), transcript variant 1, mRNA
4107	17141	30036	1.45	6.6E-02	AF260225.1	NT	Homo sapiens TESTIN 2 and TESTIN 3 genes, complete cds, alternatively spliced
5015	18029	30913	9.23	6.6E-02	Q61703	SWISSPROT	INTER-ALPHA-TRYPSIN INHIBITOR HEAVY CHAIN H2 PRECURSOR (ITI HEAVY CHAIN H2)
5015	18029	30914	9.23	6.6E-02	Q61703	SWISSPROT	INTER-ALPHA-TRYPSIN INHIBITOR HEAVY CHAIN H2 PRECURSOR (ITI HEAVY CHAIN H2)
6736	19782	33073	3.97	6.6E-02	X06411.1	NT	P. vulgaris mRNA for chalcone synthase
6967	19823	33105	0.55	6.6E-02	P25159	SWISSPROT	MATERNAL EFFECT PROTEIN STAUFEN
6967	19823	33106	0.55	6.6E-02	P25159	SWISSPROT	MATERNAL EFFECT PROTEIN STAUFEN
8152	21080		0.57	6.6E-02	D14567.1	NT	Penicillium urticae mitochondrial rRNA (large rRNA) gene and its flanking region
8279	21248	34660	1.6	6.6E-02	AF052672.1	NT	Homo sapiens chemokine receptor CXCR4 gene, promoter region and complete cds
8817	21784	35209	0.67	6.6E-02	AF006055.1	NT	Dictyostellum discoideum darlin (dar) gene, complete cds
9273	22239	35666	0.67	6.6E-02	9629193	NT	Human respiratory syncytial virus, complete genome
9273	22239	35667	0.67	6.6E-02	9629193	NT	Human respiratory syncytial virus, complete genome
10311	23235	36717	0.52	6.6E-02	AI458752.1	EST_HUMAN	ig97g06.x1 NCL_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:2149498 3'
10447	23469	36860	1.65	6.6E-02	V07848.1	NT	Homo sapiens EWS, gar22, rp22 and bam22 genes
10481	23403		0.6	6.6E-02	11430659	NT	Homo sapiens vinculin (VCL), mRNA
11310	24260	37786	4.9	6.6E-02	BF374248.1	EST_HUMAN	MR1-SN0064-010600-006-a12 SN0064 Homo sapiens cDNA
12063	24936		1.73	6.6E-02	C05789.1	EST_HUMAN	C05789 Human pancreatic islet Homo sapiens cDNA clone hbc5156
12719	25373		2.53	6.6E-02	9937991	NT	Mus musculus DIPB gene (Dipb), mRNA
13024	25572		1.31	6.6E-02	AF167430.1	NT	Rattus norvegicus cyclochrome P450 2E1 (CYP2E1) gene, 5' flanking region
584	13652	26566	2.67	6.5E-02	BF027639.1	EST_HUMAN	601671046F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3954178 5'
989	14041	26966	1.95	6.5E-02	7706068	NT	Homo sapiens E2F-like protein (LOC51270), mRNA
1392	14426	27395	3.5	6.5E-02	U47024.1	NT	Xenopus laevis alpha(E)-catenin mRNA, complete cds
1749	14778	27763	2.08	6.5E-02	AE000764.1	NT	Aquifex aeolicus section 96 of 109 of the complete genome
5638	18734	31896	1.71	6.5E-02	AA443991.1	EST_HUMAN	z448h12.s1 Soares ovary tumor NbHOT Homo sapiens cDNA clone IMAGE:756743 3' similar to gb:M26038
6683	19750	33027	0.83	6.5E-02	BF665340.1	EST_HUMAN	HLA CLASS II HISTOCOMPATIBILITY ANTIGEN, DR-3 BETA CHAIN (HUMAN); 602118687F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4276028 5'

Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7165	18396	31241	1.17	6.5E-02	U22861.1	NT	Azobacter vinelandii ATCC 9046 negative regulator MucB (mucB) gene, partial cds
10302	23227	36709	0.65	6.5E-02	BE963200.2	EST_HUMAN	601656817R1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:3865637 3'
10302	23227	36710	0.65	6.5E-02	BE963200.2	EST_HUMAN	601656817R1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:3865637 3'
10832	23753	37252	0.53	6.5E-02	BF106300.1	EST_HUMAN	601823611F1 NIH_MGC_77 Homo sapiens cDNA clone IMAGE:4043138 5'
11002	23968	37492	4.61	6.5E-02	AA196648.1	EST_HUMAN	z32g05.s1 Soares_NIHMPU_S1 Homo sapiens cDNA clone IMAGE:665144 3'
12164	25017		4.16	6.5E-02	M21498.1	NT	Rabbit microsomal epoxide hydrolase
12526	25255		7.31	6.5E-02	AF102993.1	NT	Nectria haematococca kinesin related protein 2 (KRP2) gene, complete cds
577	13946	26559	1.74	6.4E-02	X94649.1	NT	A.carteae precursor of peridinin-chlorophyll-protein (PCP) gene
1746	14775	27760	0.93	6.4E-02	AE001777.1	NT	Thermotoga maritima section 89 of 136 of the complete genome
1746	14775	27761	0.93	6.4E-02	AE001777.1	NT	Thermotoga maritima section 89 of 136 of the complete genome
4933	15085	29007	1.16	6.4E-02	6986923	NT	Mus musculus histone deacetylase 5 (Hdac5), mRNA
5282	18270		2.56	6.4E-02	AA147572.1	EST_HUMAN	z51e04.11 Soares_pregnant_uterus_NihHPU Homo sapiens cDNA clone IMAGE:506470 5' similar to contains Alu repetitive element;
5525	18624	31559	1.19	6.4E-02	AI191956.1	EST_HUMAN	qe07b01.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1738249 3' similar to contains LTR8.b3 LTR8 repetitive element;
5982	19067	32265	1.15	6.4E-02	7305186	NT	Mus musculus IFN-response element binding factor 1 (IREBF-1), mRNA
6234	19307	32539	4.16	6.4E-02	AF052733.1	NT	Heterodera glycines beta-1,4-endoglucanase-1 precursor (HG-eng-1) gene, complete cds
6234	19307	32540	4.16	6.4E-02	AF052733.1	NT	Heterodera glycines beta-1,4-endoglucanase-1 precursor (HG-eng-1) gene, complete cds
6542	19604	32866	0.72	6.4E-02	AI672896.1	EST_HUMAN	we73g12.x1 Soares_Dieckgraebe_colon_NHCD Homo sapiens cDNA clone IMAGE:2346780 3'
6900	20213	33542	4.64	6.4E-02	BE974448.1	EST_HUMAN	601680425R2 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:3950603 3'
7693	20651	34015	0.52	6.4E-02	AL16257.2	NT	Neisseria meningitidis serogroup A strain Z2491 complete genome; segment 617
8679	21647		2.79	6.4E-02	6753323	NT	Mus musculus chaperonin subunit 6a (zeta) (Cct6a), mRNA
9012	21978	35397	4	6.4E-02	AA083305.1	EST_HUMAN	k1419.seq.F Human fetal heart, Lambda ZAP Express Homo sapiens cDNA 5'
9483	22447	35887	0.92	6.4E-02	AF150106.1	EST_HUMAN	AF150195 Human mRNA from cd34+ stem cells Homo sapiens cDNA clone CBDAIA10
9944	22871		0.51	6.4E-02	BE934083.1	EST_HUMAN	RC1-OT0083-150600-014-g06 OT0083 Homo sapiens cDNA
10075	23002	36472	1.75	6.4E-02	AB011126.1	NT	Homo sapiens mRNA for KIAA0554 protein, partial cds
10824	23546	37046	0.59	6.4E-02	AF087150.1	NT	Homo sapiens DNA topoisomerase II beta (TOP2B) gene, exons 16, 17, and 18
10824	23546	37047	0.59	6.4E-02	AF087150.1	NT	Homo sapiens DNA topoisomerase II beta (TOP2B) gene, exons 16, 17, and 18
12018	24895	38492	2.18	6.4E-02	U91328.1	NT	Human hereditary haemochromatosis region, histone 2A-like protein gene, hereditary haemochromatosis (HLA-H) gene, RoRet gene, and sodium phosphate transporter (NPT3) gene, complete cds
12018	24895	38493	2.18	6.4E-02	U91328.1	NT	Human hereditary haemochromatosis region, histone 2A-like protein gene, hereditary haemochromatosis (HLA-H) gene, RoRet gene, and sodium phosphate transporter (NPT3) gene, complete cds

Single Exon Probes Expressed In Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
12424	26881		5.38	6.4E-02	AF107690.1	NT	Homo sapiens mucin 5B (MUC5B) gene, partial cds
12476	25224	31793	5.68	6.4E-02	AJ277174.1	NT	Drosophila melanogaster mRNA for mod(mdg4)51.4 protein
1769	14798	27784	2.76	6.3E-02	AF109905.1	NT	Mus musculus major histocompatibility locus class III regions Hec70t gene, partial cds; smRNP, G7A, NG23, MutS homolog, CLCP, NG24, NG25, and NG28 genes, complete cds; and unknown genes
3618	16662		2.77	6.3E-02	P37092	SWISSPROT	HEAT SHOCK PROTEIN 70 HOMOLOG
6259	19332	32563	1.06	6.3E-02	BF210736.1	EST_HUMAN	601873316F1 NIH_MGC_54 Homo sapiens cDNA clone IMAGE:4097498 5'
7453	20419		1.39	6.3E-02	X97869.1	NT	H. sapiens gene encoding La autoantigen
9846	22590	36039	1.01	6.3E-02	AJ243916.1	NT	Drosophila melanogaster Domina gene, exons 1-3
10374	23297	36773	2.98	6.3E-02	AB010162.1	NT	Hepatitis G virus RNA for polyprotein (NS5A region), partial cds, strain: CMR-152
10834	23556		0.81	6.3E-02	AV698070.1	EST_HUMAN	AY698070 GKC Homo sapiens cDNA clone GKCAHE01 5'
11070	19332	32563	2.76	6.3E-02	BF210736.1	EST_HUMAN	601873316F1 NIH_MGC_54 Homo sapiens cDNA clone IMAGE:4097498 5'
4278	17307	30186	2.48	6.2E-02	AL161572.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 68
4365	17392		1.12	6.2E-02	AF271235.1	NT	Rattus norvegicus differentiation-associated Na-dependent inorganic phosphate cotransporter (DNPI) mRNA, complete cds
4812	17633		6.56	6.2E-02	Q62191	SWISSPROT	52 KD RO PROTEIN (SJOGREN SYNDROME TYPE A ANTIGEN (SS-A)) (RO(SS-A)) (RO52)
6963	20188	33513	0.87	6.2E-02	D49530.1	NT	Spirulina platensis DNA for adenylate cyclase, complete cds
7889	20833	34212	0.79	6.2E-02	U41453.1	NT	Rattus norvegicus PKC binding protein and substrate mRNA, complete cds
8158	21096		0.56	6.2E-02	AL161543.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 45
9299	28007		0.63	6.2E-02	M61101.1	NT	Porcine group C rotavirus (strain Cowden) outer membrane protein (VP7) mRNA, complete cds
9599	22652	36106	0.53	6.2E-02	AA78450.1	EST_HUMAN	ar20a06.st Soares_tetris_Nb2HF8_9w Homo sapiens cDNA clone IMAGE:10321778 3'
9835	22771	36226	1.25	6.2E-02		NT	Mus musculus stromal cell derived factor receptor 2 (Sdfr2), mRNA
12259	25979		15.66	6.2E-02	AE000750.1	NT	Aquifex aeolicus section 82 of 109 of the complete genome
12596	25298		1.38	6.2E-02	BE793085.1	EST_HUMAN	601583773F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3337842 5'
12676	25348	31764	3.54	6.2E-02	BF112039.1	EST_HUMAN	7137h03.x1 Soares NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:3623815 3' similar to TR-Q9Y4S6 Q9Y4S6 HYPOTHETICAL 30.3 KD PROTEIN, [1];
256	13353	26278	3.09	6.1E-02	D16471.1	NT	Human mRNA, Xq terminal portion
4017	17056		15.65	6.1E-02	U73325.1	NT	Arabidopsis thaliana K+ inward rectifying channel protein (AKG1) gene, complete cds
6043	19125	32330	0.62	6.1E-02	7662463	NT	Homo sapiens KIAA1052 protein (KIAA1052), mRNA
6043	19125	32331	0.62	6.1E-02	7662463	NT	Homo sapiens KIAA1052 protein (KIAA1052), mRNA
6235	19308		1.84	6.1E-02	4507070	NT	Homo sapiens SWISNF related, matrix associated, actin dependent regulator of chromatin, subfamily a, member 3 (SMARCA3) mRNA
8606	21674	34989	3.52	6.1E-02	X95288.1	NT	H. sapiens mRNA for B-HLH DNA binding protein
9008	21974	35393	1.93	6.1E-02	BE971863.1	EST_HUMAN	601651056R1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:3934604 3'

Table 4

Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9008	21974	36394	1.93	6.1E-02	BE971853.1	EST_HUMAN	601651086R1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:3934804 3'
11082	24044	37566	3.44	6.1E-02	BE176643.1	EST_HUMAN	IL3-HT0618-110500-136-C08 HT0618 Homo sapiens cDNA
12216	25897		2.42	6.1E-02	X70969.1	NT	S. japonicum mRNA for serine-enzyme
12776	25774		1.35	6.1E-02	A886811.1	EST_HUMAN	tz56707.x1 NCI_CGAP_OV35 Homo sapiens cDNA clone IMAGE:2282901 3'
12812	25491		7.44	6.1E-02	AL163207.2	NT	Homo sapiens chromosome 21 segment HS21C007
1287	14302	27263	1.25	6.0E-02	AE001777.1	NT	Thermoplasma maritima section 89 of 136 of the complete genome
2684	15680	28698	1.17	6.0E-02	AW968948.1	EST_HUMAN	EST1380924 MAGE resequences, MAGJ Homo sapiens cDNA
2783	15775		1.98	6.0E-02	AB031289.1	NT	Mesocricetus cori mitochondrial DNA, NADH dehydrogenase subunit 4, tRNA-Gln, tRNA-Phe, tRNA-Met, ATPase subunit 6, and NADH dehydrogenase subunit 2
2948	13213	26137	1.47	6.0E-02	AA188730.1	EST_HUMAN	zp78c04.r1 Stratagene HeLa cell s3 937216 Homo sapiens cDNA clone IMAGE:626310 5'
2948	13213	26138	1.47	6.0E-02	AA188730.1	EST_HUMAN	zp78c04.r1 Stratagene HeLa cell s3 937216 Homo sapiens cDNA clone IMAGE:626310 5'
3243	16298	29222	1.52	6.0E-02	AA372376.1	EST_HUMAN	EST842268 Colon adenocarcinoma IV Homo sapiens cDNA 5' end similar to tissue-specific protein
3243	16298	29223	1.52	6.0E-02	AA372376.1	EST_HUMAN	EST842268 Colon adenocarcinoma IV Homo sapiens cDNA 5' end similar to tissue-specific protein
5472	18573		0.76	6.0E-02	AW370211.1	EST_HUMAN	RC3-BT0253-011199-013-b04 BT0253 Homo sapiens cDNA
6341	19410	32651	0.98	6.0E-02	AB07637.1	EST_HUMAN	wf48h05.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2358873 3' similar to contains L1.11 L1 repetitive element;
7180	18411	31212	2.79	6.0E-02	5174698	NT	Homo sapiens stimulated trans-acting factor (50 kDa) (STAF50) mRNA
7180	18411	31213	2.79	6.0E-02	5174698	NT	Homo sapiens stimulated trans-acting factor (50 kDa) (STAF50) mRNA
7394	20362	33714	2.08	6.0E-02	BF582349.1	EST_HUMAN	601815274F2 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4049226 5'
7508	20473	33833	0.57	6.0E-02	BF210488.1	EST_HUMAN	601874710F1 NIH_MGC_54 Homo sapiens cDNA clone IMAGE:4101074 5'
7644	20886	34277	1.71	6.0E-02	A1204275.1	EST_HUMAN	q558b08.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1754199 3'
8765	21732		0.52	6.0E-02	11486496	NT	Rec110momas americana mitochondrion, complete genome
9627	22571	36020	1.17	6.0E-02	AB23167.1	EST_HUMAN	ts78a06.x1 NCI_CGAP_GC06 Homo sapiens cDNA clone IMAGE:2237362 3'
9627	22571	36021	1.17	6.0E-02	AB23167.1	EST_HUMAN	ts78a06.x1 NCI_CGAP_GC06 Homo sapiens cDNA clone IMAGE:2237362 3'
9761	22702	36159	2.03	6.0E-02	AJ245365.1	NT	Acipenser baeri partial IGLV gene for immunoglobulin light chain variable region, exons 1-2
9761	22702	36160	2.03	6.0E-02	AJ245365.1	NT	Acipenser baeri partial IGLV gene for immunoglobulin light chain variable region, exons 1-2
10265	23190	36675	0.66	6.0E-02	AA309797.1	EST_HUMAN	EST180654 Jurkat T-cells V Homo sapiens cDNA 5' end similar to heat shock protein 1, 60 kDa-like
10265	23190	36676	0.66	6.0E-02	AA309797.1	EST_HUMAN	EST180654 Jurkat T-cells V Homo sapiens cDNA 5' end similar to heat shock protein 1, 60 kDa-like
12475	25223	31792	3.08	6.0E-02	11431702	NT	Homo sapiens DNA-dependent protein kinase catalytic subunit-interacting protein 2 (KIP2), mRNA
12845	25455		3.16	6.0E-02	AB09273.1	EST_HUMAN	wf69h03.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2360885 3' similar to TR:O60298 O60298 KIAA0551 PROTEIN;
232	13332	26255	5.34	5.9E-02	AW934719.1	EST_HUMAN	RC1-DT0001-290100-012-e10 DT0001 Homo sapiens cDNA

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Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2996	16054	28375	3.42	5.9E-02	AF190269.1	NT	Mus musculus p53 tumor suppressor gene, exon 10 and 11, partial cds; alternatively spliced
4905	17922	30814	0.94	5.9E-02	AF006304.1	NT	Saccharomyces cerevisiae protein tyrosine phosphatase (PTP3) gene, complete cds
7077	25674	33409	0.62	5.9E-02	AF145680.1	NT	Drosophila melanogaster LD23107 sting (sting) mRNA, complete cds
8964	21930	35355	1.92	5.9E-02	9055249	NT	Mus musculus Iroquois related homeobox 5 (Drosophila) (Irx5), mRNA
9806	21129		0.82	5.9E-02	BF242748.1	EST_HUMAN	601877609F1 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:4105994.5
1138	24098		3.23	5.9E-02	6679870	NT	Mus musculus follistatin-like (Fstl), mRNA
933	13886		6.03	5.8E-02	D60110.1	NT	Thiobacillus ferrooxidans merC, merA genes and URF-1
2872	15932		0.99	5.8E-02	AJ223621.1	NT	Populus trichocarpa CGAOMT1 gene, exon 1 to exon 5
3676	18719	29633	1.32	5.8E-02	AE001775.1	NT	Thermotoga maritima section 87 of 136 of the complete genome
4382	17410	30292	5.33	5.8E-02	AW051927.1	EST_HUMAN	wx24c02.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2544578.3
4382	17410	30293	5.33	5.8E-02	AW051927.1	EST_HUMAN	wx24c02.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2544578.3
4578	17600	30495	4.73	5.8E-02	A1247505.1	EST_HUMAN	qh56f01.x1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:1848697.3 similar to gb:M13142 COAGULATION FACTOR XI PRECURSOR (HUMAN);
4578	17600	30496	4.73	5.8E-02	A1247505.1	EST_HUMAN	qh56f01.x1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:1848697.3 similar to gb:M13142 COAGULATION FACTOR XI PRECURSOR (HUMAN);
4604	17625		2.93	5.8E-02	AF066264.1	NT	Gallus gallus tyrosine kinase JAK1 (JAK1) mRNA, complete cds
6014	19097	32298	0.53	5.8E-02	AA190394.1	EST_HUMAN	zp86a11.s1 StrataGene HeLa cell s3 937216 Homo sapiens cDNA clone IMAGE:627068.3
7941	20883	34273	2.52	5.8E-02	M99150.1	NT	Human polymorphic microsatellite DNA
7941	20883	34274	2.52	5.8E-02	M99150.1	NT	Human polymorphic microsatellite DNA
9014	21980	35399	0.59	5.8E-02	AL163283.2	NT	Homo sapiens chromosome 21 segment HS21C083
12655	25668		10.6	5.8E-02	AA604269.1	EST_HUMAN	no75e11.s1 NCI_CGAP_AA1 Homo sapiens cDNA clone IMAGE:1112684.3
3070	16127	29039					ou63b05.s1 NCI_CGAP_Br2 Homo sapiens cDNA clone IMAGE:1632465.3 similar to WP-C37A2.2
3086	16143	29055	1.27	5.7E-02	AJ081644.1	EST_HUMAN	CE08611;
3614	18654	29761	2.47	5.7E-02	AF11917.1	NT	Homo sapiens dopamine transporter (SLC6A3) gene, complete cds
5199	18208	31082	0.91	5.7E-02	AW966791.1	EST_HUMAN	EST378865 MAGE resequences, MAGI Homo sapiens cDNA
5306	18309		1.18	5.7E-02	AJ251973.1	NT	Homo sapiens partial steerin-1 gene
5979	19064		0.89	5.7E-02	6784525	NT	Mus musculus low density lipoprotein receptor (Ldlr), mRNA
7704	20681	34025	0.59	5.7E-02	AF275948.1	NT	Homo sapiens ABCA1 (ABCA1) gene, complete cds
7704	20661	34026	0.59	5.7E-02	BE871911.1	EST_HUMAN	601447937F1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3851985.5
7766	20739	34111	0.68	5.7E-02	BE871911.1	EST_HUMAN	601447937F1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3851985.5
7766	20739	34112	0.68	5.7E-02	D78003.1	NT	Xenopus laevis mRNA for fourth component of complement, complete cds
8495	21463	34879	1.74	5.7E-02	D78003.1	NT	Xenopus laevis mRNA for fourth component of complement, complete cds
10209	23134	36621	0.65	5.7E-02	AJ289090.1	NT	Rattus norvegicus mRNA for potassium channel, alpha subunit (Kv9.2 gene)
					6681260	NT	Mus musculus ec2 oncogene (Ec2), mRNA

Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10930	23850	37365	0.49	5.7E-02	Z49883.1	NT	L.mexicana opp1 gene
11521	24462	38013	3.22	5.7E-02	A1752885.1	EST_HUMAN	en18b09.y1 Normal Human Trabecular Bone Cells Homo sapiens cDNA clone NHTBC_en18b09 random
11521	24462	38014	3.22	5.7E-02	A1752885.1	EST_HUMAN	en18b09.y1 Normal Human Trabecular Bone Cells Homo sapiens cDNA clone NHTBC_en18b09 random
11676	24642		1.89	5.7E-02	AL163303.2	NT	Homo sapiens chromosome 21 segment HS21C103
12573	25782		8.27	5.7E-02	D50320.1	NT	Pig DNA for SPAI-2, complete cds
12794	25855		3.72	5.7E-02	AF217490.1	NT	Homo sapiens fragile 16D oxido reductase (FOR) gene, exons 8, 9, and partial cds
12930	25958		5.65	5.7E-02	AF281280.1	NT	Pan troglodytes apolipoprotein-E gene, complete cds
1529	14562	27533	1.85	5.6E-02	AF094455.1	NT	Hydrocotyle rotundifolia ribosomal protein L16 (rpl16) gene, intron; chloroplast gene for chloroplast product
4671	17692	30578	1.92	5.6E-02	AB013100.1	NT	Lycopodium esculentum LE-ACS9 mRNA for 1-aminocyclopropane-1-carboxylate synthase, complete cds
4725	17745	30636	1.21	5.6E-02	AA280599.1	EST_HUMAN	z445c01.s1 NCL_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:700416 3'
6817	19871	33160	5.93	5.6E-02	AW172708.1	EST_HUMAN	x02c10.x1 NCL_CGAP_U12 Homo sapiens cDNA clone IMAGE:2856050 3' similar to TR:O94978 O94978 KIAA0905 PROTEIN. ;
7075	20097	33407	0.77	5.6E-02	AA866182.1	EST_HUMAN	cd47f12.s1 NCL_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1371119 3' similar to contains Alu repetitive element; contains element L1 repetitive element ;
7356	20328	33677	2.94	5.6E-02	BE008001.1	EST_HUMAN	QVQ-BN0147-290400-214-g07 BN0147 Homo sapiens cDNA
8141	21078	34478	0.61	5.6E-02	A1183563.1	EST_HUMAN	q64g11.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1734308 3'
9154	22120	35548	2.47	5.6E-02	BE542663.1	EST_HUMAN	601067158F1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3453279 5'
9154	22120	35549	2.47	5.6E-02	BE542663.1	EST_HUMAN	601067158F1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3453279 5'
10171	23096	36576	1.06	5.6E-02	AA482864.1	EST_HUMAN	m48407.s1 NCL_CGAP_AVI1 Homo sapiens cDNA clone IMAGE:923245 similar to TR:G769859 G769859 LAMINA ASSOCIATED POLYPEPTIDE 1C. ;
11891	24772		1.87	5.6E-02	AF260225.1	NT	Homo sapiens TESTIN 2 and TESTIN 3 genes, complete cds, alternatively spliced
2663	15660	28678	8.23	5.6E-02	X97869.1	NT	H.sapiens gene encoding La autoantigen
3228	16283	29207	3.44	5.6E-02	6755501.1	NT	Mus musculus SH3 domain protein 1B (Sh3d1B), mRNA
4244	17273	30157	1.13	5.6E-02	L41561.1	NT	Gallid herpesvirus mRNA fragment
5742	18836	32017	3.09	5.6E-02	Q01174	SWISSPROT	TROPOMYOSIN ALPHA CHAIN, NON MUSCLE
6141	18836	32017	3.81	5.6E-02	Q01174	SWISSPROT	TROPOMYOSIN ALPHA CHAIN, NON MUSCLE
7603	20564	33925	1.85	5.6E-02	6755902.1	NT	Mus musculus tufellin 1 (Tuf1), mRNA
8457	21426	34842	0.69	5.6E-02	AF170911.1	NT	Homo sapiens sodium-dependent vitamin C transporter 1 (SVCT1) mRNA, complete cds
8457	21426	34843	0.69	5.6E-02	AF170911.1	NT	Homo sapiens sodium-dependent vitamin C transporter 1 (SVCT1) mRNA, complete cds
10013	22940	36405	0.63	5.6E-02	10947034	NT	Homo sapiens eIF4E-transporter (4E-1), mRNA

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Table 4
Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10013	22940	36406	0.63	5.5E-02	10647034	NT	Homo sapiens eIF4E-transporter (4E-T), mRNA
10107	23033	36510	1.45	5.5E-02	U69492.1	NT	Mus musculus second IL11 receptor alpha chain (IL-11Ra2) gene, exons 1 and 2
11360	24309	37835	6.48	5.5E-02	U09771.1	NT	Citrobacter freundii DSM 30040 cyclopropane fatty acid synthase (cfa) gene, partial cds, dihydroxyacetone kinase (dhaK), glycerol dehydrogenase (dhaD), transcriptional activator (dhaR), 1,3-propanediol dehydrogenase (dhaT), glycerol dehydratase (dhaB), >
13089	25920	31303	1.99	5.5E-02	11421332	NT	Homo sapiens hypothetical protein SIRP-52 (SIRP-52), mRNA
3032	18090		1.02	5.4E-02	AJ277468.1	NT	Oryza sativa rbb3-1 gene for putative Bowman Birk trypsin inhibitor
3433	18323		6.97	5.4E-02	BE073468.1	EST_HUMAN	ROS-BT0559-140200-072-C03 BT0559 Homo sapiens cDNA
3931	18971	29885	0.7	5.4E-02	U85806.1	NT	Hirudo medicinalis SNAP-25 homolog mRNA, complete cds
8462	21431		1.05	5.4E-02	Z99116.1	NT	Bacillus subtilis complete genome (section 13 of 21): from 2395261 to 2613730
9426	22390	35828	0.53	5.4E-02	AF260225.1	NT	Homo sapiens TESTIN 2 and TESTIN 3 genes, complete cds, alternatively spliced
11057	24020	37543	1.54	5.4E-02	U20790.1	NT	Neurospora crassa ubiquinol-cytochrome c oxidoreductase subunit VIII (QOR8) mRNA, complete cds
1056	14102	27052	1.91	5.3E-02	AW391248.1	EST_HUMAN	QV0-ST0213-021299-062-a09 ST0213 Homo sapiens cDNA
1056	14102	27053	1.91	5.3E-02	AW391248.1	EST_HUMAN	QV0-ST0213-021299-062-a09 ST0213 Homo sapiens cDNA
1506	14559	27511	16.63	5.3E-02	T94799.1	EST_HUMAN	ye37f12.11 Stralagene lung (#837210) Homo sapiens cDNA clone IMAGE:119951 5' similar to gb:K01508 HLA CLASS II HISTOCOMPATIBILITY ANTIGEN, DP(1) ALPHA CHAIN (HUMAN);
2604	15507	28533	2.12	5.3E-02	AJ276408.1	NT	Pseudomonas putida tfgS gene
2953	16011	28937	0.96	5.3E-02	M58417.1	NT	Drosophila melanogaster laminin B2 gene, complete cds
2953	16011	28938	0.95	5.3E-02	M58417.1	NT	Drosophila melanogaster laminin B2 gene, complete cds
3167	16222	29137	5.38	5.3E-02	AJ276408.1	NT	Pseudomonas putida tfgS gene
4641	17682	30550	0.9	5.3E-02	AJ011048.1	NT	Arabidopsis thaliana eli5 gene, exons 1-11
5125	18134	31011	8.41	5.3E-02	M80483.1	NT	Mus musculus caudal type homeobox-1 (Cdx-1) gene, complete cds
5392	18495	31372	1.8	5.3E-02	AE000527.1	NT	Helicobacter pylori 26695 section 5 of 134 of the complete genome
5392	18495	31373	1.8	5.3E-02	AE000527.1	NT	Helicobacter pylori 26695 section 5 of 134 of the complete genome
6222	19296	32530	3.03	5.3E-02	M85289.1	NT	Human heparan sulfate proteoglycan (HSPG2) mRNA, complete cds
7068	20039	33398	3.94	5.3E-02	9695413	NT	Lymphocystis disease virus 1, complete genome
7299	20271	33608	1.23	5.3E-02	U32892.1	NT	Haemophilus influenzae Rd section 147 of 163 of the complete genome
7585	20546		2.12	5.3E-02	S78221.1	NT	nuclear protein TIF1 isoform [mice, mRNA, 4053 nt]
8209	21108	34507	0.51	5.3E-02	P38742	SWISSPROT	HYPOTHETICAL 130.0 KD PROTEIN IN SNF8-SPO11 INTERGENIC REGION
8748	21716		0.5	5.3E-02	U10098.1	NT	Mus musculus 129/Sv cystatin C (cst3) gene, complete cds
9481	22448	35886	2.05	5.3E-02	X03127.1	NT	Podocarpa anserina mitochondrial epsilon-sen DNA
10491	23413	36911	0.61	5.3E-02	AB022605.1	NT	Homo sapiens hCMT1b mRNA for mRNA (guanine-7-methyltransferase, complete cds
10491	23413	36912	0.61	5.3E-02	AB022605.1	NT	Homo sapiens hCMT1b mRNA for mRNA (guanine-7-methyltransferase, complete cds

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Table 4

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10618	23540		0.6	5.3E-02	Y07907.1	NT	D. rerio mRNA for zp-23 POU gene, splice variant (neurula, 9-16 hpf and postsomitogenesis, 20-28 hpf)
10695	23617	37111	0.69	5.3E-02	X68432.1	NT	B. rerio pou3c mRNA for transcription factor
12092	24963	38558	2.06	5.3E-02	X68435.1	NT	H. sapiens mRNA for HMG-CoA-synthase
2263	15305		89.73	5.2E-02	5031908	NT	Homo sapiens meprin A, alpha (PABA peptide hydrolase) (MEP1A) mRNA
3131	16188	29097	1.98	5.2E-02	AJ277681.1	NT	Homo sapiens partial LMO1 gene for LIM domain only 1 protein, exon 1
3131	16188	29098	1.98	5.2E-02	AJ277681.1	NT	Homo sapiens partial LMO1 gene for LIM domain only 1 protein, exon 1
3960	17000	29915	0.73	5.2E-02	AF236101.1	NT	Arabidopsis thaliana putative dicarboxylate diion protein (Ctd1) mRNA, complete cds
3962	17002		0.97	5.2E-02	6671757	NT	Mus musculus cytokine inducible SH2-containing protein 3 (Cish3), mRNA
4307	17336	30214	3.36	5.2E-02	U07132.1	NT	Human steroid hormone receptor Nrl-1 mRNA, complete cds
6025	19108	32310	0.66	5.2E-02	U14731.1	NT	Saccharomyces cerevisiae Cdc54p (CDC54) gene, complete cds
6228	19302		1.22	5.2E-02	A1830965.1	EST_HUMAN	w80604.x1 NCI_CGAP_Lym12 Homo sapiens cDNA clone IMAGE:2409150 3' similar to contains MER15.b1
7489	20454	33813	1.07	5.2E-02	P36322	SWISSPROT	MER15 repetitive element
8537	21505		2.15	5.2E-02	AL163204.2	NT	DNA POLYMERASE PROCESSIVITY FACTOR (POLYMERASE ACCESSORY PROTEIN) (PAP) (DNA-BINDING GENE 18 PROTEIN)
10087	23014	36487	1.77	5.2E-02	D10927.1	NT	Homo sapiens chromosome 21 segment HS21C004
10087	23014	36488	1.77	5.2E-02	D10927.1	NT	Turnip mosaic virus genomic RNA for Capsid protein, complete cds
11888	24769	38357	5.42	5.2E-02	F32386.1	EST_HUMAN	Turnip mosaic virus genomic RNA for Capsid protein, complete cds
12693	25358	38358	5.42	5.2E-02	F32386.1	EST_HUMAN	HSPD25097 HM3 Homo sapiens cDNA clone s3000039A02
2372	15380		1.55	5.2E-02	Q03030	SWISSPROT	HSPD25097 HM3 Homo sapiens cDNA clone s3000039A02
5041	18054		0.97	5.1E-02	AL134071.1	EST_HUMAN	OXALOACETATE DECARBOXYLASE ALPHA CHAIN
6630	19884	33175	0.94	5.1E-02	AB031740.1	NT	DKFZp547D073_T1 547 (synonym: hfr1) Homo sapiens cDNA clone DKFZp547D073 5'
7039	19371	31258	1.76	5.1E-02	BF378625.1	EST_HUMAN	Homo sapiens PB1 gene for salivary proline-rich protein P-B, complete cds
8596	21564	34978	0.77	5.1E-02	M26434.1	NT	HIV-1 patient 96 from Italy protease (pol) gene, complete cds
8596	21564	34979	0.77	5.1E-02	M26434.1	NT	QV0-UM0051:250800-350-508 UM0051 Homo sapiens cDNA
8590	21668	35081	1.26	5.1E-02	AJ131966.1	NT	Human hypoxanthine phosphoribosyltransferase (HPRT) gene, complete cds
9237	22203	35634	0.61	5.1E-02	P02533	SWISSPROT	Human hypoxanthine phosphoribosyltransferase (HPRT) gene, complete cds
9237	22203	35635	0.61	5.1E-02	P02533	SWISSPROT	Spodoptera littoralis mRNA for 3-dehydrocyclohexone 3-beta-reductase
10168	23093	36571	7.1	5.1E-02	AF012898.1	NT	KERATIN, TYPE I CYTOSKELETAL 14 (CYTOKERATIN 14) (K14) (CK 14)
10542	23464	36959	1.66	5.1E-02	AF012898.1	NT	KERATIN, TYPE I CYTOSKELETAL 14 (CYTOKERATIN 14) (K14) (CK 14)
11179	24135	37665	2.19	5.1E-02	AF069303.1	SWISSPROT	Candida albicans protein, phosphatase Ssd1 homolog (SSD1) gene, complete cds
11179	24135	37666	2.19	5.1E-02	AF069303.1	NT	ANTER-SPECIFIC PROLINE-RICH PROTEIN APG (PROTEIN CEX)
11179	24135	37666	2.19	5.1E-02	AF069303.1	NT	Homo sapiens ES18 mRNA, partial cds
11179	24135	37666	2.19	5.1E-02	AF069303.1	NT	Homo sapiens ES18 mRNA, partial cds

Table 4
Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
12899	25359		1.75	5.1E-02	AF062467.1	NT	Cucumis melo polygalacturonase precursor (MPC3) mRNA, complete cds
12961	25531		1.8	5.1E-02	AA534104.1	EST_HUMAN	h7302.s1 NCI_CGAP_P10 Homo sapiens cDNA clone IMAGE:998139
483	13556	26481	2.16	5.0E-02	AF098004.1	NT	Mus musculus fatty acid amide hydrolase gene, exon 10
935	13988	26938	4.55	5.0E-02	Z38896.1	NT	O. virginianus (HEL37) microsatellite DNA
1209	14247	27205	4.03	5.0E-02	Z98104.1	NT	Bacillus subtilis complete genome (section 1 of 21): from 1 to 213080
2007	15028	28036	4.94	5.0E-02	P02810	SWISSPROT	SALIVARY ACIDIC PROLINE-RICH PHOSPHOPROTEIN 1/2 PRECURSOR (PRP-1/PRP-3) (PRP-2/PRP-4) (P1F-F/P1F-S) (PROTEIN A/PROTEIN C) [CONTAINS: PEPTIDE P-C]
2829	14040	26996	1.62	5.0E-02	U72742.1	NT	Oryctolagus cuniculus UDP-glucuronosyltransferase (UGT2B13) mRNA, complete cds
3348	16399		1.34	5.0E-02	7305610	NT	Mus musculus Uho-51 like kinase 2 (C. elegans) (Ulk2), mRNA
3609	16654		1.01	5.0E-02	U32782.1	NT	Haemophilus influenzae Rd section 97 of 163 of the complete genome
3696	16798	29662	13.82	5.0E-02	U12768.2	NT	Antheraea pernyi period clock protein homolog mRNA, complete cds
6253	19326	32557	0.77	5.0E-02	AF096264.1	NT	Gallus gallus tyrosine kinase JAK1 (JAK1) mRNA, complete cds
6441	19508		1.25	5.0E-02	AJ242623.1	NT	Mus musculus Dmp-1 gene, exons 1-6
7181	18412	31214	0.6	5.0E-02	P35616	SWISSPROT	NEUROFILAMENT TRIPLET L PROTEIN (NEUROFILAMENT LIGHT POLYPEPTIDE) (NFL)
7785	20738	34110	12.03	5.0E-02	P35616	SWISSPROT	NEUROFILAMENT TRIPLET L PROTEIN (NEUROFILAMENT LIGHT POLYPEPTIDE) (NFL)
8008	20946		0.52	5.0E-02	AW082464.1	EST_HUMAN	MR0-CT0084-100899-002-g10 CT0084 Homo sapiens cDNA
10560	23492	36977	1.26	5.0E-02	AF305238.1	NT	Mus musculus Fas-interacting serine/threonine kinase 3 (Fist3) mRNA, complete cds
11820	24703	38285	2.47	5.0E-02	U67600.1	NT	Methanococcus jannaschii section 142 of 150 of the complete genome
12226	26818		6.4	5.0E-02	Q04047	SWISSPROT	NO-ON-TRANSIENT A PROTEIN
226	13325		27.61	4.9E-02	M14230.1	NT	Chicken 28-kDa vitamin D-dependent calcium-binding protein (CaBP-28) mRNA, complete cds
369	13455	26384	2.96	4.9E-02	AF275948.1	NT	Homo sapiens ABCA1 (ABCA1) gene, complete cds
369	13455	26385	2.96	4.9E-02	AF275948.1	NT	Homo sapiens ABCA1 (ABCA1) gene, complete cds
3302	16355	29274	1.54	4.9E-02	P54258	SWISSPROT	ATROPHIN-1 (DENTATORUBRAL-PALLIDOLYSIN ATROPHY PROTEIN)
3584	16629		0.7	4.9E-02	AA188940.1	EST_HUMAN	zq48a12.s1 Striatagene hNT neuron (#337233) Homo sapiens cDNA clone IMAGE:632926 3' similar to contains Alu repetitive element/contains element MSR1 repetitive element;
3605	16650	29568	0.96	4.9E-02	AA400914.1	EST_HUMAN	Z178a03.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:728428 3'
3605	16650	29567	0.96	4.9E-02	AA400914.1	EST_HUMAN	Z178a03.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:728428 3'
4877	17894	30783	2.11	4.9E-02	AW167821.1	EST_HUMAN	xg56g10.x1 NCI_CGAP_U14 Homo sapiens cDNA clone IMAGE:2632386 3'
4877	17894	30784	2.11	4.9E-02	AW167821.1	EST_HUMAN	xg56g10.x1 NCI_CGAP_U14 Homo sapiens cDNA clone IMAGE:2632386 3'
5444	18546	31458	1.71	4.9E-02	L00122.1	NT	Rat elastase II gene, exon 6
5444	18546	31459	1.71	4.9E-02	L00122.1	NT	Rat elastase II gene, exon 6
7349	20319	33666	2.83	4.9E-02	AE000860.1	NT	Archaeoglobus fulgidus section 127 of 172 of the complete genome
8963	21928		0.91	4.9E-02	AE002309.1	NT	Chlamydia muridarum, section 40 of 85 of the complete genome
9107	22073	35500	0.8	4.9E-02	AL161559.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 59

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Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10656	23578	37075	0.53	4.9E-02	P19532	SWISSPROT	TRANSCRIPTION FACTOR E3
11730	24616	38193	3.44	4.9E-02	AF008303.1	NT	Homo sapiens prepro placental TGF-beta gene, complete cds
12879	25473		6.66	4.9E-02	M19364.1	NT	Human gamma-B-crystallin (gamma 1-2) and gamma-C-crystallin (gamma 2-1) genes, complete cds
330	13420	26344	1.06	4.8E-02	D16471.1	NT	Human mRNA, Xq terminal portion
331	13420	26344	2.41	4.8E-02	D16471.1	NT	Human mRNA, Xq terminal portion
489	13562	26486	12.99	4.8E-02	AF003100.1	NT	Arabidopsis thaliana AP2 domain containing protein RAP2.7 mRNA, partial cds
2281	15294	28318	2.24	4.8E-02	W51983.1	EST_HUMAN	gb:M30938 LUPUS KU AUTOANTIGEN PROTEIN P86 (HUMAN);
3222	16277	29202	1.93	4.8E-02	X17144.1	NT	z449b02.s1 Soares_senescent_fibroblasts_NbHSF Homo sapiens cDNA clone IMAGE:32661 1' 3' similar to
4698	17719		1.24	4.8E-02	Z54280.1	NT	Tetrahymena costrata histone H3I and histone H4II intergenic DNA
5174	18183	31060	0.63	4.8E-02	U91914.1	NT	S. scrofa gene for skeletal muscle ryanodine receptor
8477	21446	34863	1.55	4.8E-02	AW368497.1	EST_HUMAN	Streptococcus constellatus D-alanine-D-alanine ligase gene, partial cds
9485	22449	35889	0.76	4.8E-02	AJ001398.1	NT	MR2-ST0129-221099-012-b02 ST0129 Homo sapiens cDNA
9485	22449	35890	0.76	4.8E-02	AJ001398.1	NT	Fugu rubripes rps24 gene
12505	25242		1.35	4.8E-02	9632883	NT	Fugu rubripes rps24 gene
7004	20130	33445	3.77	4.7E-02	W01153.1	EST_HUMAN	Streptococcus thermophilus bacteriophage Sfi19, complete genome
7069	20091	33399	0.88	4.7E-02	BF686625.1	EST_HUMAN	y287109.r1 Soares melanocyte 2NbHM Homo sapiens cDNA clone IMAGE:281017 5' similar to contains Alu
7069	20091	33400	0.88	4.7E-02	BF686625.1	EST_HUMAN	repetitive element;
7103	20037	33340	1.56	4.7E-02	M62752.1	NT	602143554F1 NIH_MGC 46 Homo sapiens cDNA clone IMAGE:4304772 5'
8594	21562	34976	8.56	4.7E-02	X15543.1	NT	602143554F1 NIH_MGC 46 Homo sapiens cDNA clone IMAGE:4304772 5'
9305	22270	35701	1.65	4.7E-02	X89211.1	NT	Rat stathin-related protein (s1) gene, complete CDS
9327	22282		2.51	4.7E-02	AB028678.1	NT	B.taurus mRNA for RF-36-DNA-binding protein
9582	22544	35995	7.94	4.7E-02	X15543.1	NT	B.taurus mRNA for endogenous retroviral like element
10005	22932	36395	0.55	4.7E-02	BF305237.1	EST_HUMAN	Gallus gallus Wpki-8 gene, complete cds
10092	23018		0.56	4.7E-02	AI873042.1	EST_HUMAN	B.taurus mRNA for RF-36-DNA-binding protein
12783	25970		1.97	4.7E-02	P52951	SWISSPROT	601892692F1 NIH_MGC 17 Homo sapiens cDNA clone IMAGE:4198414 5'
13022	25570		1.56	4.7E-02	AJ277682.1	NT	we76c10.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2347314 3'
270	13366	26292	1.06	4.6E-02	BE153583.1	EST_HUMAN	HOMEOBOX PROTEIN GBX-2 (GASTRULATION AND BRAIN-SPECIFIC HOMEOBOX PROTEIN 2)
741	13802	26741	3.47	4.6E-02	AE000445.1	NT	Homo sapiens partial TUB gene for tubby (mouse) homolog and LIM domain only 1 protein
1361	14395	27366	3.62	4.6E-02	AV727059.1	EST_HUMAN	PMO-HT0339-251199-003-g05 HT0339 Homo sapiens cDNA
							Escherichia coli K-12 MG1655 section 335 of 400 of the complete genome
							AV727059 HTC Homo sapiens cDNA clone HTCBWC01 5'

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Single Exon Probes Expressed in Bone Marrow

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2496	15499	28525	4.32	4.6E-02	AW236023.1	EST_HUMAN	xn24f03.x1 NCI_CGAP_Kid111 Homo sapiens cDNA clone IMAGE:2694653 3' similar to SW:GRF1_HUMAN
2819	13368	26292	1.03	4.6E-02	BE153583.1	EST_HUMAN	Q12849 G-RICH SEQUENCE FACTOR-1
3020	16078	28999	0.67	4.6E-02	BE153583.1	EST_HUMAN	PM0-HT0339-251199-003-g05 HT0339 Homo sapiens cDNA
3342	16078	28999	0.67	4.6E-02	BE153583.1	EST_HUMAN	PM0-HT0339-251199-003-g05 HT0339 Homo sapiens cDNA
3607	16078	28999	0.91	4.6E-02	BE153583.1	EST_HUMAN	PM0-HT0339-251199-003-g05 HT0339 Homo sapiens cDNA
4149	17180		1.24	4.6E-02	AF220365.1	NT	Mus musculus nucleolar RNA helicase II(Gu (ddx21) gene, complete cds
5252	18260	31129	0.94	4.6E-02	AA070167.1	EST_HUMAN	zm92c10.s1 Stralagene ovarian cancer (#937219) Homo sapiens cDNA clone IMAGE:545394 3' similar to gb:X03212 KERATIN, TYPE II CYTOSKELETAL 7 (HUMAN);
5823	18913	32096	1.42	4.6E-02	AF076962.1	NT	Haplochromis burtoni gonadotropin-releasing hormone and GnRH-associated peptide precursor (GnRH2) gene, complete cds
6357	19426	32668	4.48	4.6E-02	X61624.1	NT	C.reinhardtii atp2 (atpB) mRNA
6357	19426	32669	4.48	4.6E-02	X61624.1	NT	C.reinhardtii atp2 (atpB) mRNA
6968	20191	33518	1.51	4.6E-02	AI149574.1	EST_HUMAN	gc06b06.x1 Soares_placenta_8to9weeks_2NbpHP8c9W Homo sapiens cDNA clone IMAGE:1713971 3' similar to contains L1.13 L1 repetitive element;
8134	21071	34470	0.66	4.6E-02	6978720	NT	Rattus norvegicus Cathepsin H (Ctsh), mRNA
9003	21969	35391	2.89	4.6E-02	BE154006.1	EST_HUMAN	PM0-HT0339-060400-009-G12 HT0339 Homo sapiens cDNA
11731	24617	38194	5.31	4.6E-02	AA913328.1	EST_HUMAN	ol27h09.s1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1524737 3'
12761	25967		1.99	4.6E-02	L11692.1	NT	Oryctolagus cuniculus macrophage scavenger receptor type II mRNA, complete cds
12992	25552		8.41	4.6E-02	X57808.1	NT	Human germline immunoglobulin lambda light chain gene
447	13520	26453	1.9	4.5E-02	P22448	SWISSPROT	RETINOIC ACID RECEPTOR BETA (RAR-BETA)
1222	14260	27217	0.78	4.5E-02	AF005730.1	NT	Marburg virus strain M.S.Africa/Johannesburg/1975/Ozolin VP35 gene, complete cds
1222	14260	27218	0.78	4.5E-02	AF005730.1	NT	Marburg virus strain M.S.Africa/Johannesburg/1975/Ozolin VP35 gene, complete cds
1821	14848	27841	4.23	4.5E-02	P32182	SWISSPROT	HEPATOCYTE NUCLEAR FACTOR 3-BETA (HNF-3B)
2119	15106	28156	3.34	4.5E-02	AE003964.1	NT	Xylella fastidiosa, section 110 of 228 of the complete genome
3736	16778	29691	4.42	4.5E-02	AL163278.2	NT	Homo sapiens chromosome 21 segment HS21C078
6358	19427	32670	1.63	4.5E-02	AJ400877.1	NT	Homo sapiens ASCL3 gene, CEGP1 gene, C11orf14 gene, C11orf15 gene, C11orf16 gene and C11orf17 gene
6856	19713	32990	0.94	4.5E-02	AL163280.2	NT	Homo sapiens chromosome 21 segment HS21C080
7062	20084	33392	0.96	4.5E-02	L26487.1	NT	Methanosarcina frisia carbon monoxide dehydrogenase large subunit (cdh1A) gene; carbon monoxide dehydrogenase small subunit (cdh1B) gene, complete cds
7062	20084	33393	0.96	4.5E-02	L26487.1	NT	Methanosarcina frisia carbon monoxide dehydrogenase large subunit (cdh1A) gene; carbon monoxide dehydrogenase small subunit (cdh1B) gene, complete cds
8736	21704	35128	2.34	4.5E-02	AF036684.1	NT	Arabidopsis thaliana CCAAT-box binding factor HAP3 homolog gene, complete cds

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Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10306	23233	36715	4.58	4.5E-02	AA325216.1	EST_HUMAN	EST28167 Cerebellum 11 Homo sapiens cDNA 5' end similar to similar to neuro-D4 protein
10460	23382	36875	0.43	4.5E-02	X95508.1	NT	A europaeum mRNA for legumin-like protein
10577	23499	36991	0.81	4.5E-02	AB000470.1	NT	Gallus gallus mRNA for alpha1 integrin, complete cds
12440	25203	31826	2.95	4.5E-02	11418013	NT	Homo sapiens ref finger protein-like 3 (RFPL3), mRNA
12823	25863	31440	7.3	4.5E-02	AA191097.1	EST_HUMAN	Homo sapiens ref finger protein-like 3 (RFPL3), mRNA
222	13322		4.84	4.4E-02	BE972733.1	EST_HUMAN	601652154F1 NIH_MGC_82 Homo sapiens cDNA clone IMAGE:3935388 5'
2107	15124		6.38	4.4E-02	P31568	SWISSPROT	HYPOTHETICAL PROTEIN (ORF 2280)
2498	15901	28527	2.11	4.4E-02	AW878475.1	EST_HUMAN	QV2-PT0012-010300-070-g02 PT0012 Homo sapiens cDNA
3654	16687	29612	2.01	4.4E-02	AF159160.1	NT	Mycoplasma xanthus serine/threonine kinase Pkn10 (pkn10) gene, complete cds
4657	17678	30563	1.25	4.4E-02	AF109907.1	NT	Homo sapiens S164 gene, partial cds; PS1 and hypothetical protein genes, complete cds; and S171 gene, partial cds
4657	17678	30564	1.25	4.4E-02	AF109907.1	NT	Homo sapiens S164 gene, partial cds; PS1 and hypothetical protein genes, complete cds; and S171 gene, partial cds
4771	17791		0.94	4.4E-02	AJ222689.1	NT	Ovis aries CCAAT-enhancer binding protein epsilon gene
7325	20296	33639	0.59	4.4E-02	AF095824.1	NT	Canis familiaris matrix metalloproteinase 9 (MMP-9) mRNA, partial cds
7325	20296	33640	0.59	4.4E-02	AF095824.1	NT	Canis familiaris matrix metalloproteinase 9 (MMP-9) mRNA, partial cds
9105	22071	35497	2.17	4.4E-02	AA736989.1	EST_HUMAN	mvt3n03.s1 NCJ_CGAP_SS1 Homo sapiens cDNA clone IMAGE:1239221 3'
11409	24353	37886	3.75	4.4E-02	AF060669.1	NT	Hepatitis E virus strain HEV-US2 polyprotein (ORF1), (ORF3), and capsid protein (ORF2) genes, complete cds
11533	24474	38025	2.56	4.4E-02	AA496739.1	EST_HUMAN	aa3304.r1 Gessler Wilms tumor Homo sapiens cDNA clone IMAGE:897631 5'
12159	25014		2.22	4.4E-02	AB040926.1	NT	Homo sapiens mRNA for KIAA1493 protein, partial cds
12346	25980		1.83	4.4E-02	BF241245.1	EST_HUMAN	601878746F1 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:4107418 5'
781	13841	26766	5.93	4.3E-02	AF003249.1	NT	Morone saxatilis myosin heavy chain FM3A (FM3A), complete cds
2575	15576	28595	1.4	4.3E-02	AV704878.1	EST_HUMAN	AV704878 ADB Homo sapiens cDNA clone ADBAOH08 5'
3443	16490	29409	8.93	4.3E-02	AL163210.2	NT	Homo sapiens chromosome 21 segment HS21C010
3671	16714		1.25	4.3E-02	AF060598.1	NT	Homo sapiens promyelocytic leukemia zinc finger protein (PLZF) gene, complete cds
6644	19702	32977	4.62	4.3E-02	P30427	SWISSPROT	PLECTIN
6644	19702	32978	4.62	4.3E-02	P30427	SWISSPROT	PLECTIN
6896	19848	33245	0.73	4.3E-02	AA652266.1	EST_HUMAN	ns8c12.s1 NCJ_CGAP_P12 Homo sapiens cDNA clone IMAGE:1188886
8858	21825	35248	0.9	4.3E-02	AF293359.1	NT	Homo sapiens desmocollin 3 (DSC3) gene, complete cds, alternatively spliced
9153	22119	35546	0.95	4.3E-02	X55322.1	NT	H. sapiens NCAM mRNA for neural cell adhesion molecule
9153	22119	35547	0.95	4.3E-02	X55322.1	NT	H. sapiens NCAM mRNA for neural cell adhesion molecule
823	13881	26832	1.85	4.2E-02	AU123327.1	EST_HUMAN	AU123327 NT2RM2 Homo sapiens cDNA clone NT2RM2000020 5'
867	13923		2.58	4.2E-02	AU123327.1	EST_HUMAN	AU123327 NT2RM2 Homo sapiens cDNA clone NT2RM2000020 5'

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Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
897	13952	28910	0.83	4.2E-02	AW003845.1	EST_HUMAN	w34g01.x1 NCI_CGAP_P111 Homo sapiens cDNA clone IMAGE:2545584 3' similar to TR:Q63291 Q63291
1733	14763		1.54	4.2E-02	AL445068.1	NT	L1 RETROPOSON, ORF2 MRNA; contains L1.13 L1 repetitive element;
1793	14822	27806	1.02	4.2E-02	P23091	SWISSPROT	Thermoplasma acidophilum complete genome; segment 4/5
3677	16720	28634	2.18	4.2E-02	P23091	SWISSPROT	TRANSFORMING PROTEIN MAF
4774	17784	30686	0.73	4.2E-02	BF342955.1	EST_HUMAN	TRANSFORMING PROTEIN MAF
							602017105F1 NCI_CGAP_Bn64 Homo sapiens cDNA clone IMAGE:4152672 5'
5699	18794	31967	0.85	4.2E-02	AF280107.1	NT	Homo sapiens cytochrome P450 polypeptide 43 (CYP3A43) gene, partial cds; cytochrome P450 polypeptide 4 (CYP3A4) and cytochrome P450 polypeptide 7 (CYP3A7) genes, complete cds; and cytochrome P450 polypeptide 5 (CYP3A5) gene, partial cds
5699	18794	31968	0.85	4.2E-02	AF280107.1	NT	Homo sapiens cytochrome P450 polypeptide 43 (CYP3A43) gene, partial cds; cytochrome P450 polypeptide 4 (CYP3A4) and cytochrome P450 polypeptide 7 (CYP3A7) genes, complete cds; and cytochrome P450 polypeptide 5 (CYP3A5) gene, partial cds
7175	18406	31205	0.73	4.2E-02	BE268285.1	EST_HUMAN	601124596F1 NIH_MGC_8 Homo sapiens cDNA clone IMAGE:288319 5'
7769	20722	34094	4.52	4.2E-02	AF276752.1	NT	Legionella pneumophila catalase-peroxidase (katA) gene, complete cds
7793	20745	34118	0.81	4.2E-02	AV730347.1	EST_HUMAN	AV730347 HTF Homo sapiens cDNA clone HTFAVH04 5'
9162	22128	35556	3.74	4.2E-02	P05095	SWISSPROT	ALPHA-ACTININ 3, NON MUSCULAR (F-ACTIN CROSS LINKING PROTEIN)
10525	23447	36845	1.19	4.2E-02	Q18650	SWISSPROT	T-BRAIN-1 PROTEIN (T-BOX BRAIN PROTEIN 1) (TBR-1) (TES-56)
11379	24328	37855	1.59	4.2E-02	AA976118.1	EST_HUMAN	on33b11.a1 NCI_CGAP_Lu5 Homo sapiens cDNA clone IMAGE:1558461 3' similar to gb:M65290
11637	24574	38138	2.65	4.2E-02	BE15822.1	EST_HUMAN	INTERLEUKIN-12 BETA CHAIN PRECURSOR (HUMAN);
11637	24574	38139	2.65	4.2E-02	BE15822.1	EST_HUMAN	PM3-BN0174-250500-009-d10 BN0174 Homo sapiens cDNA
12694	25908		5.02	4.2E-02	AI983494.1	EST_HUMAN	PM3-BN0174-250500-009-d10 BN0174 Homo sapiens cDNA
12990	25550		1.99	4.2E-02	D14711.1	NT	w49g10.x1 NCI_CGAP_Pan1 Homo sapiens cDNA clone IMAGE:2510850 3'
511	13582	26503	0.75	4.1E-02	AF200628.1	NT	Staphylococcus aureus HSP10 and HSP60 genes
2685	15681	28699	1.16	4.1E-02	AE002330.2	NT	Homo sapiens HPS1 gene, intron 5
4499	17524		7.84	4.1E-02	AW893484.1	EST_HUMAN	Chlamydia muridarum, section 60 of 85 of the complete genome
5302	18305	31166	0.82	4.1E-02	5902103	NT	QV1-NN0012-180400-164-r06 NN0012 Homo sapiens cDNA
5726	18820	31999	1.08	4.1E-02	BE251894.1	EST_HUMAN	Homo sapiens SRY (sex-determining region Y)-box 10 (SOX10), mRNA
5726	18820	32000	1.08	4.1E-02	BE251894.1	EST_HUMAN	601107535F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3343856 5'
7066	20088		0.9	4.1E-02	X75881.1	NT	601107535F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3343856 5'
7306	20277	33615	1.19	4.1E-02	AE002132.1	NT	A.thaliana mRNA for plasma membrane intrinsic protein 1a
7756	20709	34078	2	4.1E-02	7662347	NT	Ureaplasma urealyticum section 33 of 59 of the complete genome
							Homo sapiens KIAA0867 protein (KIAA0867), mRNA
7860	20804	34180	0.7	4.1E-02	L02110.1	NT	Mus musculus proviral retroviral insertion in the cGMP-phosphodiesterase (rd beta PDE) gene, intron 1, with the proviral insert encompassing the env pseudogene (3' end) and 3' LTR

Table 4

Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8042	20979	34375	2.63	4.1E-02	AF026198.1	NT	Fugu rubripes neural cell adhesion molecule L1 homolog (L1-CAM) gene, complete cds; putative protein 1 (PUT1) gene, partial cds; mitosis-specific chromosome segregation protein SMC1 homolog (SMC1) gene, complete cds; and calcium channel alpha-1 subunit
8549	21517	34935	0.58	4.1E-02	P07857	SWISSPROT	ADAM-TS 1 PRECURSOR (A DISINTEGRIN AND METALLOPROTEINASE WITH THROMBOSPONDIN MOTIFS 1) (ADAMTS-1) (ADAM-TS1)
8950	21956	35381	0.57	4.1E-02	P34687	SWISSPROT	GUTICLE COLLAGEN 34
9509	22472	35916	0.83	4.1E-02	AA372398.1	EST_HUMAN	EST84297 Colon adenocarcinoma IV Homo sapiens cDNA 5' end
13013	25909	31423	4.48	4.1E-02	AJ271809.1	NT	Brassica napus gln gene for plastid glutamine synthetase, exons 1-12
13102	25625	31679	1.33	4.1E-02	AF254922.1	NT	Homo sapiens SMARCA4 isoform (SMARCA4) gene, complete cds, alternatively spliced
1649	14881	27654	1.21	4.0E-02	AF675922.1	EST_HUMAN	wb98h01.x1 NCI_CGAP_P128 Homo sapiens cDNA clone IMAGE:2313745 3'
3258	16312	29233	2.57	4.0E-02	AB040904.1	NT	Homo sapiens mRNA for KIAA1471 protein, partial cds
5453	18555	31466	5.39	4.0E-02	AF280107.1	NT	Homo sapiens cytochrome P450 polypeptide 43 (CYP3A43) gene, partial cds; cytochrome P450 polypeptide 4 (CYP3A4) and cytochrome P450 polypeptide 7 (CYP3A7) genes, complete cds; and cytochrome P450 polypeptide 5 (CYP3A5) gene, partial cds
6339	19408	32649	1.43	4.0E-02	BF110434.1	EST_HUMAN	7n52h07.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3568380 3' similar to TR:O75296 O75296 R29124_1.:
7954	20895	34288	6.1	4.0E-02	L23838.1	NT	Strongylocentrotus purpuratus homolog of human bone morphogenetic protein 1 (submp) mRNA, complete cds
8028	20963	34376	0.58	4.0E-02	AL161535.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 35
8043	20980	34376	0.85	4.0E-02	AB000381.1	NT	Homo sapiens DNA for GPI-anchored molecule-like protein, complete cds
8043	20980	34377	0.85	4.0E-02	AB000381.1	NT	Homo sapiens DNA for GPI-anchored molecule-like protein, complete cds
9057	22033	35456	2.78	4.0E-02	P08640	SWISSPROT	GLUCOAMYLASE S1/S2 PRECURSOR (GLUCAN 1,4-ALPHA-GLUCOSIDASE) (1,4-ALPHA-D-GLUCAN GLUCOHYDROLASE)
10002	22929	36423	0.71	4.0E-02	BF679376.1	EST_HUMAN	602153884F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4294724 5'
10027	22954	36423	2.95	4.0E-02	AJ000941.1	NT	Methanobacterium thermoautotrophicum strain Marburg, Thiol fumarate reductase subunit A
10344	23268		0.92	4.0E-02	D43949.1	NT	Human mRNA for KIAA0092 gene, partial cds
12058	24941		1.48	4.0E-02	AJ001018.1	NT	Kluyveromyces fragilis gene for Ca++ ATPase
12331	25730	31614	3.52	4.0E-02	AJ001056.1	NT	Ovis aries mRNA for acetyl-coA carboxylase
1122	14166	27118	3.13	3.9E-02	BF516149.1	EST_HUMAN	UI-H-BW1-ans-h-08-0-JL:s1 NCI_CGAP_Sub7 Homo sapiens cDNA clone IMAGE:3084134 3'
1348	14383	27351	1.9	3.9E-02	P41047	SWISSPROT	FAS ANTIGEN LIGAND
1878	14959	28001	2.82	3.9E-02	AJ403386.1	NT	M.musculus DNA for desmin-binding fragment DesD7
2715	15709		2.12	3.9E-02	4508962	NT	Homo sapiens succinate dehydrogenase complex, subunit C, integral membrane protein, 15kD (SDHC) mRNA
5191	18200	31072	0.65	3.9E-02	AW392417.1	EST_HUMAN	RC6-ST0258-171199-021-C09 ST0258 Homo sapiens cDNA

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Table 4

Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5573	18669	31630	0.74	3.9E-02	D50608.1	NT	Rat gene for cholecystokinin type-A receptor (CCKAR), complete cds
5573	18669	31631	0.74	3.9E-02	D50608.1	NT	Rat gene for cholecystokinin type-A receptor (CCKAR), complete cds
5820	18910	32094	1.08	3.9E-02	BE988841.1	EST_HUMAN	601649874F1 NIH_MGC_74 Homo sapiens cDNA clone IMAGE:3933642 5'
5957	19042	32241	0.71	3.9E-02	BF675203.1	EST_HUMAN	602138132F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4274910 5'
7259	19994	33291	1.1	3.9E-02	BE271437.1	EST_HUMAN	601140729F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3049830 5'
8157	21105	34504	0.53	3.9E-02	P48778	SWISSPROT	ANTIGEN GOR
8172	21142	34548	1.07	3.9E-02	BF239613.1	EST_HUMAN	601906848F1 NIH_MGC_54 Homo sapiens cDNA clone IMAGE:4134779 5'
8395	21364	34772	0.63	3.9E-02	AJ229041.1	NT	Homo sapiens 959 kb contig between AML1 and CBR1 on chromosome 21q22; segment 1/3
8395	21364	34773	0.63	3.9E-02	AJ229041.1	NT	Homo sapiens 959 kb contig between AML1 and CBR1 on chromosome 21q22; segment 1/3
11737	21105	34504	1.61	3.9E-02	P48778	SWISSPROT	ANTIGEN GOR
12184	25872		14.17	3.9E-02	AB042553.1	NT	Felis catus G-CSF gene for granulocyte colony-stimulating factor, complete cds
12949	25784		5.15	3.9E-02	AL049866.2	NT	Mus musculus chromosome X contig; X-linked lymphocyte regulated 5 gene, Zinc finger protein 275, Zinc finger protein 82, mnx28orf
1969	14990	27993	1.13	3.8E-02	BE885137.1	EST_HUMAN	601510691F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3912215 5'
2129	15146		1.1	3.8E-02	AJ251973.1	NT	Homo sapiens partial steerin-1 gene
4906	17923	30815	0.92	3.8E-02	BE393275.1	EST_HUMAN	601308488F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3626757 5'
4906	17923	30816	0.92	3.8E-02	BE393275.1	EST_HUMAN	601308488F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3626757 5'
4965	17980	30870	1.4	3.8E-02	AU124122.1	EST_HUMAN	AU124122 NT2RM2 Homo sapiens cDNA clone NT2RM2001698 5'
5515	18615	31548	1.2	3.8E-02	M11228.1	NT	Human protein C gene, complete cds
6206	19280	32513	1.04	3.8E-02	P10284	SWISSPROT	HOMEOBOX PROTEIN HOX-B4 (HOX-2.6)
7540	20503	33862	1.43	3.8E-02	6005700	NT	Homo sapiens ATP-binding cassette, sub-family A (ABC1), member 8 (ABCA8), mRNA
9011	21977		1.26	3.8E-02	M60675.1	NT	Human von Willebrand factor gene, exons 23 through 34
11014	23979	37505	2.04	3.8E-02	AF143952.2	NT	Homo sapiens PELOTA (PELOTA) gene, complete cds
12009	24886	38481	1.53	3.8E-02	P01641	SWISSPROT	IG KAPPA CHAIN V-V REGION MOPC 173B PRECURSOR
12009	24886	38482	1.53	3.8E-02	P01641	SWISSPROT	IG KAPPA CHAIN V-V REGION MOPC 173B PRECURSOR
994	14045	26999	4.76	3.7E-02	P19137	SWISSPROT	LAMININ ALPHA-1 CHAIN PRECURSOR (LAMININ A CHAIN)
1389	14423	27392	0.96	3.7E-02	L14591.1	NT	Homo sapiens plasma membrane calcium ATPase isoform 1 (ATP2B1) gene, alternative splice products, partial cds
2246	15260	28287	4.98	3.7E-02	AJ884806.1	EST_HUMAN	vr85e08.x1 NC1_OGAP_Kid11 Homo sapiens cDNA clone IMAGE:2494502 3'
3063	16120	29034	1.27	3.7E-02	P79944	SWISSPROT	EOMESODERMIN
3065	16122	29035	4.14	3.7E-02	BF312663.1	EST_HUMAN	601896233F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4125584 5'
3468	16514		1.03	3.7E-02	6680541	NT	Mus musculus potassium large conductance pH-sensitive channel, subfamily M, alpha member 3 (Kcma3), mRNA
5279	18285	31148	0.76	3.7E-02	AF168106.1	NT	Bubo virginianus cytochrome b gene, partial cds; mitochondrial gene for mitochondrial product

Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7281	25998		0.79	3.7E-02	AF000093.1	NT	Aeropyrum pernix genomic DNA, section 87
7956	20897	34290	0.84	3.7E-02	AE003975.1	NT	Xylella fastidiosa, section 121 of 229 of the complete genome
10375	23288		0.98	3.7E-02	AA782516.1	EST_HUMAN	ai55c09.s1 Soares_papathroid_tumor_NHHPA Homo sapiens cDNA clone 1360912 3'
12225	25051	38628	5.94	3.7E-02	BF124974.1	EST_HUMAN	601762117F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:4024973 5'
12883	25782	31520	2.34	3.7E-02	11418392	NT	Homo sapiens solute carrier family 22 (organic cation transporter), member 1 (SLC22A1), mRNA
3667	16710	29625	1.04	3.6E-02	X73221.1	NT	H. vulgare Sst1 gene for sucrose synthase
3674	16717	29631	0.75	3.6E-02	AL096806.1	NT	Homo sapiens genomic region containing hypervariable minisatellites chromosome 10(10q26.3) of Homo sapiens
5253	18261	31130	2.27	3.6E-02	AL096810.1	NT	Homo sapiens genomic region containing hypervariable minisatellites chromosome 10(10q26.3) of Homo sapiens
5501	18601	31514	0.8	3.6E-02	X59403.1	NT	C. glutamicum gap, pgk and tpi genes for glyceraldehyde-3-phosphate, phosphoglycerate kinase and triosephosphate isomerase
5501	18601	31530	0.8	3.6E-02	X59403.1	NT	C. glutamicum gap, pgk and tpi genes for glyceraldehyde-3-phosphate, phosphoglycerate kinase and triosephosphate isomerase
5578	18874	31638	0.68	3.6E-02	AF181722.1	NT	Homo sapiens R2AS (R2) mRNA, complete cds
6865	19918	33212	4.97	3.6E-02	AW945516.1	EST_HUMAN	CM2-EN0013-110500-192-b10 EN0013 Homo sapiens cDNA
6865	19918	33213	4.97	3.6E-02	AW945516.1	EST_HUMAN	CM2-EN0013-110500-192-b10 EN0013 Homo sapiens cDNA
7150	18382	31270	0.5	3.6E-02	U67575.1	NT	Methanococcus jannaschii section 117 of 160 of the complete genome
7291	20263	33597	1.7	3.6E-02	AF025952.1	NT	Chromatium vinosum sulfur globule protein Cx2 precursor (sgp2) gene, complete cds
7527	20491	33853	2.75	3.6E-02	AA714521.1	EST_HUMAN	nm20e05.s1 NCI_CGAP_GCB0 Homo sapiens cDNA clone IMAGE:1241024 3' similar to gb:J00314_ma2
7895	20838	34218	1.08	3.6E-02	BE143078.1	EST_HUMAN	TUBULIN BETA-1 CHAIN (HUMAN);
9746	22687	36142	1.85	3.6E-02	U20608.1	NT	MRO-HT0158-030200-003-b08 HT0158 Homo sapiens cDNA
9746	22687	36143	1.85	3.6E-02	U20608.1	NT	Dictpostellum discoidium unknown spore germination-specific protein-like protein, orf1, orf2 and orf3 genes, complete cds
9971	22898	36361	0.68	3.6E-02	BF347686.1	EST_HUMAN	802020463F1 NCI_CGAP_Bn67 Homo sapiens cDNA clone IMAGE:4156116 5'
896	13951	26909	0.9	3.5E-02	U09506.1	NT	Drosophila melanogaster tiggerin mRNA, complete cds
1010	14059	27011	1.38	3.5E-02	AF263417.1	NT	Homo sapiens microsomal epoxide hydrolase (EPHX1) gene, complete cds
1566	14599	27574	1.3	3.5E-02	BF678085.1	EST_HUMAN	602085136F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4249377 5'
1566	14599	27575	1.3	3.5E-02	BF678085.1	EST_HUMAN	602085136F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4249377 5'
4241	17270	30155	1.95	3.5E-02	AE001773.1	NT	Thermococcus maritima section 85 of 136 of the complete genome
4344	17371	30253	3.67	3.5E-02	P53780	SWISSPROT	CYSTATHIONINE BETA-LYASE PRECURSOR (CBL) (BETA-CYSTATHIONASE) (CYSTEINE LYASE)

Table 4

Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5265	18273		1.04	3.5E-02	P47144	SWISSPROT	HYPOTHETICAL 80.7 KD PROTEIN IN SOD1-CPA2 INTERGENIC REGION
6347	19416	32857	1.74	3.5E-02	J01238.1	NT	Maize actin 1 gene (MAc1), complete cds
8310	21279		0.78	3.5E-02	H29951.1	EST_HUMAN	yp44a05.r1 Soares retina N255HR Homo sapiens cDNA clone IMAGE:180256 5' similar to cortals Alu repetitive element;
8970	21936	35362	2.87	3.5E-02	BE988970.1	EST_HUMAN	601644701R2 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:3928737 3'
10378	23301	36777	1.99	3.5E-02	X76642.1	NT	Lactis MG1363 grPE and dnaK genes
10425	23347	36832	0.47	3.5E-02	BE581042.1	EST_HUMAN	601344861F1 NIH_MGC_8 Homo sapiens cDNA clone IMAGE:3677654 5'
11823	24706	38288	1.61	3.5E-02	AW681641.1	EST_HUMAN	PM1-CT0326-291289-002-103 CT0326 Homo sapiens cDNA
11823	24706	38289	1.61	3.5E-02	AW681641.1	EST_HUMAN	PM1-CT0326-291289-002-103 CT0326 Homo sapiens cDNA
12877	25806		5.77	3.5E-02	BE276948.1	EST_HUMAN	601178755F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3543833 5'
580	13849	26562	0.91	3.4E-02	AK024424.1	NT	Homo sapiens mRNA for FLJ00013 protein, partial cds
580	13849	26563	0.91	3.4E-02	AK024424.1	NT	Homo sapiens mRNA for FLJ00013 protein, partial cds
581	13849	26562	3.42	3.4E-02	AK024424.1	NT	Homo sapiens mRNA for FLJ00013 protein, partial cds
581	13849	26563	3.42	3.4E-02	AK024424.1	NT	Homo sapiens mRNA for FLJ00013 protein, partial cds
1053	14099	27049	2.4	3.4E-02	AW274020.1	EST_HUMAN	xc26d07.x1 Soares NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2814253 3' similar to SW:C211_HUMAN P83801 PUTATIVE SURFACE GLYCOPROTEIN C21ORF1 PRECURSOR;
1211	14249		6.51	3.4E-02	11345459	NT	Homo sapiens hypothetical protein FLJ13220 (FLJ13220), mRNA
2401	15408	28432	2.61	3.4E-02	T57160.1	EST_HUMAN	yc20d06.r1 Stragene lung (#937210) Homo sapiens cDNA clone IMAGE:81250 5' similar to contains MER29 repetitive element
3444	18491	29410	1.19	3.4E-02	AL163208.2	NT	Homo sapiens chromosome 21 segment HS21C008
3942	16982	29897	3.71	3.4E-02	AW794952.1	EST_HUMAN	RC8-UM0015-210200-021-A10 UM0015 Homo sapiens cDNA
4628	17849	30537	3.06	3.4E-02	X59789.1	NT	M.musculus S-antigen gene promoter region
5100	18110		2.48	3.4E-02	Q28457	SWISSPROT	LA PROTEIN HOMOLOG (LA RIBONUCLEOPROTEIN) (LA AUTOANTIGEN HOMOLOG)
5114	18124	30899	1.93	3.4E-02	AJ012469.1	NT	Caenorhabditis elegans mRNA for DYS-1 protein, partial
6330	19400		0.63	3.4E-02	BF131628.1	EST_HUMAN	601820445F1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:4052434 5'
7032	19364	31251	3.97	3.4E-02	U24393.1	NT	Human lysyl oxidase-like protein gene, exon 3
8604	21572		3.14	3.4E-02	A1888929.1	EST_HUMAN	w199d04.x1 NCJ_CGAP_Brn25 Homo sapiens cDNA clone IMAGE:2433031 3'
9100	22068	35492	1.56	3.4E-02	AA684886.1	EST_HUMAN	nu70f08.s1 NCJ_CGAP_Alv1 Homo sapiens cDNA clone IMAGE:1216071 similar to contains Alu repetitive element; contains element MER25 MER25 repetitive element;
							zq04f11.s1 Stragene muscle 937208 Homo sapiens cDNA clone IMAGE:628749 3' similar to TR:G1017425 G1017425
9268	22234		6.2	3.4E-02	AA194906.1	EST_HUMAN	IPISGKPLPKVTLNRDGVPLKATMRPNTAENLTNLKESVTADAGRYEITANSSGTTKAFINIVLDRPG
10136	23062		0.84	3.4E-02	A1092719.1	EST_HUMAN	PPT GPVVISDITEESVTLKWEPPKYDGGQVNTYLLKRETSVAVWTEVSATVARTMMKVMKL ...;
							ca29h08.x1 Soares parathyroid_tumor_NHHPA Homo sapiens cDNA clone IMAGE:1883519 3'

Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
372	13458		9.24	3.3E-02	AA398735.1	EST_HUMAN	z75e08.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:728198 3'
1171	14212	27166	14.49	3.3E-02	AB038897.1	NT	Cricetulus griseus CYP2A17 mRNA for cytochrome P450 2A17, complete cds
1645	14677	27650	1.73	3.3E-02	AF110783.1	NT	Homo sapiens skeletal muscle LIM-protein 1 (FHL1) gene, complete cds
1753	14782		1.29	3.3E-02	AE000700.1	NT	Aquifex aeolicus section 32 of 109 of the complete genome
2096	15113		1.76	3.3E-02	R09112.1	EST_HUMAN	y25c09.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:127888 5'
2458	15462	28485	1.31	3.3E-02	6755862	NT	Mus musculus tumor rejection antigen gp96 (Tra1), mRNA
3372	16422	29347	8.85	3.3E-02	H02389.1	EST_HUMAN	y35h02.r1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:150771 5'
4206	14677	27650	2.36	3.3E-02	AF110783.1	NT	Homo sapiens skeletal muscle LIM-protein 1 (FHL1) gene, complete cds
4494	17516	30407	1.81	3.3E-02	6755862	NT	Mus musculus tumor rejection antigen gp96 (Tra1), mRNA
4848	17865	30759	0.86	3.3E-02	AW275696.1	EST_HUMAN	xp40b04.x1 NCI_CGAP_HN11 Homo sapiens cDNA clone IMAGE:2742799 3'
6570	19630	32896	20.14	3.3E-02	BF245995.1	EST_HUMAN	601853910F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4073787 5'
6570	19630	32897	20.14	3.3E-02	BF245995.1	EST_HUMAN	601853910F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4073787 5'
9677	22630	36084	0.71	3.3E-02	BF115621.1	EST_HUMAN	7m92b04.x1 NCI_CGAP_Bm23 Homo sapiens cDNA clone IMAGE:3562423 3'
9677	22630	36085	0.71	3.3E-02	BF115621.1	EST_HUMAN	7m92b04.x1 NCI_CGAP_Bm23 Homo sapiens cDNA clone IMAGE:3562423 3'
9779	22720	36174	0.72	3.3E-02	AA488202.1	EST_HUMAN	ad08f09.s1 Soares NBHFB Homo sapiens cDNA clone IMAGE:877673 3' similar to gb:X70944_cds1
9779	22720	36175	0.72	3.3E-02	AA488202.1	EST_HUMAN	ad08f09.s1 Soares NBHFB Homo sapiens cDNA clone IMAGE:877673 3' similar to gb:X70944_cds1
10964	23884		0.46	3.3E-02	H38108.1	EST_HUMAN	yp51f11.s1 Soares retina N2b4HR Homo sapiens cDNA clone IMAGE:190989 3'
11455	24398	37845	2.47	3.3E-02	BF691107.1	EST_HUMAN	60224717F1 NIH_MGC_62 Homo sapiens cDNA clone IMAGE:4332497 5'
12425	25193		3.71	3.3E-02	T96545.1	EST_HUMAN	ye49f11.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:121101 5'
12547	25270		1.69	3.3E-02	AF289665.1	NT	Mus musculus EIF4H gene, partial cds; LIMK1 gene, complete cds; and ELN gene, partial cds
12577	25286		3.04	3.3E-02	M81800.1	NT	Human Interleukin 11 (IL11) gene, complete mRNA
132	13237	26168	1.27	3.2E-02	AJ002005.1	NT	Oryctolagus cuniculus gene encoding ileal sodium-dependent bile acid transporter
1128	14171	27122	10.01	3.2E-02	AF098275.1	NT	Drosophila melanogaster heat shock protein 68 (hsp68) gene, hsp68 allele, complete cds
1128	14171	27123	10.01	3.2E-02	AF098275.1	NT	Drosophila melanogaster heat shock protein 68 (hsp68) gene, hsp68 allele, complete cds
2127	15144		3.6	3.2E-02	P28955	SWISSPROT	LARGE TEGUMENT PROTEIN
3151	16208	29122	9.61	3.2E-02	BE967353.1	EST_HUMAN	601442431F1 NIH_MGC_69 Homo sapiens cDNA clone IMAGE:3846727 5'
4246	17275		16.99	3.2E-02	X94788.1	NT	H. sapiens RP3 gene (XLRP gene 3)
4801	17818	30712	3.75	3.2E-02	AF114182.1	NT	Sadfraga nidifica maturase (matK) gene, chloroplast gene encoding chloroplast protein, partial cds
5303	18306		1.34	3.2E-02	Y08924.1	NT	P. falciparum mRNA for AARP2 protein
5613	18709	31866	1.56	3.2E-02	X68709.1	NT	S. griseocarinum whiG-Stv gene
5613	18709	31867	1.56	3.2E-02	X68709.1	NT	S. griseocarinum whiG-Stv gene

Table 4
Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6673	19730	33008	2.23	3.2E-02	M32437.1	NT	Rat polyomavirus left junction in cell line W98.14
6676	19733		30.53	3.2E-02	T89387.1	EST_HUMAN	y433h12.s1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:110087 3' similar to contains Alu repetitive element; contains LTR1 repetitive element;
6783	19817	33097	4.01	3.2E-02	AF173845.1	NT	Sagittaria oedipus tissue kallikrein gene, complete cds
8039	20976	34372	0.82	3.2E-02	11424049	NT	Homo sapiens cytochrome P450, subfamily 1B (phenobarbital-inducible) (CYP2B), mRNA
8843	21611	36033	2.84	3.2E-02	6680565	NT	Mus musculus kinesin family member 3c (Kif3c), mRNA
9283	22259		0.7	3.2E-02	AF109718.1	NT	Homo sapiens chromosome 3 subtelomeric region
9580	22542	35992	1.02	3.2E-02	AI278971.1	EST_HUMAN	qm17b04.x1 NCL CGAP_Lu5 Homo sapiens cDNA clone IMAGE:1882063 3'
9580	22542	35993	1.02	3.2E-02	AI278971.1	EST_HUMAN	qm17b04.x1 NCL CGAP_Lu5 Homo sapiens cDNA clone IMAGE:1882063 3'
10417	23339		4.18	3.2E-02	AA179795.1	EST_HUMAN	zg54b12.s1 Soares_pineal_gland_N3HPG Homo sapiens cDNA clone IMAGE:397151 3' similar to gb:U08441 CYTOCHROME C OXIDASE POLYPEPTIDE III (HUMAN);
10723	23845	37138	0.98	3.2E-02	U96762.1	NT	Macaca mulatta chemokine receptor COR5 mRNA, complete cds
12812	25978		1.43	3.2E-02	V00574.1	NT	Human germ line gene homologous to bladder carcinoma oncogene T24 (Gene code c-Ha-ras-1) with four exons
1285	14300		2.28	3.1E-02	4503416	NT	Homo sapiens dual specificity phosphatase 4 (DUSP4) mRNA
1308	14344	27309	1.67	3.1E-02	P18845	SWISSPROT	NEURONAL ACETYLCHOLINE RECEPTOR PROTEIN, ALPHA-3 CHAIN PRECURSOR (GF-ALPHA-3)
1909	14933	27929	1	3.1E-02	6671564	NT	Mus musculus adaptor-related protein complex AP-3, delta subunit (Ap3d), mRNA
1991	16012		1.18	3.1E-02	Z50097.1	NT	Drosophila melanogaster mRNA for headcase protein
5336	18441	31194	1.28	3.1E-02	U78104.1	NT	Human leukemia inhibitory factor receptor (LIFR) gene, promoter and partial exon 1
5434	18536		2.28	3.1E-02	AA278478.1	EST_HUMAN	zs81a06.r1 NCL CGAP_G08T Homo sapiens cDNA clone IMAGE:703858 5'
5731	18825	32005	0.81	3.1E-02	BF687742.1	EST_HUMAN	602068783.F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4065789 5'
5803	25945	32078	0.52	3.1E-02	AJ391284.1	NT	Neisseria meningitidis DNA for region 2 (flaB- and flaC-homologs, unknown genes) and flanking genes, strain FAM18
10391	23313	36793	2.55	3.1E-02	AF034779.1	NT	Enterococcus faecalis surface protein precursor, gene, complete cds
1627	14860		2.21	3.0E-02	AF187125.1	NT	Pityoketines minutus cytochrome oxidase I gene, partial cds; mitochondrial gene for mitochondrial product z66h03.r1 Soares_fetal_liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:727253 5'
2590	15591	28508	0.97	3.0E-02	AA402242.1	EST_HUMAN	Saccharomyces cerevisiae stem-loop mutation suppressor SSL2 gene, complete cds
3579	16524	29545	0.91	3.0E-02	M64176.1	NT	Pseudomonas fluorescens family II aminotransferase gene, complete cds
3666	16709	29624	2.77	3.0E-02	AF247844.1	NT	QV2-ST0286-150200-040-e09 ST0286 Homo sapiens cDNA
3758	18789		0.98	3.0E-02	AW620223.1	EST_HUMAN	EST74530 Pineal gland II Homo sapiens cDNA
3669	17009		1.45	3.0E-02	AA364003.1	EST_HUMAN	Homo sapiens neuropilin 2 (NRP2) gene, complete cds, alternatively spliced
5092	18102	30977	7.41	3.0E-02	AF281074.1	NT	Homo sapiens neuropilin 2 (NRP2) gene, complete cds, alternatively spliced
5092	18102	30978	7.41	3.0E-02	AF281074.1	NT	Homo sapiens neuropilin 2 (NRP2) gene, complete cds, alternatively spliced
5485	18567		2.99	3.0E-02	AB046793.1	NT	Homo sapiens mRNA for KIAA1573 protein, partial cds

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6383	19451	32693	0.58	3.0E-02	N99615.1	EST_HUMAN	z39a10.1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:294908 5' similar to contains element TAR1 repetitive element;
6383	19451	32694	0.58	3.0E-02	N99615.1	EST_HUMAN	z39a10.1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:294908 5' similar to contains element TAR1 repetitive element;
6957	20182	33505	3.17	3.0E-02	AJ242906.1	NT	Cyprinid carp mRNA for inducible nitric oxide synthase (NOS gene)
7091	20025	33327	2.8	3.0E-02	BE889948.1	EST_HUMAN	601512206F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3913848 5'
7091	20025	33328	2.8	3.0E-02	BE889948.1	EST_HUMAN	601512206F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3913848 5'
7274	20009	33310	2.29	3.0E-02	AF213884.1	NT	Homo sapiens nuclear factor of kappa light polypeptide gene enhancer in B-cells 1 (NFKB1) gene, complete cds
7274	20009	33311	2.29	3.0E-02	AF213884.1	NT	Homo sapiens nuclear factor of kappa light polypeptide gene enhancer in B-cells 1 (NFKB1) gene, complete cds
7442	20408	33760	1.29	3.0E-02	M86624.1	NT	Human dystrophin gene
7836	20783		0.76	3.0E-02	BF246361.1	EST_HUMAN	601854981F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4074548 5'
8463	21432		0.48	3.0E-02	BF679706.1	EST_HUMAN	602154364F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4285654 5'
8988	21954	35378	0.74	3.0E-02	BF353889.1	EST_HUMAN	IL5-HT0704-280600-108-c04 HT0704 Homo sapiens cDNA
9145	22111		1.62	3.0E-02	AF275654.1	NT	Ornithorhynchus anatinus coagulation factor X mRNA, complete cds
10828	23747	37248	1.66	3.0E-02	AE001797.1	NT	Thermotoga maritima section 109 of 136 of the complete genome
11596	24506	38063	2.36	3.0E-02	M81357.1	NT	Human coagulation factor VII (F7) gene exon 1 and factor X (F10) gene, exon 1
11997	24874	38470	7.84	3.0E-02	AA483216.1	EST_HUMAN	ne87f04.s1 NCL CGAP_Kid1 Homo sapiens cDNA clone IMAGE:911283
12528	25960	31316	2.02	3.0E-02	R32019.1	EST_HUMAN	Yh63d04.s1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:134407 3'
12868	25470		2.06	3.0E-02	AW895585.1	EST_HUMAN	QV4-NN0038-270400-187-r05 NN0038 Homo sapiens cDNA
12908	25954		1.96	3.0E-02	AF048887.1	NT	Rattus norvegicus UDP-Galactose 4-epimerase beta-1,4-galactosyltransferase mRNA, complete cds
2442	15893	28467	1	2.9E-02	AF228703.1	NT	Homo sapiens mitochondrial glutathione reductase and cytosolic glutathione reductase (GRD1) gene, complete cds, alternatively spliced
3005	16063	28982	1.14	2.9E-02	BE565844.1	EST_HUMAN	601338428F1 NIH_MGC_53 Homo sapiens cDNA clone IMAGE:3680695 5'
3005	16063	28983	1.14	2.9E-02	BE565844.1	EST_HUMAN	601338428F1 NIH_MGC_53 Homo sapiens cDNA clone IMAGE:3680695 5'
3573	16618	29540	0.8	2.9E-02	X55284.1	NT	Sheep gene for ultra high-sulphur keratin protein
3950	16990	29908	0.72	2.9E-02	H72805.1	EST_HUMAN	yao7e10.1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:233130 5'
6181	19256	32489	1.13	2.9E-02	AF060221.1	NT	Sus scrofa deoxyribonuclease II mRNA, complete cds
6424	19491	32743	7.33	2.9E-02	BF032233.1	EST_HUMAN	601452661F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3856598 5'
7142	20118	33431	0.52	2.9E-02	AJ391284.1	NT	Neisseria meningitidis DNA for region 2 (thaB- and thaC-homologs, unknown genes) and flanking genes, strain FAM18
7460	20426	33752	10.95	2.9E-02	BE271437.1	EST_HUMAN	601140729F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3049830 5'

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Table 4
Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7657	20817	33982	0.67	2.9E-02	D29214.1	EST_HUMAN	HUMNK262 Human epidermal keratinocyte Homo sapiens cDNA clone 262
8169	21107	34506	0.53	2.9E-02	AE003932.1	NT	Xyella fastidiosa, section 78 of 229 of the complete genome
8331	21300	34716	0.83	2.9E-02	AF129279.1	NT	Buchnera aphidicola natural-host Schlectendallia chinensis gluconate-6-phosphate dehydrogenase (gnd) gene, partial cds
8331	21300	34717	0.83	2.9E-02	AF129279.1	NT	Buchnera aphidicola natural-host Schlectendallia chinensis gluconate-6-phosphate dehydrogenase (gnd) gene, partial cds
10016	22943	36409	2.26	2.9E-02	AW875979.1	EST_HUMAN	CM3-PT0014-071299-051-04 PT0014 Homo sapiens cDNA
10016	22943	36410	2.26	2.9E-02	AW875979.1	EST_HUMAN	CM3-PT0014-071299-051-04 PT0014 Homo sapiens cDNA
10233	23159		0.67	2.9E-02	AW976597.1	EST_HUMAN	EST388706 MAGE resequences, MAGN Homo sapiens cDNA
10710	23632	37127	1.07	2.9E-02	AP000064.1	NT	Aeropyrum pernix genomic DNA, section 777
11388	16618	29540	1.6	2.9E-02	X55294.1	NT	Sheep gene for ultra high-sulphur keratin protein
12531	25870		1.48	2.9E-02	AU135817.1	EST_HUMAN	AU13817 PLACE1 Homo sapiens cDNA clone PLACE1002962 5'
567	13637		1.93	2.8E-02	AW970153.1	EST_HUMAN	EST382234 MAGE resequences, MAGN Homo sapiens cDNA
3380	16429	29355	1.27	2.8E-02	AF066063.1	NT	Homo sapiens retinal fascic (FSCN2) gene, exon 2
3380	16429	29356	1.27	2.8E-02	AF066063.1	NT	Homo sapiens retinal fascic (FSCN2) gene, exon 2
4341	17368		0.67	2.8E-02	8393751	NT	Rattus norvegicus microtubule-associated protein tau (Mapt), mRNA
5206	18215	31090	3.2	2.8E-02	N87073.1	EST_HUMAN	L2083F Human fetal heart, Lambda ZAP Express Homo sapiens cDNA clone L2083 5' similar to TRNA-GUANINE TRANSGLYCOSYLASE
5294	18299		0.93	2.8E-02	M58493.1	NT	Dengue virus type 2 non-structural protein 1 (NS1) gene, partial cds
5565	18662	31622	10.89	2.8E-02	BE741083.1	EST_HUMAN	601594078F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3948067 5'
6981	20204	33533	1.13	2.8E-02	T78960.1	EST_HUMAN	yd21b08.r1 Soares fetal liver spleen 1NFL3 Homo sapiens cDNA clone IMAGE:108855 5'
8671	21639	35063	2.24	2.8E-02	AJ005820.1	NT	Craterosigma plantagineum mRNA for homeodomain leucine zipper protein (hb-1)
9371	22336	35766	0.82	2.8E-02	AA260762.1	EST_HUMAN	z396c06.r1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:711466 5'
9563	22525	35974	1.03	2.8E-02	AF187672.1	NT	Cavia porcellus inwardly-rectifying potassium channel Kir2.1 (KCNJ2) gene, complete cds
9667	22620	36071	0.71	2.8E-02	AE001092.1	NT	Archaeoglobus fulgidus section 15 of 172 of the complete genome
10980	23900	37413	0.42	2.8E-02	BF527244.1	EST_HUMAN	602039477F2 NCI_CGAP_Bm67 Homo sapiens cDNA clone IMAGE:4177267 5'
12809	29801		1.6	2.8E-02	R08966.1	EST_HUMAN	yf12h02.r1 Soares fetal liver spleen 1NFL3 Homo sapiens cDNA clone IMAGE:126675 5'
12815	25438		1.57	2.8E-02	X06322.1	NT	Yeast CN31C chromosome III RAHS DNA (right arm transcription hot-spot)
							Human germline T-cell receptor beta chain Dopamine-beta-hydroxylase-like, TRY1, TRY2, TRY3, TORBV27S1P, TORBV22S1A2N1T, TORBV6S1A1T, TORBV7S1A1N2T, TORBV5S1A1T, TORBV5S1A1T, TORBV5S7P, TORBV7S2A2T, TORBV13S2A1T, TORBV6S2A2PT, TORBV7S2A1N4T, TORBV13S9/13S>
1485	14518	27491	1.07	2.7E-02	U66059.1	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 6
3445	16492	29411	1.88	2.7E-02	AL161494.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 6
4230	17259	30143	2.01	2.7E-02	N47258.1	EST_HUMAN	y98h12.r1 Soares multiple sclerosis 2NBHMSHP Homo sapiens cDNA clone IMAGE:280487 5'

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Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4230	17256	30144	2.01	2.7E-02	N47258.1	EST_HUMAN	y86h12.r1 Soares_multiple_sclerosis_2NbHMSP Homo sapiens cDNA clone IMAGE:280487 5'
5319	18425	31176	0.52	2.7E-02	BF245672.1	EST_HUMAN	60186481F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4083075 5'
5516	18616	31549	1.09	2.7E-02	R12245.1	EST_HUMAN	y33d09.r1 Soares fetal liver spleen 1NPLS Homo sapiens cDNA clone IMAGE:128657 5' similar to SP-JC2284 JC2284 TISSUE FACTOR PATHWAY INHIBITOR - RHESUS ;
6005	19038	32288	0.68	2.7E-02	X61670.1	NT	T.aestivum pTTH20 mRNA for wheat type V thionin
6087	19187	32379	0.51	2.7E-02	AB004799.1	NT	Oryza sativa mRNA for ascorbate oxidase, partial cds
6754	19808		1.03	2.7E-02	X97580.1	NT	A.bisporus pgkA gene
7289	20004	33304	1.93	2.7E-02	AA993571.1	EST_HUMAN	096h03.s1 Soares_total_fetus_Nb2HF8_9w Homo sapiens cDNA clone IMAGE:1624661 3'
8140	21077		0.53	2.7E-02	AK024456.1	NT	Homo sapiens mRNA for FLJ00048 protein, partial cds
8160	21098	34497	0.59	2.7E-02	9256542	NT	Mus musculus G21 protein (G21), mRNA
8697	21665		1.23	2.7E-02	A1377036.1	EST_HUMAN	tc28g08.x1 Soares_total_fetus_Nb2HF8_9w Homo sapiens cDNA clone IMAGE:2065982 3' similar to contains Alu repetitive element;
573	13642	26556	1.25	2.6E-02	AL163282.2	NT	Homo sapiens chromosome 21 segment HS21C082
2374	15382	28404	2.54	2.6E-02	AA490021.1	EST_HUMAN	ab02b02.s1 Stralagene fetal retina 937202 Homo sapiens cDNA clone IMAGE:839595 3'
2376	15384	28406	3.05	2.6E-02	6754241	NT	Mus musculus histidine rich calcium binding protein (Hrc), mRNA
2376	15384	28407	3.05	2.6E-02	6754241	NT	Mus musculus histidine rich calcium binding protein (Hrc), mRNA
2926	15934		1.52	2.6E-02	AF109906.1	NT	Mus musculus MHC class III region RD gene, partial cds; Bf, C2, G9A, NG22, G9, HSP70, HSP70, HSC70;
3988	17028		0.91	2.6E-02	AW181045.1	EST_HUMAN	and snRNP genes, complete cds; G7A gene, partial cds; and unknown genes
4942	17858	30848	3.25	2.6E-02	L12032.1	NT	x165i09.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2662409 3'
5104	18114	30987	1.8	2.6E-02	AE002014.1	NT	Chicken dorsalin-1 mRNA, complete cds
5128	18137	31014	3.05	2.6E-02	AW241154.1	EST_HUMAN	Deinococcus radiodurans R1 section 151 of 229 of the complete chromosome 1
5944	19030		0.6	2.6E-02	AL161563.2	NT	Q15041 HYPOTHETICAL PROTEIN KIAA0069 ;
5992	19076		0.55	2.6E-02	AL161563.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 63
6345	19414		6.36	2.6E-02	AL206030.1	EST_HUMAN	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 63
6565	19625	32890	1.88	2.6E-02	BE621748.1	EST_HUMAN	gg27f11.x1 NCL_CGAP_K1d3 Homo sapiens cDNA clone IMAGE:1762317 3'
7001	20127	33441	0.82	2.6E-02	Z99084.1	NT	601493473T1 NIH_MGC_70 Homo sapiens cDNA clone IMAGE:3895578 3'
7001	20127	33442	0.82	2.6E-02	Z99084.1	NT	Vaccinia virus ORF1L strain Wyeth
7095	20029	33333	6.03	2.6E-02	6981271	NT	Vaccinia virus ORF1L strain Wyeth
7516	20481	33842	0.55	2.6E-02	P21894	SWISSPROT	Rattus norvegicus Nerve growth factor receptor, fast (Ngfr), mRNA
8950	21817	35237	0.71	2.6E-02	AA860946.1	EST_HUMAN	ALANYL-TRNA SYNTHETASE (ALANINE-TRNA LIGASE) (ALARS)
9715	22743	36104	1.27	2.6E-02	11432020	NT	ak22f04.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1406719 3'
							Homo sapiens KIAA1070 protein (KIAA1070), mRNA

Table 4

Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10072	22999	38468	0.7	2.6E-02	AF114952.1	NT	Saccharomyces dairenensis NRRL Y-12639(T) ATP synthase subunit 9 (ATP9) gene, mitochondrial gene encoding mitochondrial protein, complete cds
10072	22999	36469	0.7	2.6E-02	AF114952.1	NT	Saccharomyces dairenensis NRRL Y-12639(T) ATP synthase subunit 9 (ATP9) gene, mitochondrial gene encoding mitochondrial protein, complete cds
10768	23689	37186	4.31	2.6E-02	AL163303.2	NT	Homo sapiens chromosome 21 segment HS21C103
11717	24980		2.02	2.6E-02	AA279351.1	EST_HUMAN	zs84c02.f1 NCL CGAP_GC81 Homo sapiens cDNA clone IMAGE:704162 5'
11889	24770	38359	1.61	2.6E-02	AA279351.1	EST_HUMAN	U14F-BNO-akf-e-10-Q-U1.r NIH_MGC_50 Homo sapiens cDNA clone IMAGE:3077466 5'
12457	25944	31313	1.96	2.6E-02	BF343827.1	EST_HUMAN	602015501F1 NCL CGAP_Bm64 Homo sapiens cDNA clone IMAGE:4150944 5'
533	13604	26522	1.86	2.5E-02	A1793130.1	EST_HUMAN	on26f06.y5 NCL CGAP_Lu5 Homo sapiens cDNA clone IMAGE:1557827 5'
533	13604	26523	1.85	2.5E-02	A1793130.1	EST_HUMAN	on26f06.y5 NCL CGAP_Lu5 Homo sapiens cDNA clone IMAGE:1557827 5'
810	13668	26817	9.19	2.5E-02	BE974314.1	EST_HUMAN	601680308R2 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:3950665 3'
870	13926	26884	6.9	2.5E-02	BE974314.1	EST_HUMAN	601680308R2 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:3950665 3'
2773	15765		2.26	2.5E-02	U12571.1	NT	Rattus norvegicus rapthillin-3A mRNA, complete cds
2968	16028	28949	3.43	2.5E-02	X99697.1	NT	H. carterae mRNA for fucoxanthin chlorophyll a/c binding protein, Fcp1
2968	16028	28950	3.43	2.5E-02	X99697.1	NT	H. carterae mRNA for fucoxanthin chlorophyll a/c binding protein, Fcp1
4075	18316	30005	1.02	2.5E-02	BE701165.1	EST_HUMAN	PM2-NN0128-080700-001-a12 NN0128 Homo sapiens cDNA
4075	18316	30006	1.02	2.5E-02	BE701165.1	EST_HUMAN	PM2-NN0128-080700-001-a12 NN0128 Homo sapiens cDNA
4233	17282	30146	6.52	2.5E-02	AW592114.1	EST_HUMAN	h136h08.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2634015 3'
5799	18891	32073	0.65	2.5E-02	A1732776.1	EST_HUMAN	z683c10.x5 Soares ovary tumor NBHOT Homo sapiens cDNA clone IMAGE:810354 3'
6317	19388		4.71	2.5E-02	BE670128.1	EST_HUMAN	7e30e09.x1 NCL CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3284008 3' similar to contains L1.1.L1
6334	19403		4.42	2.5E-02	BE746888.1	EST_HUMAN	repetitive element 1
6470	19535	32783	0.97	2.5E-02	L29029.1	NT	601579393F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3328054 5'
7927	20870	34258	1.48	2.5E-02	BF526722.1	EST_HUMAN	Chlamydomonas reinhardtii VSP-3 mRNA, complete cds
7927	20870	34259	1.48	2.5E-02	BF526722.1	EST_HUMAN	602070562F1 NCL CGAP_Bm64 Homo sapiens cDNA clone IMAGE:4213408 5'
8137	21074	34474	0.54	2.5E-02	AF129458.1	NT	602070562F1 NCL CGAP_Bm64 Homo sapiens cDNA clone IMAGE:4213408 5'
9177	22143	35570	0.82	2.5E-02	Q91713	SWISSPROT	Chlamydomonas reinhardtii class II DNA photolyase (PHR2) gene, complete cds
9315	22280	35710	0.46	2.5E-02	AW025821.1	EST_HUMAN	CHORDIN PRECURSOR (ORGANIZER-SPECIFIC SECRETED DORSALIZING FACTOR)
10428	23348		0.55	2.5E-02	X71303.1	NT	w408c10.x1 NCL CGAP_GC6 Homo sapiens cDNA clone IMAGE:2516370 3'
10847	23867	37381	0.67	2.5E-02	A1147615.1	EST_HUMAN	D radicum 28S ribosomal RNA, D2 domain
11161	24119	37646	2.15	2.5E-02	Q10335	SWISSPROT	qb22a08.x1 Soares_pregnant uterus_NHPU Homo sapiens cDNA clone IMAGE:1696982 3'
11161	24119	37647	2.15	2.5E-02	Q10335	SWISSPROT	HYPOTHETICAL 46.7 KD PROTEIN C19G10.05 IN CHROMOSOME I

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Table 4

Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
11227	24180		3.01	2.5E-02	AF050157.1	NT	Mus musculus major histocompatibility locus class II region; major histocompatibility protein class II alpha chain (Aalpha) and major histocompatibility protein class II beta chain (Ebeta) genes; complete cds; butyrophilin-like (NGS), butyrophilin-lp
12059	24932		1.47	2.5E-02	AB007546.1	NT	Homo sapiens gene for LECT2, complete cds
12416	25885		3.35	2.5E-02		NT	Homo sapiens similar to ALEX3 protein (H. sapiens) (LOC636334), mRNA
12598	25751		1.47	2.5E-02	11420078	NT	Homo sapiens mitogen-activated protein kinase kinase 13 (MAP3K13), mRNA
12686	25353		2.24	2.5E-02	U00189.1	NT	Dicotyledon discoidium putative protein kinase MkcA (mkcA) gene, complete cds
12709	25385	31770	3.42	2.5E-02	BE973327.1	EST_HUMAN	601662365R2 NIH_MGC_82 Homo sapiens cDNA clone IMAGE:3935513 3'
175	13276	26203	0.69	2.4E-02	A1378592.1	EST_HUMAN	tc72007.x1 Soares_NhHMP_u_S1 Homo sapiens cDNA clone IMAGE:2070156 3'
1802	14634	27610	2.24	2.4E-02	H65884.1	EST_HUMAN	y75f11.r1 Soares fetal liver spleen TNFSL Homo sapiens cDNA clone IMAGE:211149 5'
2060	15884	28098	1.73	2.4E-02	P01901	SWISSPROT	H-2 CLASS I HISTOCOMPATIBILITY ANTIGEN, K-B ALPHA CHAIN PRECURSOR (H-2K(B))
2060	16884	28099	1.73	2.4E-02	P01901	SWISSPROT	H-2 CLASS I HISTOCOMPATIBILITY ANTIGEN, K-B ALPHA CHAIN PRECURSOR (H-2K(B))
4396	17424	30308	1.43	2.4E-02	J05110.1	NT	T. thermophila calcium-binding 25 kDa (TCBP 25) protein mRNA, complete cds
4549	17572	30461	1.43	2.4E-02	P01901	SWISSPROT	H-2 CLASS I HISTOCOMPATIBILITY ANTIGEN, K-B ALPHA CHAIN PRECURSOR (H-2K(B))
5227	18235	30462	1.43	2.4E-02	P01901	SWISSPROT	H-2 CLASS I HISTOCOMPATIBILITY ANTIGEN, K-B ALPHA CHAIN PRECURSOR (H-2K(B))
6340	19409	32650	0.9	2.4E-02	AL161595.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 91
6496	19560	32811	0.97	2.4E-02	W86680.1	EST_HUMAN	zh63h04.s1 Soares_fetal_liver_spleen_TNFSL_S1 Homo sapiens cDNA clone IMAGE:416791 3'
6496	19560	32812	0.65	2.4E-02	M31650.1	NT	Chicken myristoylated alanine-rich C kinase substrate (MARCKS) mRNA, complete cds
7431	20398	33750	1.38	2.4E-02	Z20573.1	EST_HUMAN	Chicken myristoylated alanine-rich C kinase substrate (MARCKS) mRNA, complete cds
7448	20414	33767	1.05	2.4E-02	X12925.1	NT	HSAACCKVX T, Human adult Rhabdomyosarcoma cell-line Homo sapiens cDNA
7448	20414	33768	1.05	2.4E-02	X12925.1	NT	Rat gene for uncoupling protein (UCP)
8156	21097	34493	0.52	2.4E-02	P98092	SWISSPROT	Rat gene for uncoupling protein (UCP)
8156	21097	34496	0.52	2.4E-02	P98092	SWISSPROT	HEMOCYTIN PRECURSOR (HUMORAL LECTIN)
8222	21191		0.57	2.4E-02	AW813007.1	EST_HUMAN	HEMOCYTIN PRECURSOR (HUMORAL LECTIN)
8275	21244		0.58	2.4E-02	M16780.1	NT	RC3-ST0186-230300-019-h08 ST0186 Homo sapiens cDNA
8784	21751		0.53	2.4E-02	H78376.1	EST_HUMAN	Human retrotransposon 3' long terminal repeat
8876	21843	35265	11.43	2.4E-02	N69442.1	EST_HUMAN	yu12a05.s1 Soares_fetal_liver_spleen_TNFSL_Homo sapiens cDNA clone IMAGE:233576 3' similar to contains
9338	22303	35731	0.49	2.4E-02	AE001125.1	NT	Alu repetitive element; contains A3R repetitive element;
							z635q11.s1 Soares_fetal_liver_spleen_TNFSL_Homo sapiens cDNA clone IMAGE:294598 3' similar to
							gbK02009RATSR7K Rat (rRNA); contains A3R.b1 A3R repetitive element;
							Borrelia burgdorferi (section 11 of 70) of the complete genome
							zu91c06.s1 Soares_testis_NHT_Homo sapiens cDNA clone IMAGE:745354 3' similar to gbJ04422 ISLET
							AMYLOID POLYPEPTIDE PRECURSOR (HUMAN); contains Alu repetitive element; contains element XTR
9363	22328	35757	0.81	2.4E-02	AA625660.1	EST_HUMAN	XTR repetitive element;

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Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10050	22977	36443	0.46	2.4E-02	AF124160.1	NT	Arabidopsis thaliana molybdopterin synthase sulphurylase (cnx5) gene, complete cds
10050	22977	36444	0.46	2.4E-02	AF124160.1	NT	Arabidopsis thaliana molybdopterin synthase sulphurylase (cnx5) gene, complete cds
10165	23090	36568	2.57	2.4E-02	AV692954.1	EST_HUMAN	AV692954 GKCC Homo sapiens cDNA clone GKDCSC03.5
10340	23264	36743	2.76	2.4E-02	AA493894.1	EST_HUMAN	nh07b12.s1 NCI_CGAP_Thy1 Homo sapiens cDNA clone IMAGE:943583 similar to contains Alu repetitive element; contains element PTR5 repetitive element
10976	23896		1.35	2.4E-02	BE387111.1	EST_HUMAN	601274962F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3615902.5
11900	24781	38368	1.81	2.4E-02	AF109905.1	NT	Mus musculus major histocompatibility locus class III regions Hsc70T gene, partial cds; smRNP, G7A, NG23, MutS homolog, CLCP, NG24, NG25, and NG26 genes, complete cds; and unknown genes
11900	24781	38369	1.81	2.4E-02	AF109905.1	NT	Mus musculus major histocompatibility locus class III regions Hsc70T gene, partial cds; smRNP, G7A, NG23, MutS homolog, CLCP, NG24, NG25, and NG26 genes, complete cds; and unknown genes
12209	25050		2.39	2.4E-02	9627909	NT	Bacteriophage b1L67, complete genome
12363	25152	31855	1.7	2.4E-02	6753335	NT	Mus musculus DnB1 homolog 1 (E. coli) (DnB1), mRNA
12418	25188	31823	3.48	2.4E-02	BE928899.1	EST_HUMAN	MR0-FT0175-310900-202-606 FT0175 Homo sapiens cDNA
12474	25222	31791	1.59	2.4E-02	U78167.1	NT	Rattus norvegicus cAMP-regulated guanine nucleotide exchange factor 1 (cAMP-GEF1) mRNA, complete cds
12474	25222	31833	1.59	2.4E-02	U78167.1	NT	Rattus norvegicus cAMP-regulated guanine nucleotide exchange factor 1 (cAMP-GEF1) mRNA, complete cds
12843	25327		7.88	2.4E-02	AB008599.1	NT	Caenorhabditis elegans mRNA for iron-sulfur subunit of mitochondrial succinate dehydrogenase, complete cds
1898	14913		5.26	2.3E-02	W05340.1	EST_HUMAN	z84-g08.r1 Scores_fetal_lung_NHL19W Homo sapiens cDNA clone IMAGE:289284.5
1904	14928		8.44	2.3E-02	U64165.1	NT	4 Homo sapiens mammary tumor-associated protein INT6 (INT6) gene, exon 4
2358	15366	28388	3.16	2.3E-02	Z74293.1	NT	S. cerevisiae chromosome IV reading frame ORF YDL245c
3694	16737	29650	4.2	2.3E-02	Z20377.1	EST_HUMAN	HSAAACADH.P, Human foetal Brain Whole tissue Homo sapiens cDNA
4176	17207	30093	0.8	2.3E-02	L24799.1	NT	Gallus gallus connexin 45.6 (Cx45.6) gene, complete cds
4176	17207	30094	0.8	2.3E-02	L24799.1	NT	Gallus gallus connexin 45.6 (Cx45.6) gene, complete cds
4450	17476	30364	1.52	2.3E-02	AW899107.1	EST_HUMAN	GM4-NN0080-290400-160-504 NN0080 Homo sapiens cDNA
4477	17503	30388	0.78	2.3E-02	BE935225.1	EST_HUMAN	CM3-MT0118-010900-318-g07 MT0118 Homo sapiens cDNA
4477	17503	30389	0.78	2.3E-02	BE935225.1	EST_HUMAN	CM3-MT0118-010900-318-g07 MT0118 Homo sapiens cDNA
4478	18317	30390	1.23	2.3E-02	AW593693.1	EST_HUMAN	xs25d08.x1 NCI_CGAP_U2 Homo sapiens cDNA clone IMAGE:2770671.3
4478	18317	30391	1.23	2.3E-02	AW593693.1	EST_HUMAN	xs25d08.x1 NCI_CGAP_U2 Homo sapiens cDNA clone IMAGE:2770671.3
4625	17646	30534	2.89	2.3E-02	BF028487.1	EST_HUMAN	601672279F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3955386.5
4625	17646	30535	2.89	2.3E-02	BF028487.1	EST_HUMAN	601672279F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3955386.5

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Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5203	18212	31086	1.19	2.3E-02	AF257110.1	NT	Rattus norvegicus guanine nucleotide binding protein gamma subunit 11 mRNA, complete cds
5203	18212	31087	1.19	2.3E-02	AF257110.1	NT	Rattus norvegicus guanine nucleotide binding protein gamma subunit 11 mRNA, complete cds
5449	18551	31463	3.35	2.3E-02	U88303.1	NT	Caulobacter crescentus topoisomerase IV ParE subunit (parE) gene, complete cds, and propionyl-CoA carboxylase beta chain (pcdB) homolog gene, partial cds
6363	19432	32675	0.55	2.3E-02	BF106464.1	EST_HUMAN	601822921R1 NIH_MGC_77 Homo sapiens cDNA clone IMAGE:4042829 3'
6774	19829	33112	4.22	2.3E-02	AL161505.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 17
7172	18403	31201	0.84	2.3E-02	BE141475.1	EST_HUMAN	MRC-HT0080-011099-002-09 HT0080 Homo sapiens cDNA
7693	20653	34016	0.52	2.3E-02	AL163303.2	NT	Homo sapiens chromosome 21 segment HS21C103
8208	21178	34686	5.65	2.3E-02	U63610.1	NT	Human plectin (PLEC1) gene, exons 3-32, and complete cds
8815	21782	35207	0.87	2.3E-02	AJ298105.1	NT	Homo sapiens PDX1 gene for lipoyl-containing component X, exons 1-11
8815	21782	35208	0.87	2.3E-02	AJ298105.1	NT	Homo sapiens PDX1 gene for lipoyl-containing component X, exons 1-11
9044	22010	35431	0.74	2.3E-02	AI685380.1	EST_HUMAN	wa76h10.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2302147 3'
9044	22010	35432	0.74	2.3E-02	AI685380.1	EST_HUMAN	wa76h10.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2302147 3'
9493	22457	35897	0.89	2.3E-02	P41996	SWISSPROT	HYPOTHETICAL 55.6 KD PROTEIN B0280.5 IN CHROMOSOME III PRECURSOR
10218	23143	36632	0.77	2.3E-02	P50532	SWISSPROT	CHROMOSOME ASSEMBLY PROTEIN XCAP-C
10360	23312	36791	1.47	2.3E-02	AE000199.1	NT	Escherichia coli K-12 MG1655 section 89 of 400 of the complete genome
10360	23312	36792	1.47	2.3E-02	AE000199.1	NT	Escherichia coli K-12 MG1655 section 89 of 400 of the complete genome
11135	24095	37624	1.71	2.3E-02	P08840	SWISSPROT	GLUCOAMYLASE S1/S2 PRECURSOR (GLUCAN 1,4-ALPHA-GLUCOSIDASE) (1,4-ALPHA-D-GLUCAN GLUCOHYDROLASE)
12336	26738		7.98	2.3E-02	BE278331.1	EST_HUMAN	601179958F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3546567 5'
12742	25392	31755	1.5	2.3E-02	BF528482.1	EST_HUMAN	602043629F1 NCI_CGAP_Bm87 Homo sapiens cDNA clone IMAGE:4181454 5'
12742	25392	31756	1.5	2.3E-02	BF528482.1	EST_HUMAN	602043629F1 NCI_CGAP_Bm87 Homo sapiens cDNA clone IMAGE:4181454 5'
12843	25453	31724	3.2	2.3E-02	U93994.1	NT	Streptomyces sp. alpha-1,3/4-fucosidase precursor gene, complete cds
12897	25983		2.48	2.3E-02	U11077.1	NT	Dicotylellum discoideum extracellular signal-regulated protein kinase (ERK1) mRNA, complete cds
13100	25533		1.82	2.3E-02	11426388	NT	Homo sapiens dead ringer (Drosophila)-like 1 (DRL1), mRNA
739	13800	26739	4.3	2.2E-02	AF018287.1	NT	Columbia livia nucleoside diphosphate kinase (NDPK) gene, nuclear gene encoding mitochondrial protein, complete cds
1762	14791		1.59	2.2E-02	4557448	NT	Homo sapiens chromodomain helicase DNA binding protein 2 (CHD2) mRNA
2031	15050	28065	1.68	2.2E-02	Z82001.1	NT	S.pneumoniae pcgA gene and open reading frames
3448	16495		2.16	2.2E-02	AA577785.1	EST_HUMAN	m24804.s1 NCI_CGAP_Gas1 Homo sapiens cDNA clone IMAGE:1084782 3'
3660	16703		3.48	2.2E-02	AF083094.1	NT	Infectious bursal disease virus segment B strain IL4 VP1 gene, complete cds
3867	16906	29814	1.26	2.2E-02	AF060137.1	EST_HUMAN	PM0-BT0340-170100-004-b03 BT0340 Homo sapiens cDNA
3941	16981	29898	0.74	2.2E-02	Z74293.1	NT	S.cerevisiae chromosome IV reading frame ORF YDL248c

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5105	18115	30988	1.17	2.2E-02	Z73997.1	NT	S.cerevisiae chromosome XVI reading frame ORF YPL241c
7458	20424	33780	3.37	2.2E-02	AV699721.1	EST_HUMAN	AV699721 GKB Homo sapiens cDNA clone GKBAND03 3'
8714	21682	35109	2.28	2.2E-02	AL161515.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 27
8714	21682	35110	2.28	2.2E-02	AL161515.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 27
9161	22127	35555	0.77	2.2E-02	X79468.1	NT	P.vulgaris alpha tub 2 mRNA
10045	22972	36438	2.26	2.2E-02	AB026898.1	NT	Homo sapiens DNA, DLEC1 to ORCTL4 gene region, section 1/2 (DLEC1, ORCTL3, ORCTL4 genes, complete cds)
10045	22972	36439	2.26	2.2E-02	AB026898.1	NT	Homo sapiens DNA, DLEC1 to ORCTL4 gene region, section 1/2 (DLEC1, ORCTL3, ORCTL4 genes, complete cds)
10565	23487		0.91	2.2E-02	6678140	NT	Mus musculus Sjogren syndrome antigen A1 (Ssa1), mRNA
11540	24481	38033	1.8	2.2E-02	BE797601.1	EST_HUMAN	601584309F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3938571 5'
12602	25304		5.72	2.2E-02	AA503553.1	EST_HUMAN	ne47107.s1 NCI_CGAP_Co3 Homo sapiens cDNA clone IMAGE:900541 3' similar to contains Alu repetitive element
419	13492		5.37	2.1E-02	AV761502.1	EST_HUMAN	AV761502 MDS Homo sapiens cDNA clone MDSADG01 5'
449	13522		8.77	2.1E-02	AF029726.1	NT	Dicystellum discoideum histidine kinase C (dhkC) mRNA, complete cds
1268	14303	27264	8.3	2.1E-02	U72073.1	NT	Bacillus subtilis cotKLM cluster, CotK (cotK), and spore coat protein CotM (cotM) genes, complete cds
1387	14420	27389	0.98	2.1E-02	AF204395.1	NT	Mus musculus macrophage migration inhibitory factor (MIF) gene, 5' flanking region and partial cds
1387	14420	27390	0.99	2.1E-02	AF204395.1	NT	Mus musculus macrophage migration inhibitory factor (MIF) gene, 5' flanking region and partial cds
1797	14826	27611	1.26	2.1E-02	P02438	SWISSPROT	KERATIN, HIGH-SULFUR MATRIX PROTEIN, B2A
1797	14826	27612	1.26	2.1E-02	P02438	SWISSPROT	KERATIN, HIGH-SULFUR MATRIX PROTEIN, B2A
1797	14826	27613	1.26	2.1E-02	P02438	SWISSPROT	KERATIN, HIGH-SULFUR MATRIX PROTEIN, B2A
1980	15001	28004	1.01	2.1E-02	AF190899.1	NT	Tegula aureolincta major acrosomal protein precursor (TIMAP) mRNA, complete cds
2050	15069	28089	0.9	2.1E-02	BE072546.1	EST_HUMAN	PM2-BT0546-120100-001-f11 BT0546 Homo sapiens cDNA
2050	15069	28090	0.9	2.1E-02	BE072546.1	EST_HUMAN	PM2-BT0546-120100-001-f11 BT0546 Homo sapiens cDNA
2591	15592	28609	1.04	2.1E-02	AA226095.1	EST_HUMAN	nc21g03.r1 NCI_CGAP_P1 Homo sapiens cDNA clone IMAGE:1008820
2827	13839	26784	4.46	2.1E-02	N29266.1	EST_HUMAN	y443107.1 Soares melanocyte 2N6HM Homo sapiens cDNA clone IMAGE:796121 5'
3164	15069	28089	1.02	2.1E-02	BE072546.1	EST_HUMAN	PM2-BT0546-120100-001-f11 BT0546 Homo sapiens cDNA
3164	15069	28090	1.02	2.1E-02	BE072546.1	EST_HUMAN	PM2-BT0546-120100-001-f11 BT0546 Homo sapiens cDNA
3597	16842	29561	0.98	2.1E-02	AA461271.1	EST_HUMAN	z63309.r1 Soares total Telus Nb2-HF8_9w Homo sapiens cDNA clone IMAGE:796121 5'
4028	17066	29987	0.97	2.1E-02	BF203457.1	EST_HUMAN	60186580F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4098407 5'
4157	17188	30076	0.84	2.1E-02	Z74283.1	NT	S.cerevisiae chromosome IV reading frame ORF YDL245c
4339	17366	30249	1.4	2.1E-02	BF343655.1	EST_HUMAN	60201500F1 NCI_CGAP_Bn84 Homo sapiens cDNA clone IMAGE:4151161 5'
4473	17499	30384	2.15	2.1E-02	U44914.1	NT	Borrelia burgdorferi plasmid cp32-2, erpC and erpD genes, complete cds, and unknown genes

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Table 4

Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4483	17508	30397	1.13	2.1E-02	AI768127.1	EST_HUMAN	wg81d11.x1 Scores_NSF_F8_GW_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:2371509 3'
4739	17759	30654	5.69	2.1E-02	Y08501.1	NT	A.thaliana mitochondrial genome, part A
4761	17761	30677	1.5	2.1E-02	AA665737.1	EST_HUMAN	ag55g12.s1 Gessler Wilms tumor Homo sapiens cDNA clone IMAGE:1126918 3'
5256	18264	31133	1.07	2.1E-02	BF026405.1	EST_HUMAN	601671411F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3694410 5'
5723	18817	31996	0.75	2.1E-02	AW379528.1	EST_HUMAN	CM4-HT0244-111199-040-n05 HT0244 Homo sapiens cDNA
7268	20003	33303	0.66	2.1E-02	BF086199.1	EST_HUMAN	QV3-GN0058-120900-329-a12 GN0058 Homo sapiens cDNA
8864	21831	35264	0.68	2.1E-02	9790238	NT	Mus musculus sorting nexin 1 (Sxn1), mRNA
9861	22797	36250	0.51	2.1E-02	AA984288.1	EST_HUMAN	an83d07.s1 Stratagene schizo brain S11 Homo sapiens cDNA clone IMAGE:1629732 3' similar to contains
9889	22916	36381	2.63	2.1E-02	AJ243213.1	NT	Alu repetitive element contains element MER11 repetitive element
9989	22916	36382	2.63	2.1E-02	AJ243213.1	NT	Homo sapiens partial 5-HT4 receptor gene, exons 2 to 5
10343	23267	36746	1.13	2.1E-02	L29324.1	NT	Homo sapiens partial 5-HT4 receptor gene, exons 2 to 5
10421	23343	36829	0.68	2.1E-02	AA984288.1	EST_HUMAN	Streptococcus pneumoniae integrase, excisionase, repressor protein, relaxase, UmuC MucB homolog, and
12584	18345		8.95	2.1E-02	Y19213.1	NT	UmuD MucA homolog genes, complete cds; and unknown genes
12624	25735	31617	1.4	2.1E-02	L34170.1	NT	an83d07.s1 Stratagene schizo brain S11 Homo sapiens cDNA clone IMAGE:1629732 3' similar to contains
13003	25567	31693	3.5	2.1E-02	AF183913.1	NT	Alu repetitive element contains element MER11 repetitive element
19	13139	26037	1.39	2.0E-02	BF002932.1	EST_HUMAN	Homo sapiens putative psliHbA pseudogene for hair keratin, exons 2 to 7
20	13140	26038	10.76	2.0E-02	AW895655.1	EST_HUMAN	Human germline UBE1L gene similar to the gene for ubiquitin-activating enzyme, exons 1-22
259	13356	26280	3.29	2.0E-02	6753635	NT	Azospirillum brasilense major outer membrane protein OmaA precursor (omaA) gene, complete cds
295	13399	26317	2.95	2.0E-02	AA456538.1	EST_HUMAN	7g51c08.x1 NCI_CGAP_P228 Homo sapiens cDNA clone IMAGE:3309998 3' similar to contains MER1.13
799	13858	26805	1.27	2.0E-02	6753635	NT	MER1 repetitive element
1089	14133	27086	1.03	2.0E-02	AL096805.1	NT	QV4-NN0038-270400-167-n05 NN0038 Homo sapiens cDNA
1204	14243	27201	0.79	2.0E-02	8922391	NT	Mus musculus DinB homolog 1 (E. coli) (Dinb1), mRNA
1204	14243	27202	0.79	2.0E-02	8922391	NT	aa15b10.f1 Scores_NhMMPu_S1 Homo sapiens cDNA clone IMAGE:813307 5'
1890	14915	27909	2.08	2.0E-02	8922453	NT	Mus musculus DinB homolog 1 (E. coli) (Dinb1), mRNA
1890	14915	27910	2.08	2.0E-02	8922453	NT	Homo sapiens genomic region containing hypervariable minisatellites chromosome 1(p36.33) of Homo
2810	15802		4.57	2.0E-02	AL167532.2	NT	sapiens
3095	13139	26037	1.61	2.0E-02	BF002832.1	EST_HUMAN	Homo sapiens hypothetical protein FLJ10379 (FLJ10379), mRNA
							Homo sapiens hypothetical protein FLJ10379 (FLJ10379), mRNA
							Homo sapiens hypothetical protein FLJ10486 (FLJ10486), mRNA
							Homo sapiens hypothetical protein FLJ10486 (FLJ10486), mRNA
							Homo sapiens hypothetical protein FLJ10486 (FLJ10486), mRNA
							Arabidopsis thaliana DNA chromosome 4, contig fragment No. 32
							7g51c08.x1 NCI_CGAP_P228 Homo sapiens cDNA clone IMAGE:3309998 3' similar to contains MER1.13
							MER1 repetitive element

Table 4

Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3159	16216		1.83	2.0E-02	7305474	NT	Mus musculus sema domain, transmembrane domain (TM), and cytoplasmic domain, (semaphorin) 6B (Semab6), mRNA
3241	16296		1.8	2.0E-02	AF095888.1	NT	Arabidopsis thaliana C2H2 zinc finger protein FZF mRNA, complete cds
4032	17070	28971	1.4	2.0E-02	M18095.1	NT	P. vulgaris hydroxyproline-rich glycoprotein (HRGP) mRNA, 3' end
5153	18163		0.7	2.0E-02	AI271985.1	EST_HUMAN	q83603.x1 NCL CGAP_K1d3 Homo sapiens cDNA clone IMAGE:1866076 3'
5175	18184	31061	0.94	2.0E-02	AL163278.2	NT	Homo sapiens chromosome 21 segment HS21C078
5718	18812	31991	0.59	2.0E-02	U34778.1	NT	Caenorhabditis elegans sma-2 mRNA, complete cds
6000	19083	32282	0.73	2.0E-02	L35321.2	NT	Dicystelium discoideum class VII unconventional myosin (myoI) gene, complete cds
7199	20751	34126	1.09	2.0E-02	AP000004.1	NT	Pyrococcus horikoshii OT3 genomic DNA, 777001-994000 nt, position (417)
7799	20751	34127	1.09	2.0E-02	AP000004.1	NT	Pyrococcus horikoshii OT3 genomic DNA, 777001-994000 nt, position (417)
10236	23161		1.99	2.0E-02	U70408.1	NT	Japanese encephalitis virus envelope protein mRNA, partial cds
10726	23548	37141	1.54	2.0E-02	AI640342.1	EST_HUMAN	wa17b02.x1 NCL CGAP_K1d11 Homo sapiens cDNA clone IMAGE:2288315 3'
11005	23671	37495	1.84	2.0E-02	Z73986.1	NT	Mycobacterium tuberculosis H37RV complete genome, segment 93/162
11699	24664	38241	2.26	2.0E-02	D88184.1	NT	Equus caballus DNA for 17alpha-hydroxylase/17,20-lyase, complete cds
12148	18351	31296	3.03	2.0E-02	AA456538.1	EST_HUMAN	aat15b10.r1 Soares NIHMPu_S1 Homo sapiens cDNA clone IMAGE:813307 5'
12621	15802		1.99	2.0E-02	AL161532.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 32
13078	25008		3.4	2.0E-02	T80037.1	EST_HUMAN	yd04c09.r1 Soares infant brain 1NIB Homo sapiens cDNA clone IMAGE:24675 5'
694	13756	26886	2.55	1.9E-02	AA572764.1	EST_HUMAN	m19a07.s1 NCL CGAP_P1 Homo sapiens cDNA clone IMAGE:914196 similar to contains L1.11 L1 repetitive element
1819	14652	27628	1.03	1.9E-02	P18488	SWISSPROT	EMPTY SPIRACLES HOMEOTIC PROTEIN
2055	15074	28093	3.04	1.9E-02	AL163303.2	NT	Homo sapiens chromosome 21 segment HS21C103
2055	15074	28094	3.04	1.9E-02	AL163303.2	NT	Homo sapiens chromosome 21 segment HS21C103
2314	15517	28540	1.07	1.9E-02	AL161550.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 50
2916	15974	28897	8.5	1.9E-02	AA713855.1	EST_HUMAN	hw04f05.s1 NCL CGAP_SS1 Homo sapiens cDNA clone IMAGE:1238337 3'
2964	16022	28947	1.46	1.9E-02	AV648669.1	EST_HUMAN	AV048669.G1C Homo sapiens cDNA clone GLCBLH07 3'
3273	16327		0.72	1.9E-02	AB033611.1	NT	Utricularia talpoides mitochondrial gene for cytochrome b, complete cds
3625	16666		1.36	1.9E-02	N52280.1	EST_HUMAN	yz28b02.s1 Soares multiple sclerosis_2NblHNSP Homo sapiens cDNA clone IMAGE:284331 3'
3718	16761		8.23	1.9E-02	BE738088.1	EST_HUMAN	601572882F1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:3839564 5'
3727	16769	29681	0.69	1.9E-02	AI301183.1	EST_HUMAN	qn04c07.x1 NCL CGAP_Lu5 Homo sapiens cDNA clone IMAGE:1897280 3' similar to contains Alu repetitive element
4077	17112	30008	1.59	1.9E-02	AF141940.1	NT	Mycoplasma imitans Vira1 precursor (vira1) and Vira2 precursor (vira2) genes, partial cds
4222	17261	30137	1.62	1.9E-02	P09081	SWISSPROT	HOMEOTIC BICOID PROTEIN (PRD-4)
4222	17251	30138	1.62	1.9E-02	P09081	SWISSPROT	HOMEOTIC BICOID PROTEIN (PRD-4)

Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4572	17594	30488	3.65	1.9E-02	AI452999.1	EST_HUMAN	y46d04.x1 Soares_NSF_F8_gw_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:2144551 3' similar to contains Alu repetitive element;
5048	15517	28540	2.68	1.9E-02	AL161550.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 50
5389	18482	31359	0.91	1.9E-02	AF037382.1	NT	Mus musculus T cell receptor gamma locus, TCR gamma 1 and gamma 3 gene clusters
5544	18641	31581	1.25	1.9E-02	L47572.1	NT	Meleagris gallopavo paraoxonase-2 (PON2) mRNA, complete cds
5885	18974		1.24	1.9E-02	AB019507.1	NT	Drosophila kaneli gene for glyceral-3-phosphate dehydrogenase, complete cds
7308	20279	33617	1.34	1.9E-02	U19241.1	NT	Homo sapiens interferon-gamma receptor alpha chain gene, exon 1
7308	20278	33618	1.34	1.9E-02	U19241.1	NT	Homo sapiens interferon-gamma receptor alpha chain gene, exon 1
8917	21883		1.2	1.9E-02	AL162754.2	NT	Neisseria meningitidis serogroup A strain Z2491 complete genome, segment 3/7
9686	22639	36096	0.78	1.9E-02	BF316129.1	EST_HUMAN	601856130F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4125462 5'
10071	22968	36467	0.43	1.9E-02	L10114.1	NT	Nicotiana tabacum type II phytochrome (phyB) gene, complete cds
10405	23327	36811	1.09	1.9E-02	BF695832.1	EST_HUMAN	601852385F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4076253 5'
10510	23432	36929	0.45	1.9E-02	N39180.1	EST_HUMAN	y46d08.s1 Soares_multiple_sclerosis_ZNBMSP Homo sapiens cDNA clone IMAGE:276639 3'
10614	23535	37034	0.5	1.9E-02	D84001.1	NT	Synechocystis sp. POC8803 complete genome, 20/27, 2539000-2844794
12372	25742	31620	3.14	1.9E-02	AF101065.1	NT	Hirudo medicinalis intermediate filament gllarin mRNA, complete cds
13026	25574	31696	1.4	1.9E-02	X68271.1	NT	H.sapiens MUC18 gene exon 16
346	13435	26357	1.35	1.8E-02	AW771104.1	EST_HUMAN	hn52c06.x1 NCL_CGAP_Co17 Homo sapiens cDNA clone IMAGE:3027274 3' similar to contains element MER29 repetitive element ;
686	13749	26875	1.39	1.8E-02	BF308122.1	EST_HUMAN	601894329F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4139983 5'
1164	14205	27159	1.87	1.8E-02	X17694.1	NT	H.francisci mRNA for myelin basic protein (MBP)
2687	15683	28701	1.78	1.8E-02	AE004544.1	EST_HUMAN	Pseudomonas aeruginosa PAO1, section 105 of the complete genome
3224	16279		1.06	1.8E-02	AI805829.1	EST_HUMAN	te52a09.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2090296 3'
3902	16942	29853	1.01	1.8E-02	AW879122.1	EST_HUMAN	MR1-OT0011-280300-009-g04 OT0011 Homo sapiens cDNA
3902	16942	29854	1.01	1.8E-02	AW879122.1	EST_HUMAN	MR1-OT0011-280300-009-g04 OT0011 Homo sapiens cDNA
4113	17147		1.04	1.8E-02	AA881446.1	EST_HUMAN	ak24h04.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1406935 3'
4461	17487	30374	1.49	1.8E-02	AW936363.1	EST_HUMAN	QV4-DT0021-301299-071-b11 DT0021 Homo sapiens cDNA
4992	18007	30895	0.98	1.8E-02	O60810	SWISSPROT	HYPOTHETICAL PROTEIN DJ845024.2
5287	18283	31154	0.68	1.8E-02	AF255711.1	NT	Oryza sativa putative histone deacetylase HD2 mRNA, complete cds
6524	19587	32845	0.59	1.8E-02	AE002518.1	NT	Neisseria meningitidis serogroup B strain MC58 section 160 of the complete genome
6524	19587	32846	0.59	1.8E-02	AE002518.1	NT	Neisseria meningitidis serogroup B strain MC58 section 160 of the complete genome
6982	20205	33534	4.59	1.8E-02	P14310	SWISSPROT	HYPOTHETICAL 7.9 KD PROTEIN IN FIXW 5REGION
7699	20657	34021	0.65	1.8E-02	BF125690.1	EST_HUMAN	601763268F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:4026280 5'
7722	20657	34021	0.58	1.8E-02	BF125690.1	EST_HUMAN	601763268F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:4026280 5'
8467	21436	34854	0.77	1.8E-02	U37091.1	NT	Mus musculus carbonic anhydrase IV gene, complete cds

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Table 4
Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8811	21778	35203	0.79	1.8E-02	AW905327.1	EST_HUMAN	QV2-NN1073-220400-159-h09 NN1073 Homo sapiens cDNA
8857	21824	35247	0.75	1.8E-02	6678943	NT	Mus musculus microtubule-associated protein 2 (Map2), mRNA
9849	22785	36238	0.5	1.8E-02	BF241924.1	EST_HUMAN	601877028F1 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:4105303 5'
9849	22785	36239	0.5	1.8E-02	BF241924.1	EST_HUMAN	601877028F1 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:4105303 5'
10000	22927		2.03	1.8E-02	AA897543.1	EST_HUMAN	af62109.s1 Soares testis NHT Homo sapiens cDNA clone IMAGE:1394921 3' similar to gb:L11672 ZINC FINGER PROTEIN 91 (HUMAN);
10423	23345	36830	1.65	1.8E-02	BE778274.1	EST_HUMAN	601463548F1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:3866963 5'
10586	23508	37000	1.2	1.8E-02	X98933.1	NT	L. stagnalis mRNA for myomodulin neuropeptide precursor
11765	23920	37438	1.7	1.8E-02	AB002337.2	NT	Homo sapiens mRNA for KIAA0339 protein, partial cds
11765	23920	37439	1.7	1.8E-02	AB002337.2	NT	Homo sapiens mRNA for KIAA0339 protein, partial cds
11935	24818	38413	2.73	1.8E-02	AP000006.1	NT	Pyrococcus horikoshii OT3 genomic DNA, 1166001-1485000 nt, position (87)
11948	24827	38422	3.16	1.8E-02	U62749.1	NT	Zea mays acidic ribosomal protein P2a-3 (pp2a-3) mRNA, partial cds
13105	25626	31680	1.35	1.8E-02	R40255.1	EST_HUMAN	yf60401.s1 Soares infant brain 1N1B Homo sapiens cDNA clone IMAGE:29985 3' similar to gb:M62783 ALPHA-N-ACETYL GALACTOSAMINIDASE PRECURSOR (HUMAN);
13105	25626	31681	1.35	1.8E-02	R40255.1	EST_HUMAN	yf60401.s1 Soares infant brain 1N1B Homo sapiens cDNA clone IMAGE:29985 3' similar to gb:M62783 ALPHA-N-ACETYL GALACTOSAMINIDASE PRECURSOR (HUMAN);
907	13962	26918	0.8	1.7E-02	BE394869.1	EST_HUMAN	601310526F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3632190 5'
1806	14834	27823	2.15	1.7E-02	AW573183.1	EST_HUMAN	hf34a03.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2933740 3' similar to contains L1.1t L1 repetitive element;
1806	14834	27824	2.15	1.7E-02	AW573183.1	EST_HUMAN	hf34a03.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2933740 3' similar to contains L1.1t L1 repetitive element;
1887	14912		4.23	1.7E-02	AL163204.2	NT	Homo sapiens chromosome 21 segment HS21C004
2121	15138		11.19	1.7E-02	AB004816.1	NT	Oryctolagus cuniculus mRNA for mitsugumin29, complete cds
2301	15313	28333	1.03	1.7E-02	S74186.1	NT	[microsatellite INRA41] [Ovis aries=sheep, Genomic, 361 nt, segment 1 of 2]
2648	15645		1.18	1.7E-02		NT	Homo sapiens putative Rabs GDP/GTP exchange factor homologue (RABEX5), mRNA
3011	16069	28990	0.96	1.7E-02	A1147615.1	EST_HUMAN	qb22a08.x1 Soares_pregnant_uterus_NbHPU Homo sapiens cDNA clone IMAGE:1696982 3'
3523	16569		5.52	1.7E-02	AW827368.1	EST_HUMAN	hm45a04.x1 NCI CGAP_RDF1 Homo sapiens cDNA clone IMAGE:3015534 3' similar to contains MER19.b1 MER19 repetitive element;
4198	17229		0.96	1.7E-02	AA669618.1	EST_HUMAN	ac19f04.s1 Stratagene ovary (R937217) Homo sapiens cDNA clone IMAGE:856927 3' similar to contains Alu repetitive element; contains element MER24 repetitive element;
4228	17257		2.04	1.7E-02	R02506.1	EST_HUMAN	ye86f08.r1 Soares fetal liver spleen 1N1FL Homo sapiens cDNA clone IMAGE:124647 5'
4482	17507	30396	0.7	1.7E-02	A105279.1	EST_HUMAN	qm08g07.x1 NCI CGAP_Lu5 Homo sapiens cDNA clone IMAGE:1881276 3' similar to gb:X52359 ZINC FINGER PROTEIN 30 (HUMAN);

Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4557	17580	30471	1.52	1.7E-02	AW573183.1	EST_HUMAN	h34a03.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2633740 3' similar to contains L1.1 L1 repetitive element:
4744	17764	30658	1.54	1.7E-02	V00941.1	NT	Messenger RNA for anglerfish (<i>Lophius americanus</i>) somatostatin II
4851	17868		7.05	1.7E-02	A015076.1	EST_HUMAN	ov61602.s1 Soares_tasitis_NHT Homo sapiens cDNA clone IMAGE:1640858 3'
5106	18116	30989	0.74	1.7E-02	6981289	NT	Rattus norvegicus N-arginine dibasic convertase 1 (Nr41), mRNA
5229	18237		0.91	1.7E-02	AJ229041.1	NT	Homo sapiens 959 kb contig between AML1 and CBR1 on chromosome 21q22; segment 1/3
6248	19321	32551	1.63	1.7E-02	A1769247.1	EST_HUMAN	wg35109.x1 Soares_NSF_F8_gw_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:2367113 3' similar to contains Alu repetitive element;
6618	19676		0.64	1.7E-02	Z28383.1	NT	T.niveum (ATCC34821) simA gene for cyclosporine synthetase
6731	19787	33065	1.37	1.7E-02	A038280.1	EST_HUMAN	ov65103.x1 Soares_fetal_liver_spleen_INFLS_S1 Homo sapiens cDNA clone IMAGE:1872861 3'
7251	19986	33284	1.31	1.7E-02	AF190930.1	NT	Macaca fascicularis protein tyrosine phosphatase (PRL-1) mRNA, complete cds
7411	20378	33729	1.95	1.7E-02	8400718	NT	Homo sapiens nebulin (NEB), mRNA
7581	20543	33902	0.85	1.7E-02	L07899.1	NT	Human apolipoprotein (a) gene, exon 1
7581	20543	33903	0.85	1.7E-02	L07899.1	NT	Human apolipoprotein (a) gene, exon 1
8016	20954		1.98	1.7E-02	AJ010770.1	NT	Homo sapiens hyaluron gene, exons 1-50
9791	21114	34514	0.91	1.7E-02	U21854.1	NT	Caenorhabditis elegans cCAF1 protein gene, complete cds
10057	22984	36453	1.31	1.7E-02	AL040554.1	EST_HUMAN	DKFZp434i0314_r1_434 (synonym: htes3) Homo sapiens cDNA clone DKFZp434i0314 5'
12084	24956	38551	1.59	1.7E-02	5902007	NT	Homo sapiens serum constituent protein (MSE55), mRNA
12910	25910	31424	3.15	1.7E-02	AW903482.1	EST_HUMAN	GM4-NN1030-040400-130-06 NN1030 Homo sapiens cDNA
13059	25595	31687	1.31	1.7E-02	AA846926.1	EST_HUMAN	oe08d04.s1 NCI_CGAP_Ov2 Homo sapiens cDNA clone IMAGE:1385287 similar to contains element MSRT repetitive element;
512	13583		2.22	1.6E-02	AL021929.1	NT	Mycobacterium tuberculosis H37Rv complete genome; segment 13/162
1665	14697	27673	0.91	1.6E-02	Y18899.1	NT	Treponema maltophilum flaB2, flaB3 and flilD genes for flagellin subunit proteins and CAP protein homologue
2572	15573	28593	0.95	1.6E-02	AJ008345.1	NT	Homo sapiens KVLQ11 gene
2651	15648	28671	1.45	1.6E-02	AA484872.1	EST_HUMAN	ne81d06.s1 NCI_CGAP_Ew1 Homo sapiens cDNA clone IMAGE:910667
2704	15700		1.37	1.6E-02	AB014534.1	NT	Homo sapiens mRNA for KIAA0334 protein, partial cds
3537	15583	29506	4.46	1.6E-02	AW850652.1	EST_HUMAN	IL3-CT0219-160200-063-C07 CT0219 Homo sapiens cDNA
							Mus musculus major histocompatibility complex region NG27, NG28, RPS28, NADH oxidoreductase, NG29, KIFC1, Fas-binding protein, BING1, tapasin, RalGDS-like, KE2, BING4, beta 1,3-galactosyl transferase, and RPS18 genes, complete cds; Secm21 gene, partial>
4204	17235		2.14	1.6E-02	AF110520.1	NT	QV2-PT0012-140100-030-f07 PT0012 Homo sapiens cDNA
4328	17357	30245	0.96	1.6E-02	AW875407.1	EST_HUMAN	RPS18 genes, complete cds; Secm21 gene, partial>
5172	18181		0.76	1.6E-02	N80156.1	EST_HUMAN	2a65e07.s1 Soares fetal liver spleen INFLS Homo sapiens cDNA clone IMAGE:287444 3'
5325	18431	31183	0.49	1.6E-02	AJ281385.1	EST_HUMAN	qu42b09.x1 NCI_CGAP_Lym5 Homo sapiens cDNA clone IMAGE:1987417 3'

Table 4

Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6705	18800	31977	1.33	1.6E-02	6871715	NT	Mus musculus CD5 antigen (Cd5), mRNA
6789	19853	33138	2.07	1.6E-02	AB015281.1	NT	Candida albicans CaGCR3 gene, complete cds
7117	20051	33354	0.83	1.6E-02	AB027571.1	NT	Saccharomyces cerevisiae CAD2 gene for cadmium resistance protein, complete cds
7117	20051	33355	0.83	1.6E-02	AB027571.1	NT	Saccharomyces cerevisiae CAD2 gene for cadmium resistance protein, complete cds
7878	20917	34308	1.03	1.6E-02	AL161508.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 20
8458	21427	34844	0.72	1.6E-02	AL277662.1	NT	Homo sapiens partial TUB gene for tubby (mouse) homolog and LMO1 gene for LIM domain only 1 protein
8518	21487		1.5	1.6E-02	X05151.1	NT	Human apoC-II gene for preproapoprotein C-II
10400	23322		1.98	1.6E-02	AF078764.1	NT	Drosophila melanogaster enhancer of polycomb (E(Pc)) mRNA, complete cds
10785	23706	37206	1.2	1.6E-02	AA572818.1	EST_HUMAN	nf19g03.s1 NCI_CGAP_P1 Homo sapiens cDNA clone IMAGE:914260 similar to SW:TELO_RABIT P29284 TELOKIN. [1]:
10785	23706	37207	1.2	1.6E-02	AA572818.1	EST_HUMAN	nf19g03.s1 NCI_CGAP_P1 Homo sapiens cDNA clone IMAGE:914260 similar to SW:TELO_RABIT P29284 TELOKIN. [1]:
11255	25705	37730	1.83	1.6E-02	Z94828.1	NT	Gallus microsatellite DNA (LEI0280 (=T16III11))
11547	24488	38042	1.7	1.6E-02	AL161508.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 20
11547	24488	38043	1.7	1.6E-02	AL161508.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 20
11839	24722	38307	1.66	1.6E-02	AL161508.2	EST_HUMAN	g298e10.x1 Soares_pregnant_uterus_NhhPU Homo sapiens cDNA clone IMAGE:2042442 3'
12347	18334	31172	1.39	1.6E-02	Q64176	SWISSPROT	LIVER CARBOXYLESTERASE 22 PRECURSOR (EGASYN) (ESTERASE-22)
12347	18334	31173	1.39	1.6E-02	Q64176	SWISSPROT	LIVER CARBOXYLESTERASE 22 PRECURSOR (EGASYN) (ESTERASE-22)
752	13813		20.75	1.5E-02	8923734	NT	Homo sapiens transcription factor (HSA130894), mRNA
2152	15169	28184	4.44	1.5E-02	N39521.1	EST_HUMAN	y27b07.s1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:243925 3'
2185	15200	28220	1.82	1.5E-02	AL161594.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 90
3074	16131	29043	2.54	1.5E-02	AJ008216.1	NT	Homo sapiens CACNA1F gene, exons 1 to 48
3074	16131	29044	2.54	1.5E-02	AJ008216.1	NT	Homo sapiens CACNA1F gene, exons 1 to 48
3737	18779	29692	1.06	1.5E-02	BF092942.1	EST_HUMAN	MR4-TN0115-080900-201-b12 TN0115 Homo sapiens cDNA
6426	19493	32745	1.33	1.5E-02	Q09711	SWISSPROT	HYPOTHETICAL CALCIUM-BINDING PROTEIN C18B11.04 IN CHROMOSOME 1
7541	20504		1.59	1.5E-02	11467282	NT	Cyanophora paradoxa cyanelle, complete genome
7631	20591	33954	1.38	1.5E-02	11418713	NT	Homo sapiens KIAA1009 protein (KIAA1009), mRNA
8206	21176	34585	1.5	1.5E-02	AL163303.2	NT	Homo sapiens chromosome 21 segment HS21C103
8213	21182	34593	4.62	1.5E-02	11417739	NT	Homo sapiens vavl-mRNA synthetase 2 (VAR52), mRNA
9182	22148	35575	0.93	1.5E-02	BF345554.1	EST_HUMAN	602019135F1 NCI_CGAP_Bm67 Homo sapiens cDNA clone IMAGE:4164504 5'
9823	22672		0.98	1.5E-02	AF096774.1	NT	Homo sapiens kinase-related protein isoform 1 mRNA, complete cds
9829	22812	36266	1.88	1.5E-02	D44608.1	NT	Saccharomyces cerevisiae chromosome VI plasmid GapC
10170	23095	36574	0.95	1.5E-02	R32667.1	EST_HUMAN	y154b10.1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:133531 5'

Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10170	23095	36575	0.95	1.5E-02	R32867.1	EST_HUMAN	yt54b10.t1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:133531.5
11503	24445	37997	2.75	1.5E-02	L40809.1	NT	Plasmodium falciparum (strain FCR3) variant-specific surface protein (var-2, var-3) genes, complete cds
11537	24478	38028	2.52	1.5E-02	AL111238.1	NT	Botrytis cinerea strain T4 cDNA library under conditions of nitrogen deprivation
12564	25783		2.04	1.5E-02	AW750834.1	EST_HUMAN	RC4-CN0049-140100-011-c11 CN0049 Homo sapiens cDNA
13078	25610		1.3	1.5E-02	A1763127.1	EST_HUMAN	w06h03.x1 NCI_CGAP_G1.1 Homo sapiens cDNA clone IMAGE:2389493.3 similar to contains Alu repetitive element; contains element MER26 MSR1 repetitive element
417	13490		1.99	1.4E-02	AE002230.2	NT	Chlamydia pneumoniae AR39, section 58 of 94 of the complete genome
1120	14164	27115	5.44	1.4E-02	7705980	NT	Homo sapiens NESH protein (LOC51225), mRNA
1281	14296		1.74	1.4E-02	U32800.1	NT	Haemophilus influenzae Rd section 115 of 163 of the complete genome
1301	14337		3.4	1.4E-02	U67779.1	NT	Xenopus laevis neurogenin related 1b (X-NGNR-1b) mRNA, complete cds
1520	14552		1.03	1.4E-02	AV723785.1	EST_HUMAN	AV723785 HTB Homo sapiens cDNA clone HTBAHH11.5
3226	16281	29204	2.04	1.4E-02	AF160959.2	NT	Blifobacterium longum Na+/H+ antiporter (nhab), cytosine deaminase, and alpha-galactosidase (aglL) genes, complete cds; and N-acetylglucosamine/xylose repressor protein (nagCxyR) gene, partial cds
3409	16458	29380	0.98	1.4E-02	AW074212.1	EST_HUMAN	x09c09.x1 NCI_CGAP_GU1 Homo sapiens cDNA clone IMAGE:2575783.3
3496	16543	29467	6.29	1.4E-02	AL161586.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 82
3496	16543	29468	6.29	1.4E-02	AL161586.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 82
3689	16712	29627	6.89	1.4E-02	6996918	NT	Mus musculus histocompatibility 2, complement component factor B (H2-B), mRNA
4516	17541	30427	6.1	1.4E-02	AW962888.1	EST_HUMAN	EST374761 IMAGE resequences, MAGG Homo sapiens cDNA
4516	17541	30428	6.1	1.4E-02	AW962888.1	EST_HUMAN	EST374761 IMAGE resequences, MAGG Homo sapiens cDNA
4911	17928	30818	8.08	1.4E-02	BE733142.1	EST_HUMAN	601567403F1 NIH_MGC 21 Homo sapiens cDNA clone IMAGE:3842280.5
4911	17928	30819	8.08	1.4E-02	BE733142.1	EST_HUMAN	601567403F1 NIH_MGC 21 Homo sapiens cDNA clone IMAGE:3842280.5
5130	18139	31017	1.01	1.4E-02	AW948453.1	EST_HUMAN	CM0-FN0041-120500-370-F09 FN0041 Homo sapiens cDNA
5888	25992		0.95	1.4E-02	X91338.1	NT	H. sapiens LaSS-B pseudogene 3
6555	19615	32890	4.9	1.4E-02	AA559030.1	EST_HUMAN	nt11c04.s1 NCI_CGAP_Br2 Homo sapiens cDNA clone IMAGE:1029980.3 similar to contains Alu repetitive element;
6555	19615	32881	4.9	1.4E-02	AA559030.1	EST_HUMAN	nt11c04.s1 NCI_CGAP_Br2 Homo sapiens cDNA clone IMAGE:1029980.3 similar to contains Alu repetitive element;
8478	21447		1.61	1.4E-02	AL02073.1	NT	Mycobacterium tuberculosis H37Rv complete genome; segment 88/162
9249	22215	35645	0.77	1.4E-02	M81702.1	NT	Candida boldii melharal oxidase (AOD1) gene, complete cds
9510	22473	35917	0.9	1.4E-02	AJ272865.1	NT	Homo sapiens SPP2 gene for secreted phosphoprotein 24 precursor, exons 1-8
9755	22696	36153	2.15	1.4E-02	BE644661.1	EST_HUMAN	601078239F1 NIH_MGC 12 Homo sapiens cDNA clone IMAGE:3464241.5
10923	23843		0.58	1.4E-02	AL163218.2	NT	Homo sapiens chromosome 21 segment HS21C018

Table 4
Single Exon Probes Expressed In Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
12254	25080	38172	2.14	1.4E-02	X60459.1	NT	Human IFNAR gene for interferon alpha/beta receptor
12616	25312		1.47	1.4E-02	AF324985.1	NT	Arabidopsis thaliana F21J9.2 mRNA, complete cds
12882	25474		1.96	1.4E-02	11426988	NT	Homo sapiens sperm associated antigen 7 (SPAG7), mRNA
1972	14993	27894	2.05	1.3E-02	AL163201.2	NT	Homo sapiens chromosome 21 segment HS21C001
3227	16282	29205	2.31	1.3E-02	BF697081.1	EST_HUMAN	602129475F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4286203 5'
3227	16282	29206	2.31	1.3E-02	BF697081.1	EST_HUMAN	602129475F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4286203 5'
3993	17033		1.38	1.3E-02	AF169288.1	NT	Mus musculus beta-sarcoglycan gene, complete cds
4964	17979	30869	1.06	1.3E-02	U66061.1	NT	Human germline T-cell receptor beta chain TCRBV17S1A1T, TCRBV2S1, TCRBV10S1P, TCRBV29S1P, TCRBV19S1P, TCRBV15S1, TCRBV11S1A1T, HVB relic, TCRBV28S1P, TCRBV34S1, TCRBV14S1, TCRBV3S1, TCRBV4S1A1T, TRY4, TRY5, TRY6, TRY7, TRY8, TCRBD1, TCRBJ1S1, TCRBJ1S2>
5317	18423	31225	1.79	1.3E-02	AL049866.2	NT	Mus musculus chromosome X contigB; X-linked lymphocyte regulated 5 gene, Zinc finger protein 275, Zinc finger protein 92, mnxq28orf
5317	18423	31226	1.79	1.3E-02	AL049866.2	NT	Mus musculus chromosome X contigB; X-linked lymphocyte regulated 5 gene, Zinc finger protein 275, Zinc finger protein 92, mnxq28orf
6298	19360	32597	1.21	1.3E-02	U80017.1	NT	Homo sapiens basic transcription factor 2 p44 (btf2p44) gene, partial cds, neuronal apoptosis inhibitory protein (naip) and survival motor neuron protein (smn) genes, complete cds
6322	19393	32634	0.7	1.3E-02	M62982.1	NT	C.reinhardtii ribulose 1,5-bisphosphate carboxylase/oxygenase activase mRNA, complete cds
7154	18386	31228	1.25	1.3E-02	AL161546.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 46
7154	18386	31229	1.25	1.3E-02	AL161546.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 46
7829	20777	34155	4.86	1.3E-02	A031593.1	EST_HUMAN	ow06g05.x1 Soares_parathyroid_tumor_NbHPA Homo sapiens cDNA clone IMAGE:1646072 3' similar to contains Alu repetitive element;
8826	21793	35216	1.48	1.3E-02	AF156961.1	NT	Homo sapiens human endogenous retrovirus W gagC3.37 G gag (gag) gene, complete cds
10567	23489	36981	2.18	1.3E-02	M63707.1	NT	Mouse kidney androgen-regulated protein (KAP) gene, complete cds
10641	23563	37059	0.63	1.3E-02	AE001304.1	NT	Chlamydia trachomatis section 31 of 87 of the complete genome
10988	23908	37421	0.44	1.3E-02	AA707741.1	EST_HUMAN	zh24e07.s1 Soares_pituitary_gland_N3HPG Homo sapiens cDNA clone IMAGE:412980 3'
11336	24286	37809	3.74	1.3E-02	AW268563.1	EST_HUMAN	xx34e03.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2815036 3'
11336	24286	37810	3.74	1.3E-02	AW268563.1	EST_HUMAN	xx34e03.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2815036 3'
12622	25023		1.4	1.3E-02	Z99117.1	NT	Bacillus subtilis complete genome (section 14 of 21); from 2559451 to 2812870
12714	25368		2.51	1.3E-02	9633063	NT	Human herpesvirus 6B, complete genome
12856	25718		16.88	1.3E-02	AF152238.1	NT	Homo sapiens V1b vasopressin receptor (VPR3) gene, complete cds
214	13314		0.67	1.2E-02	X87344.1	NT	H.sapiens DMA, DMB, HLA-Z1, IP2, LMP2, TAP1, LMP2, DOB, DQ82 and RING8, 9, 13 and 14 genes

Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
355	13443	26368	4.67	1.2E-02	AA050299.1	EST_HUMAN	z65g01.r1 Soares retina N2b4HR Homo sapiens cDNA clone IMAGE:381840 5' similar to contains element L1 repetitive element:
453	13526	26456	1.81	1.2E-02	P38898	SWISSPROT	HYPOTHETICAL 17.1 KD PROTEIN IN PUR5 3'REGION
740	13801	26740	3.32	1.2E-02	A1183522.1	EST_HUMAN	q68e12.x1 Soares testis_NHT Homo sapiens cDNA clone IMAGE:1734670 3' similar to contains L1.1 L1 repetitive element:
2187	15202	28222	1.82	1.2E-02	AL163213.2	NT	Homo sapiens chromosome 21 segment HS21C013
2190	15205	28225	1.44	1.2E-02	AV731704.1	EST_HUMAN	AV731704 HTF Homo sapiens cDNA clone HTFBHG11 5'
2448	15454	28476	1.65	1.2E-02	AW172350.1	EST_HUMAN	x37e09.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2659432 3'
2505	15508	28534	0.99	1.2E-02	BE538310.1	EST_HUMAN	601088406F1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3454608 5'
2505	15508	28535	0.99	1.2E-02	BE538310.1	EST_HUMAN	601088406F1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3454608 5'
2643	15454	28476	1.31	1.2E-02	AW172350.1	EST_HUMAN	x37e09.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2659432 3'
3118	16175	29273	6.56	1.2E-02	AA075418.1	EST_HUMAN	zm88e03.r1 Stratagene ovarian cancer (#837219) Homo sapiens cDNA clone IMAGE:545020 5'
3301	16354	29273	2.62	1.2E-02	R62805.1	EST_HUMAN	y11b08.s1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:138903 3'
4917	17834	30826	8.36	1.2E-02	6754367	NT	Mus musculus interferon regulatory factor 5 (irf5), mRNA
4953	17968	30858	1.66	1.2E-02	U91328.1	NT	Human hereditary haemochromatosis region, histone 2A-like protein gene, hereditary haemochromatosis (HLA-H) gene, RoRet gene, and sodium phosphate transporter (NPT3) gene, complete cds
5080	18030		1.54	1.2E-02	AB019786.1	NT	Cynops pyrrhogaster CpUbiqT mRNA, partial cds
5121	18131	31008	2.09	1.2E-02	AV731704.1	EST_HUMAN	AV731704 HTF Homo sapiens cDNA clone HTFBHG11 5'
5259	18267	31135	1.01	1.2E-02	AF185576.1	NT	Mus musculus POZ/zinc finger transcription factor ODA-8 mRNA, complete cds
5769	18861		0.5	1.2E-02	AA759018.1	EST_HUMAN	a28f10.s1 Soares testis_NHT Homo sapiens cDNA clone 1344235 3'
5846	18936	32120	1.72	1.2E-02	D75589.1	NT	Rana rugosa mRNA for calcitriol, complete cds
6238	19311	32543	0.58	1.2E-02	AF045555.1	NT	Homo sapiens wiscr1 (WBSCR1) and wiscr5 (WBSCR5) genes, complete cds, alternatively spliced and replication factor C subunit 2 (RFC2) gene, complete cds
7203	20227	33560	5.57	1.2E-02	AF178412.1	NT	Mus musculus DNA methyltransferase (Dnmt1) gene, exons 2, 3, 4, and 5
7510	20475	33836	1.07	1.2E-02	H02197.1	EST_HUMAN	y34h12.s1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:150686 3'
7534	20497	33858	8.5	1.2E-02	AV732093.1	EST_HUMAN	AV732093 HTF Homo sapiens cDNA clone HTFBUC09 5'
7805	20755	34131	0.54	1.2E-02	BF216650.1	EST_HUMAN	601882949F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4095253 5'
8330	21299	34715	2.29	1.2E-02	Q11205	SWISSPROT	CMP-N-ACETYLNEURAMINATE-BETA-GALACTOSAMIDE-ALPHA-2,3-SIALYLTRANSFERASE (BETA-GALACTOSIDE ALPHA-2,3-SIALYLTRANSFERASE) (ALPHA 2,3-ST) (GAL-NAc6S) (GAL-BETA-1,3-GALNAc-ALPHA-2,3-SIALYLTRANSFERASE) (ST3GAL4.2) (SIAT4-B)
8534	21502	34919	1.31	1.2E-02	AF193612.1	NT	Homo sapiens fringe protein mRNA, partial cds
8534	21502	34920	1.31	1.2E-02	AF193612.1	NT	Homo sapiens fringe protein mRNA, partial cds
9242	22208		1.1	1.2E-02	T76987.1	EST_HUMAN	y172c08.s1 Soares fetal liver spleen 1N1FLS Homo sapiens cDNA clone IMAGE:113774 3'

Table 4
Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9997	22824	36389	2.63	1.2E-02	AB031013.1	NT	Nonwalk-like virus genogroup 2 gene for capsid protein, complete cds
10030	22957	36425	1.29	1.2E-02	AJ246003.1	NT	Homo sapiens Spast gene for spastin protein
12310	25118	31841	2.74	1.2E-02	O15534	SWISSPROT	PERIOD CIRCADIAN PROTEIN 1 (CIRCADIAN PACEMAKER PROTEIN RIGU1) (HPER)
12896	25482		5.61	1.2E-02	C18119.1	EST_HUMAN	C18119 Human placenta cDNA (TFujiwara) Homo sapiens cDNA clone GEN-557G06 5'
1274	14309	27270	1.14	1.1E-02	AA070364.1	EST_HUMAN	zn69e11.s1 Stratagene neuroepithelium (#837231) Homo sapiens cDNA clone IMAGE:530824 3'
1719	14749	27734	1.8	1.1E-02	X75491.1	NT	H. sapiens LIPA gene, exon 4
1719	14749	27735	1.8	1.1E-02	X75491.1	NT	H. sapiens LIPA gene, exon 4
2054	15073	28092	4.08	1.1E-02	BF345263.1	EST_HUMAN	602018037F1 NCL_CGAP_Bn67 Homo sapiens cDNA clone IMAGE:4153808 5'
2889	15948		3.91	1.1E-02	N99523.1	EST_HUMAN	za40e05.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:285040 5'
3535	16581	29505	2.75	1.1E-02	AI653508.1	EST_HUMAN	iq95b10.x1 NCL_CGAP_Ov23 Homo sapiens cDNA clone IMAGE:2216539 3' similar to SW:XPFF_HUMAN
4051	17088		1.52	1.1E-02	BE144837.1	EST_HUMAN	Q92889 DNA-REPAIR PROTEIN COMPLEMENTING XP-F CELL ;
4133	17165		0.71	1.1E-02	AW813796.1	EST_HUMAN	PN3-HT0175-300999-001-h06 HT0175 Homo sapiens cDNA
4867	17884	30772	2.22	1.1E-02	AL048983.2	EST_HUMAN	RC3-ST0197-120200-015-g11 ST0197 Homo sapiens cDNA
							DKFZp566E0924 s1 586 (synonym: hute1) Homo sapiens cDNA clone DKFZp566E0824
6272	19345	32578	1.02	1.1E-02	U66480.1	NT	Bacillus subtilis SpoVK (spoVK), YnaA (ybaA), YnaB (ybaB), GlnR (glnR), glutamine synthetase (glnA), YnaH (ybaH), YnaI (ybaI), YnaJ (ybaJ), YnaD (ybaD), YnaE (ybaE), YnaF (ybaF), YnaG (ybaG), YnaH (ybaH)
7855	20800	34176	2.47	1.1E-02	BE149811.1	EST_HUMAN	RC1-HT0256-100300-016-h07 HT0256 Homo sapiens cDNA
8105	21042	34441	3.79	1.1E-02	9631294	NT	Melanoplus sanguinipes entomopoxvirus, complete genome
8987	21953	35377	0.7	1.1E-02	AW996160.1	EST_HUMAN	QY3-BN0045-220300-128-h02 BN0045 Homo sapiens cDNA
9174	22140	35566	0.66	1.1E-02	C04803.1	EST_HUMAN	C04803 Human heart cDNA (Ynakamura) Homo sapiens cDNA clone 3NH4C4040
9253	22219	36650	7.21	1.1E-02	Q61982	SWISSPROT	NEUROGENIC LOCUS NOTCH 3 PROTEIN
10289	23214	36698	2.1	1.1E-02	AA082578.1	EST_HUMAN	zn24a01.r1 Stratagene neuroepithelium NT2RAM1 937234 Homo sapiens cDNA clone IMAGE:548328 5'
10454	23376	36869	3.79	1.1E-02	AA314866.1	EST_HUMAN	EST186494 Colon carcinoma (HCC) cell line II Homo sapiens cDNA 5' end
11324	24274	37802	2.01	1.1E-02	11435505	NT	Homo sapiens T-box 5 (TBX5), mRNA
12194	25039		3.52	1.1E-02	AA668239.1	EST_HUMAN	ab77711.s1 Stratagene fetal retina 937202 Homo sapiens cDNA clone IMAGE:853005 3' similar to contains
12960	17165		1.67	1.1E-02	AW813796.1	EST_HUMAN	Alu repetitive element
7	13127	26027	6.08	1.0E-02	AW846120.1	EST_HUMAN	RC3-ST0197-120200-015-g11 ST0197 Homo sapiens cDNA
1526	14559	27530	1.07	1.0E-02	AW368128.1	EST_HUMAN	MR3-CT0176-111098-003-e10 CT0176 Homo sapiens cDNA
2578	15579		1.26	1.0E-02	AA080388.1	EST_HUMAN	CM2-HT0177-041099-017-h12 HT0177 Homo sapiens cDNA
3106	16163	29075	2.7	1.0E-02	BE835556.1	EST_HUMAN	cc22n08.s1 NCL_CGAP_GGB1 Homo sapiens cDNA clone IMAGE:1350495 3'
3276	16330	29251	1.33	1.0E-02	BE868999.1	EST_HUMAN	RCO-FN0025-250500-021-d02 FN0025 Homo sapiens cDNA
							601649967R1 NIH_MGC_74 Homo sapiens cDNA clone IMAGE:3933889 3'

Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3620	16586		0.65	1.0E-02	AW945621.1	EST_HUMAN	MR0-CT0060-081099-003-h10 CT0060 Homo sapiens cDNA
3895	16935	29845	0.75	1.0E-02	A065086.1	EST_HUMAN	HA0921 Human fetal liver cDNA library Homo sapiens cDNA
3911	16981	29862	1.06	1.0E-02	AL163302.2	NT	Homo sapiens chromosome 21 segment HS21C102
4811	17828	30725	4.97	1.0E-02	6753521	NT	Mus musculus corticotropin releasing hormone receptor 2 (Chr2), mRNA
4881	17888	30787	5.01	1.0E-02	R96567.1	EST_HUMAN	yq54h01.1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:199633 5'
5036	18049	30929	0.63	1.0E-02	AL161593.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 89
5490	18590	31501	0.86	1.0E-02	H52681.1	EST_HUMAN	yq36h11.1 Soares ovary tumor NbhOT Homo sapiens cDNA clone IMAGE:235941 5'
5840	18930	32114	0.82	1.0E-02	AF309388.1	NT	Mus musculus transcription complex subunit NF-ATc4 (Nfatc4) gene, exons 1 and 2
6237	19310	32542	1.02	1.0E-02	AF257303.1	NT	Mus musculus synaptotagmin II (Sy2) gene, complete cds
6305	19376	32614	2.49	1.0E-02	AW577113.1	EST_HUMAN	MR4-BT0356-070100-201-h01 BT0356 Homo sapiens cDNA
6305	19376	32615	2.49	1.0E-02	AW577113.1	EST_HUMAN	MR4-BT0356-070100-201-h01 BT0356 Homo sapiens cDNA
6926	20150	33470	2.15	1.0E-02	Z29642.1	NT	Z.mays U3snRNA pseudogene
9748	22689	36145	4.19	1.0E-02	BF036331.1	EST_HUMAN	601459570F1 NIH_MGC 66 Homo sapiens cDNA clone IMAGE:3863177 5'
9748	22689	36146	4.19	1.0E-02	BF036331.1	EST_HUMAN	601459570F1 NIH_MGC 66 Homo sapiens cDNA clone IMAGE:3863177 5'
11594	24532		1.96	1.0E-02	AF157559.1	NT	Orithidia fasciculata 27 kDa guide RNA-binding protein mRNA, complete cds; mitochondrial gene for mitochondrial product
11695	24680	38238	2.05	1.0E-02	AV760016.1	EST_HUMAN	AV760016 MDS Homo sapiens cDNA clone MDSBDC10 5'
12091	24962		1.47	1.0E-02	AL163282.2	NT	Homo sapiens chromosome 21 segment HS21C082
12276	25990		1.99	1.0E-02	Q62203	SWISSPROT	SPLICOSOME ASSOCIATED PROTEIN 62 (SAP 62) (SPLICING FACTOR 3A SUBUNIT 2) (SF3A66)
12337	25757	31518	3.9	1.0E-02	AW685621.1	EST_HUMAN	RC2-DT0007-120200-016-h02 DT0007 Homo sapiens cDNA
12356	25816		5.96	1.0E-02	S70330.1	NT	Homo sapiens renal dipeptidase (RDP) gene, complete cds
12722	25789		2.07	1.0E-02	AJ276505.1	NT	Mus musculus genomic fragment, 279 Kb, chromosome 7
12873	25873		4.76	1.0E-02	X62654.1	NT	H.sapiens gene for Me491/CD63 antigen
13094	25620	31676	1.7	1.0E-02	AB039887.1	NT	Homo sapiens WDR4 gene for WD repeat protein, complete cds
894	13949	26907	1.77	9.0E-03	AI796126.1	EST_HUMAN	WM4209.x1 NCI_CGAP_Kid111 Homo sapiens cDNA clone IMAGE:2383433 3' similar to contains element
1269	14304		1.88	9.0E-03	BE781889.1	EST_HUMAN	MER22 MER22 repetitive element
1476	14510	27485	0.97	9.0E-03	AE001270.1	NT	601470242F1 NIH_MGC 67 Homo sapiens cDNA clone IMAGE:3873346 5'
2405	15412	28436	2.87	9.0E-03	AL161559.2	NT	Treponema pallidum section 86 of 87 of the complete genome
2413	15420	28444	0.95	9.0E-03	AF099934.1	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 59
2917	15975	28898	0.69	9.0E-03	AI251744.1	EST_HUMAN	Mus musculus MHC class III protein RPI (Rpi) mRNA, partial cds
2917	15975	28899	0.69	9.0E-03	AI251744.1	EST_HUMAN	qh90f09.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1854281 3'
3682	16725	29638	0.87	9.0E-03	JO5184.1	NT	qh90f09.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1854281 3'
5061	18071	30950	1.01	9.0E-03	T70044.1	EST_HUMAN	S.acidocaldarius thermophilin gene, complete cds
							ye17608.s1 Stragene lung (#937210) Homo sapiens cDNA clone IMAGE:80919 3'

Table 4

Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5061	18071	30951	1.01	9.0E-03	170044.1	EST_HUMAN	yc17b08.s1 Stratagene lung (#937210) Homo sapiens cDNA clone IMAGE:80919 3'
5280	18268	31136	0.95	9.0E-03	6753321	NT	Mus musculus corticotropin releasing hormone receptor 2 (Chr2), mRNA
5908	18694		1.2	9.0E-03	A1809792.1	EST_HUMAN	w77704.x1 Soares_NFL_T_G8C_S1 Homo sapiens cDNA clone IMAGE:2361631 3'
6785	19840		4	9.0E-03	BE745988.1	EST_HUMAN	601573439F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3834752 5'
7688	20658	34020	0.83	9.0E-03	A1242219.1	EST_HUMAN	qh87c12.x1 Soares_NFL_T_G8C_S1 Homo sapiens cDNA clone IMAGE:1853974 3'
7712	20669	34036	0.81	9.0E-03	8922570	NT	Homo sapiens hypothetical protein FLJ10650 (FLJ10650), mRNA
8207	21177		0.89	9.0E-03	AL039991.1	EST_HUMAN	DKFZp434L0412.1 434 (synonym: htes3) Homo sapiens cDNA clone DKFZp434L0412 5'
8592	21560		0.55	9.0E-03	AF223391.1	NT	Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced
10221	23146	36635	1.42	9.0E-03	P20908	SWISSPROT	COLLAGEN ALPHA 1(V) CHAIN PRECURSOR
11331	24281		1.6	9.0E-03	Y18000.1	NT	Homo sapiens NF2 gene
12690	25985		2.12	9.0E-03	BE348385.1	EST_HUMAN	hw17b09.x1 NCL_GGAP_Lu24 Homo sapiens cDNA clone IMAGE:3183181 3'
12989	25549		15.47	9.0E-03	BF351141.1	EST_HUMAN	PM1-HT0452-291299-001-e09 HT0452 Homo sapiens cDNA
502	13574		3.01	8.0E-03	AA723007.1	EST_HUMAN	zh30e03.s1 Soares_pineal_gland_N3HPG Homo sapiens cDNA clone IMAGE:413596 3' similar to contains Alu repetitive element
891	14043	26997	19.52	8.0E-03	AF108856.1	NT	Homo sapiens adenylosuccinate lyase gene, complete cds
2166	15182	28202	1.66	8.0E-03	AL163283.2	NT	Homo sapiens chromosome 21 segment HS21C083
3321	16372	29293	1.12	8.0E-03	BE171225.1	EST_HUMAN	RC1-HT0545-120200-011-b09 HT0545 Homo sapiens cDNA
3370	16420	29345	0.93	8.0E-03	AL131016.1	NT	Homo sapiens SCL gene locus
3889	16732	29644	1.25	8.0E-03	P32644	SWISSPROT	HYPOTHETICAL 127.0 KD PROTEIN IN RAD24-BMH1 INTERGENIC REGION
3889	16732	29645	1.25	8.0E-03	P32644	SWISSPROT	HYPOTHETICAL 127.0 KD PROTEIN IN RAD24-BMH1 INTERGENIC REGION
4285	17314	30183	1.08	8.0E-03	BE840049.1	EST_HUMAN	QV0-FN0181-140700-304-g10 FN0181 Homo sapiens cDNA
4410	17438	30326	5.3	8.0E-03	BF363327.1	EST_HUMAN	GM4-NN0119-300600-223-505 NN0119 Homo sapiens cDNA
4747	17767	30662	0.65	8.0E-03	P03181	SWISSPROT	HYPOTHETICAL BHLF1 PROTEIN
4747	17767	30663	0.65	8.0E-03	P03181	SWISSPROT	HYPOTHETICAL BHLF1 PROTEIN
5901	18697	31698	2.68	8.0E-03	AF110520.1	NT	Mus musculus major histocompatibility complex region NG27, NG28, RPS28, NADH oxidoreductase, NG28, KIFC1, Fas-binding protein, BING1, tapasin, RalGDS-like KE2, BING4, beta 1,3-galactosyl transferase, and RPS18 genes, complete cds; Sacm21 gene, partial>
6323	25658	32835	1.39	8.0E-03	AP000002.1	NT	Pyrococcus horikoshii OT3 genomic DNA, 287001-544000 nt, position (2/7)
6913	19965	33261	4.24	8.0E-03	P55577	SWISSPROT	PROBABLE PEPTIDASE Y4NA
7104	20038		1.4	8.0E-03	V01109.1	NT	Human BK virus (strain MM) genome. (Closely related to SV40)
7415	20382	33733	1.88	8.0E-03	M17197.1	NT	A. californica (marine gastropod mollusc) neuropeptide gene (bag cell), exon 1, 5' end
7790	20743		1.81	8.0E-03	AB038267.1	NT	Tursiops truncatus mRNA for p40-phox, complete cds

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Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9235	22201	35631	0.58	8.0E-03	P98160	SWISSPROT	BASEMENT MEMBRANE-SPECIFIC HEPARAN SULFATE PROTEOGLYCAN CORE PROTEIN
9261	22227	35657	3.77	8.0E-03	AW808692.1	EST_HUMAN	PRECURSOR (HSPG) (PERLECAN) (PLC)
9270	22236	35665	0.52	8.0E-03	AL139075.2	NT	MR1-ST0111-111199-011-103 ST0111 Homo sapiens cDNA
9331	22296	35726	0.58	8.0E-03	9789956	NT	Campylobacter jejuni NCTC11168 complete genome; segment 2/6
10308	23232		5.16	8.0E-03	BE066609.1	EST_HUMAN	Mus musculus fusion 2 (human) (Fus2), mRNA
11118	24078	37802	1.96	8.0E-03	BE788441.1	EST_HUMAN	QV1-BT0677-040400-131-g03 BT0677 Homo sapiens cDNA
11330	24280		2.68	8.0E-03	Z49852.1	NT	601475619F1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3878405 5'
11849	24586	38158	2.59	8.0E-03	BF33327.1	EST_HUMAN	S.cerevisiae chromosome X reading frame ORF YJR152w
11710	24675	38252	1.55	8.0E-03	AA828817.1	EST_HUMAN	GM4-NN0119-300600-223-b05 NN0119 Homo sapiens cDNA
11710	24675	38253	1.55	8.0E-03	AA828817.1	EST_HUMAN	cd80a09.s1 NCL_CGAP_Ov2 Homo sapiens cDNA clone IMAGE:1374232
12024	24900	38495	3.74	8.0E-03	AF084589.1	NT	cd80a09.s1 NCL_CGAP_Ov2 Homo sapiens cDNA clone IMAGE:1374232
12205	25047		2.04	8.0E-03	M69035.1	NT	Homo sapiens melanoma-associated antigen (MAGE-C1) gene, complete cds
12249	25077		2.6	8.0E-03	AB038161.1	NT	Oryctolagus cuniculus eIF-2a kinase mRNA, complete cds
695	13757	26687	18.14	7.0E-03	AF097183.1	NT	Homo sapiens ABCG1 gene for ABC transporter (ATP-binding cassette, sub-family G (WHITE), member 1), complete cds
695	13757	26688	18.14	7.0E-03	AF097183.1	NT	Cryptosporidium parvum HC-10 gene, complete cds
878	14029	26983	4.66	7.0E-03	AF243376.1	NT	Cryptosporidium parvum HC-10 gene, complete cds
1118	14162	27113	4.38	7.0E-03	AV731712.1	EST_HUMAN	Glycine max glutathione S-transferase GST 21 mRNA, partial cds
1366	14400		1.16	7.0E-03	Q61060	SWISSPROT	AV731712 HTF Homo sapiens cDNA clone HTFAZF10 5'
1366	14430	27359	3.03	7.0E-03	AA668298.1	EST_HUMAN	FORHEAD BOX PROTEIN D3 (HNF3/PH TRANSCRIPTION FACTOR GENESIS) (HEPATOCYTE
1502	14535	27506	3.04	7.0E-03	AW303599.1	EST_HUMAN	NUCLEAR FACTOR 3 FORKHEAD HOMOLOG 2 (HFF-2)
1756	14785	27769	1.03	7.0E-03	AW950556.1	EST_HUMAN	ab79609.s1 Stratagene fetal retina 937202 Homo sapiens cDNA clone IMAGE:853145 3'
1756	14785	27770	1.03	7.0E-03	AW950556.1	EST_HUMAN	xx21b02.x1 Soares_NFL_I_GBC_S1 Homo sapiens cDNA clone IMAGE:2813739 3'
2267	15888	28307	2.08	7.0E-03	P04929	SWISSPROT	EST362626 MAGE resequences, MAGA Homo sapiens cDNA
3571	16616	29537	0.67	7.0E-03	AI150273.1	EST_HUMAN	EST362626 MAGE resequences, MAGA Homo sapiens cDNA
3778	16820	29728	0.93	7.0E-03	AW444463.1	EST_HUMAN	HISTIDINE-RICH GLYCOPROTEIN PRECURSOR
3825	18865	29769	1.45	7.0E-03	AF196344.1	NT	q347402.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1751955 3'
4048	16820	29728	0.83	7.0E-03	AW444463.1	EST_HUMAN	UI-H-B13-akb-c-10-Q-JJ.s1 NCL_CGAP_Sub5 Homo sapiens cDNA clone IMAGE:2733691 3'
4366	17393		0.96	7.0E-03	U60086.1	NT	Dictyostelium discoideum multidrug resistance transporter/Ser protease (tagC) mRNA, complete cds

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Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4565	17588		1	7.0E-03	AW117711.1	EST_HUMAN	xe34f09.x1 NCI CGAP_U11 Homo sapiens cDNA clone IMAGE:2608033 3' similar to TR:Q12987 Q12987
4628	17650		1.47	7.0E-03	AW630888.1	EST_HUMAN	ACIDIC 82 KDA PROTEIN. ;
5024	18038		1.81	7.0E-03	AL163278.2	NT	hh89a05.y1 NCI CGAP_GUT Homo sapiens cDNA clone IMAGE:2669836 5'
5228	18234	31108	1.4	7.0E-03	AV724419.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C078
5228	18234	31109	1.4	7.0E-03	AV724419.1	EST_HUMAN	AV724419 HTB Homo sapiens cDNA clone HTBCE08 5'
5918	19004		0.83	7.0E-03	H71108.1	EST_HUMAN	AV724419 HTB Homo sapiens cDNA clone HTBCE08 5'
6233	25656		5.11	7.0E-03	AW861059.1	EST_HUMAN	y82g01.11 Soares fetal liver spleen INFLS Homo sapiens cDNA clone IMAGE:211824 5' similar to
6447	19512	32762	1.38	7.0E-03	W68251.1	EST_HUMAN	gbx14723 CLUSTERIN PRECURSOR (HUMAN);
6687	19744	33019	3.16	7.0E-03	AA327129.1	EST_HUMAN	RC1-CT0286-050400-018-c08 CT0286 Homo sapiens cDNA
6717	19773	33052	0.91	7.0E-03	BE857385.1	EST_HUMAN	z833f10.11 Soares fetal heart NBHH19W Homo sapiens cDNA clone IMAGE:342475 5'
7284	20061	33367	1.92	7.0E-03	BE928133.1	EST_HUMAN	EST30674 Colon I Homo sapiens cDNA 5' end
7763	20716	34088	5.31	7.0E-03	Z35838.1	NT	7g54b10.x1 NCI CGAP_Brn23 Homo sapiens cDNA clone IMAGE:3308347 3' similar to TR:Q13387
7763	20716	34089	5.31	7.0E-03	Z35838.1	NT	Q13387 HYPOTHETICAL PROTEIN 384D8_2, contains TAR1.2 TAR1 repetitive element ;
8180	21150	34557	0.45	7.0E-03	AJ229043.1	NT	CM2-CT0478-230800-347-b11 CT0478 Homo sapiens cDNA
8180	21150	34558	0.45	7.0E-03	AJ229043.1	NT	S.cerevisiae chromosome II reading frame ORF YBL077w
8448	21417	34830	2.46	7.0E-03	BE175667.1	EST_HUMAN	S.cerevisiae chromosome II reading frame ORF YBL077w
8981	21927	35354	0.48	7.0E-03	AF281074.1	NT	Homo sapiens 959 kb contig between AML1 and CBR1 on chromosome 21q22, segment 3/3
9752	22693		0.71	7.0E-03	AF11168.2	NT	Homo sapiens 959 kb contig between AML1 and CBR1 on chromosome 21q22, segment 3/3
9853	22880	36344	0.85	7.0E-03	N52378.1	EST_HUMAN	RC5-HT0582-160300-011-D02 HT0582 Homo sapiens cDNA
10078	23005	36475	2.84	7.0E-03	P48982	SWISSPROT	Homo sapiens serine palmitoyl transferase, subunit II gene, complete cds; and unknown genes
10078	23005	36476	2.84	7.0E-03	P48982	SWISSPROT	y49c10.s1 Soares fetal liver spleen INFLS Homo sapiens cDNA clone IMAGE:248086 3' similar to contains
10668	23590		1.06	7.0E-03	AV687379.1	EST_HUMAN	Alu repetitive element;
10853	23773		0.85	7.0E-03	AI799734.1	EST_HUMAN	BETA-GALACTOSIDASE PRECURSOR (LACTASE)
11175	24132	37662	2.23	7.0E-03	AB008862.1	NT	BETA-GALACTOSIDASE PRECURSOR (LACTASE)
11248	24201	37722	1.51	7.0E-03	AJ004862.1	NT	AV687379 GKX Homo sapiens cDNA clone GKXAF007 5'
11248	24201	37723	1.51	7.0E-03	AJ004862.1	NT	wc37e09.x1 NCI CGAP_P128 Homo sapiens cDNA clone IMAGE:2320840 3'
12734	25977		1.53	7.0E-03	H64065.1	EST_HUMAN	Bos taurus mRNA for NDP52, complete cds
12741	25391		1.91	7.0E-03	BE263263.1	EST_HUMAN	Homo sapiens partial MUC5B gene, exon 1-29
12834	25451		1.99	7.0E-03	Y17455.1	NT	Homo sapiens partial MUC5B gene, exon 1-29
							W15h01.s1 Soares fetal liver spleen INFLS Homo sapiens cDNA clone IMAGE:242833 3' similar to contains
							Alu repetitive element;
							601145154F2 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:3160476 5'
							Homo sapiens LSFR2 gene, penultimate exon

Single Exon Probes Expressed In Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1245	14282	27244	9.96	6.0E-03	AW511148.1	EST_HUMAN	h22a05.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2910224 3' similar to SW:PXR_HUMAN 076469 ORPHAN NUCLEAR RECEPTOR PXR ;
1245	14282	27245	9.96	6.0E-03	AW511148.1	EST_HUMAN	h22a05.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2910224 3' similar to SW:PXR_HUMAN 076469 ORPHAN NUCLEAR RECEPTOR PXR ;
2782	15774	28793	1.32	6.0E-03	AF112374.1	NT	Danio rerio odorant receptor gene cluster
2901	15960	28879	4.82	6.0E-03	AA759135.1	EST_HUMAN	ah78e11.s1 Soares_testis_NHT Homo sapiens cDNA clone 1321772 3'
2901	15960	28880	4.82	6.0E-03	AA759135.1	EST_HUMAN	ah78e11.s1 Soares_testis_NHT Homo sapiens cDNA clone 1321772 3'
3280	16314		2.26	6.0E-03	H75690.1	EST_HUMAN	y77h04.1 Soares fetal liver spleen 1NFSL Homo sapiens cDNA clone IMAGE:211351 5'
3393	16442	29368	1.3	6.0E-03	U90880.1	NT	Fugu rubripes zinc finger protein, isotocin, fatty acid binding protein, sepiapterin reductase and vasotocin genes, complete cds
3393	16442	29369	1.3	6.0E-03	U90880.1	NT	Fugu rubripes zinc finger protein, isotocin, fatty acid binding protein, sepiapterin reductase and vasotocin genes, complete cds
3557	16603		1.28	6.0E-03	W37985.1	EST_HUMAN	zc13a11.1 Soares_parathyroid_tumor_NbHPA Homo sapiens cDNA clone IMAGE:322172 5'
3672	16715	29629	4.48	6.0E-03	BF510986.1	EST_HUMAN	UIH-B14-epm-c-08-Q-UI.s1 NCL CGAP_Sub8 Homo sapiens cDNA clone IMAGE:3087754 3'
3708	16751	29657	1.21	6.0E-03	BE077356.1	EST_HUMAN	RC1-BT0606-260400-014-a07 BT0606 Homo sapiens cDNA
3790	16831	29737	1.19	6.0E-03	6754029	NT	Mus musculus glucosamine-8-phosphate deaminase (Gnp1), mRNA
3944	16984	29900	0.87	6.0E-03	AW847284.1	EST_HUMAN	RC0-GT0204-240989-021-b10 CT0204 Homo sapiens cDNA
3979	17019		0.9	6.0E-03	BE250108.1	EST_HUMAN	600842904F1 NIH_MGC_15 Homo sapiens cDNA clone IMAGE:2969513 5'
4391	17419		1.81	6.0E-03	A016833.1	EST_HUMAN	ox33c11.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1639124 3'
4724	17744	30635	5.97	6.0E-03	AA324242.1	EST_HUMAN	EST27116 Cerebellum II Homo sapiens cDNA 5' and similar to EST containing Alu repeat
6276	25637	32581	0.9	6.0E-03	9627521	NT	Varicella virus, complete genome
6989	20212	33541	0.87	6.0E-03	O14994	SWISSPROT	SYNAPSIN III
7034	18386	31253	0.84	6.0E-03	BE253748.1	EST_HUMAN	601112353F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3353172 5'
7461	20427	33783	0.83	6.0E-03	AA299442.1	EST_HUMAN	EST11949 Uterus tumor I Homo sapiens cDNA 5' end
7461	20427	33784	0.83	6.0E-03	AA299442.1	EST_HUMAN	EST11949 Uterus tumor I Homo sapiens cDNA 5' end
7908	20851	34238	0.63	6.0E-03	AF128894.1	NT	Homo sapiens telomerase reverse transcriptase (TERT) gene, exons 7-16 and complete cds
8100	21036	34436	0.62	6.0E-03	P17984	SWISSPROT	RAS-RELATED PROTEIN RAP-2B
8136	21073	34473	0.5	6.0E-03	AJ243211.1	NT	Homo sapiens DMBT1 candidate tumour suppressor gene, exons 1 to 65
8191	21161	34571	6.56	6.0E-03	A033980.1	EST_HUMAN	ow13a04.x1 Soares_parathyroid_tumor_NbHPA Homo sapiens cDNA clone IMAGE:1846870 3' similar to contains MER10.b1 MER10 repetitive element ;
8307	21276	34637	2.64	6.0E-03	AW799337.1	EST_HUMAN	RC0-UM0051-210300-032-q02 UM0051 Homo sapiens cDNA
8381	21350		1.51	6.0E-03	BF038108.1	EST_HUMAN	601454615F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3858626 5'
9912	22733	36188	8.57	6.0E-03	D10548.1	NT	Subacute sclerosing panencephalitis (SSPE) virus mRNA for fusion protein

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Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10403	23325		2.08	6.0E-03	AI432681.1	EST_HUMAN	t22c02.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2131202 3' similar to SW:R13A_HUMAN
10523	23445	36943	0.87	6.0E-03	AJ011849.1	NT	P40429 60S RIBOSOMAL PROTEIN L13A ;
10659	23581		1.03	6.0E-03	AF084555.1	NT	Bacillus subtilis fenD gene
10769	23690	37187	0.88	6.0E-03	X68396.1	NT	Homo sapiens okadaic acid-inducible and cAMP-regulated phosphoprotein 19 (ARPP-19) mRNA, complete cds
11096	24056	37580	1.61	6.0E-03	AW962164.1	EST_HUMAN	M.thermoformicum complete plasmid pFV1 DNA
11162	24120		1.55	6.0E-03	U154581.4	NT	EST374237 MAGE resequences, MAGE Homo sapiens cDNA
11327	24277		3.99	6.0E-03	U14556.1	NT	Homo sapiens hypothetical zinc finger protein FLJ14011 (FLJ14011), mRNA
11328	24278	37805	2.55	6.0E-03	BE737895.1	EST_HUMAN	Mus musculus zinc-finger protein mRNA, complete cds
12319	25123		2.28	6.0E-03	AF010493.1	NT	601572746F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:3889747 5'
12422	25812		1.52	6.0E-03	BF671185.1	EST_HUMAN	Rhodobacter capsulatus strain SB1003, partial genome
12446	25744		5.26	6.0E-03	AE000833.1	NT	602151024F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4292212 5'
12525	25807		2.71	6.0E-03	U30790.1	NT	Methanobacterium thermoautotrophicum from bases 428192 to 450298 (section 39 of 148) of the complete genome
12576	25285		1.48	6.0E-03	Q62209	SWISSPROT	Pneumocystis carinii f. sp. ratti guanine nucleotide binding protein alpha subunit (pcg 1) gene, complete cds
12850	25459		2.16	6.0E-03	BE788019.1	EST_HUMAN	SYNAPTONEMAL COMPLEX PROTEIN 1 (SCP-1) PROTEIN
12859	25471		1.53	6.0E-03	AJ245480.1	NT	601482621F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3885388 5'
13043	25584		1.76	6.0E-03	BF10298.1	EST_HUMAN	Brassica napus sig gene for S-locus glycoprotein, cultivar T2
670	13735	26661	2.34	5.0E-03	L25105.1	NT	7n366T1.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3566564 3'
670	13735	26662	2.34	5.0E-03	L25105.1	NT	Chlamydia trachomatis partial ORFB; aminoacyl-tRNA synthase, complete cds; complete ORFA, and grpE-like protein, complete cds
671	13735	26661	3.43	5.0E-03	L25105.1	NT	Chlamydia trachomatis partial ORFB; aminoacyl-tRNA synthase, complete cds; complete ORFA, and grpE-like protein, complete cds
671	13735	26662	3.43	5.0E-03	L25105.1	NT	Chlamydia trachomatis partial ORFB; aminoacyl-tRNA synthase, complete cds; complete ORFA, and grpE-like protein, complete cds
1114	14158	27109	1.03	5.0E-03	AJ010457.1	NT	Chlamydia trachomatis partial ORFB; aminoacyl-tRNA synthase, complete cds; complete ORFA, and grpE-like protein, complete cds
1574	14607		1.02	5.0E-03	AI138977.1	EST_HUMAN	Arabidopsis thaliana mRNA for DEAD box RNA helicase RH3
2690	15686	28703	2.63	5.0E-03	AB033006.1	NT	q679405.x1 Soares_Jesfis_NHT Homo sapiens cDNA clone IMAGE:1735689 3'
2947	16005	28930	3.66	5.0E-03	BE266057.1	EST_HUMAN	Homo sapiens mRNA for KIAA1180 protein, partial cds
3163	16210	29125	3.98	5.0E-03	T67923.1	EST_HUMAN	601194796F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3538799 5'
3169	16224		3.05	5.0E-03	AL161491.2	NT	y681f09.s1 Soares infant brain TNIS Homo sapiens cDNA clone IMAGE:22395 3'
							Arabidopsis thaliana DNA chromosome 4, contig fragment No. 3

Table 4

Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3181	16236	29153	1.22	5.0E-03	R71794.1	EST_HUMAN	y86g02.s1 Scores breast 2NBHst Homo sapiens cDNA clone IMAGE:155666 3'
3291	16344		0.94	5.0E-03	AJ297357.1	NT	Homo sapiens partial LIMD1 gene for LIM domains containing protein 1 and KIAA0851 gene
3679	16722	29635	0.97	5.0E-03	AL163285.2	NT	Homo sapiens chromosome 21 segment HS21C085
3713	16756	29670	4.03	5.0E-03	AF147449.2	NT	Pseudomonas aeruginosa strain PAO1 penicillin-binding protein 1B (ponB) gene, complete cds
3771	16813	29722	1	5.0E-03	U38914.1	NT	Citrus sinensis seed storage protein cDNA, complete cds
3995	17035		2	5.0E-03	AA299675.1	EST_HUMAN	EST12218 Uterus tumor 1 Homo sapiens cDNA 5' end
4333	17361	30246	0.69	5.0E-03	H78355.1	EST_HUMAN	y779g10.r1 Scores fetal liver spleen 1NLS Homo sapiens cDNA clone IMAGE:240068 5'
4335	16813	29722	1.02	5.0E-03	U38914.1	NT	Citrus sinensis seed storage protein cDNA, complete cds
4601	17622	30515	1.02	5.0E-03	U46991.1	NT	Human putative chromatin structure regulator (SUPT6H) mRNA, complete cds
4638	17659	30548	1.13	5.0E-03	AJ131018.1	NT	Homo sapiens SCL gene locus
4749	17769	30665	1.34	5.0E-03	AJ752367.1	EST_HUMAN	cn15c02.x1 Normal Human Trabecular Bone Cells Homo sapiens cDNA clone NH7BC_cn15c02 random
4970	17985	30875	1.08	5.0E-03	P15265	SWISSPROT	SPERM MITOCHONDRIAL CAPSULE SELENOPROTEIN (MCS)
5222	18230	31105	1.69	5.0E-03	6754029	NT	Mus musculus glucosaminide-6-phosphate deaminase (Gnp), mRNA
5893	18981	32172	5.69	5.0E-03	P35500	SWISSPROT	SODIUM CHANNEL PROTEIN PARA (PARALYTIC PROTEIN)
6162	19237	32468	2.97	5.0E-03	O00507	SWISSPROT	PROBABLE UBIQUITIN CARBOXYL-TERMINAL HYDROLASE FAF-Y (UBIQUITIN THIOLESTERASE FAF-Y) (UBIQUITIN-SPECIFIC PROCESSING PROTEASE FAF-Y) (DEUBIQUITINATING ENZYME FAF-Y) (FAT FACETS PROTEIN RELATED, Y-LINKED) (UBIQUITIN-SPECIFIC PROTEASE 9, Y CHROMOSOME)
6198	19272		0.89	5.0E-03	AE002234.2	NT	Chlamydomonas reinhardtii AR39, section 62 of 94 of the complete genome
6747	19801		7.44	5.0E-03	BE300091.1	EST_HUMAN	800944564 T1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:2960871 3'
7023	18355	31274	7.12	5.0E-03	AB025024.1	NT	Mus musculus AMD1 gene for S-adenosylmethionine decarboxylase, complete cds
7240	19976		0.82	5.0E-03	AB038287.1	NT	Tursiops truncatus mRNA for p40-phox, complete cds
7295	20267	33602	0.57	5.0E-03	6753551	NT	Mus musculus dynein, axon, heavy chain 11 (Dnaic11), mRNA
7727	20683	34047	0.62	5.0E-03	T05124.1	EST_HUMAN	EST03012 Fetal brain, Striatum (cat#36206) Homo sapiens cDNA clone HFBOR93 similar to EST containing Alu repeat
7856	20801		1.17	5.0E-03	AW854327.1	EST_HUMAN	RC3-CT0255-031099-011-407 CT0255 Homo sapiens cDNA
8044	20981	34378	6.8	5.0E-03	AB016816.1	NT	Homo sapiens MASL1 mRNA, complete cds
8097	21033	34431	0.49	5.0E-03	Q9R001	SWISSPROT	ADAM-TS 5 PRECURSOR (A DISINTEGRIN AND METALLOPROTEINASE WITH THROMBOSPONDIN MOTIFS 5) (ADAMTS-5) (ADAM-TS5) (AGGRECANASE-2) (ADMP-2) (IMPLANTIN)
8097	21033	34432	0.49	5.0E-03	Q9R001	SWISSPROT	ADAM-TS 5 PRECURSOR (A DISINTEGRIN AND METALLOPROTEINASE WITH THROMBOSPONDIN MOTIFS 5) (ADAMTS-5) (ADAM-TS5) (AGGRECANASE-2) (ADMP-2) (IMPLANTIN)
8581	21549	34967	2.12	5.0E-03	P48982	SWISSPROT	BETA-GALACTOSIDASE PRECURSOR (LACTASE)
8959	21925		5.83	5.0E-03	M61132.1	NT	Mouse complement receptor (CR2) mRNA, 3' end

Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9159	22125	35554	1.08	5.0E-03	D90723.1	NT	Escherichia coli genomic DNA. (19.1 - 19.4 min)
9292	22258	35688	0.61	5.0E-03	M25090.1	NT	Rabbit uteroglobin (UGL) gene, exon 1
10199	23124	36611	0.97	5.0E-03	L21710.1	NT	Plasmidium berghel 58 kDa phosphoprotein mRNA, partial cds
10330	23254	36732	0.68	5.0E-03	AW821888.1	EST_HUMAN	RC3-ST0379-210100-032-c02 ST0379 Homo sapiens cDNA
10518	23440	36938	0.44	5.0E-03	AA533143.1	EST_HUMAN	h46h10.s1 NCI CGAP_P19 Homo sapiens cDNA clone IMAGE:995587
10686	23618	37112	0.47	5.0E-03	7662557	NT	Homo sapiens PRO0471 protein (PRO0471), mRNA
10844	23764		0.51	5.0E-03	AA653261.1	EST_HUMAN	eg49c10.s1 Gessler Wilms tumor Homo sapiens cDNA clone IMAGE:1126290 3'
11075	24037		4.17	5.0E-03	T19586.1	EST_HUMAN	694F Heart Homo sapiens cDNA clone 694
11287	24237	37764	2.15	5.0E-03	AW170334.1	EST_HUMAN	xt59g05.x1 Soares_NHCEC_cervical_tumor Homo sapiens cDNA clone IMAGE:2698040 3' similar to contains L1.12 L1 repetitive element ;
11287	24237	37765	2.15	5.0E-03	AW170334.1	EST_HUMAN	xt59g05.x1 Soares_NHCEC_cervical_tumor Homo sapiens cDNA clone IMAGE:2698040 3' similar to contains L1.12 L1 repetitive element ;
11381	24328	37857	1.55	5.0E-03	T49163.1	EST_HUMAN	y099e04.r1 Stralagene placenta (#937225) Homo sapiens cDNA clone IMAGE:70886 5'
11659	24595		3.62	5.0E-03	BE048055.1	EST_HUMAN	tz46c04.y1 NCI CGAP_Brm52 Homo sapiens cDNA clone IMAGE:2291622 5'
12463	25938		5.42	5.0E-03	AF047874.1	NT	Gallus gallus glyceraldehyde-3-phosphate dehydrogenase mRNA, complete cds
12595	25298		3.7	5.0E-03	AF067253.1	NT	Brugia malayi Y chromosome marker
12888	25355		3.19	5.0E-03	L10347.1	NT	Human pro-alpha1 type II collagen (COL2A1) gene exons 1-54, complete cds
12718	25372		1.89	5.0E-03	AA456597.1	EST_HUMAN	z075a03.s1 Soares ovary tumor NBHOT Homo sapiens cDNA clone IMAGE:809548 3' similar to
12743	25752		5.67	5.0E-03	BF572332.1	EST_HUMAN	SW-DXA2_MOUSE P14685 PROBABLE DIPHENOL OXIDASE A2 COMPONENT ;
12922	25498	31702	3.21	5.0E-03	AW449109.1	EST_HUMAN	602077774F1 NIH_MGC_62 Homo sapiens cDNA clone IMAGE:4252002 5'
235	13335	26259	2.6	4.0E-03	AW500196.1	EST_HUMAN	UH-B13-akf-4-08-0-J1.s1 NCI CGAP_Sub5 Homo sapiens cDNA clone IMAGE:2734215 3'
321	13413	26337	2.12	4.0E-03	R46482.1	EST_HUMAN	UI-HF-BNO-akc-H-04-0-J1.r1 NIH_MGC_50 Homo sapiens cDNA clone IMAGE:3076831 5'
443	13516	26449	1.15	4.0E-03	P54675	SWISSPROT	y051e04.s1 Soares Infant brain T1NB Homo sapiens cDNA clone IMAGE:35988 3'
605	13672	26586	4.63	4.0E-03	AA939339.1	EST_HUMAN	PHOSPHATIDYLINOSITOL 3-KINASE 3 (PI3-KINASE) (PTDINS-3-KINASE) (PI3K)
878	13833	26803	1.9	4.0E-03	R46482.1	EST_HUMAN	on75g12.s1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1562566 3'
912	13987		3.64	4.0E-03	AW749101.1	EST_HUMAN	y051e04.s1 Soares Infant brain T1NB Homo sapiens cDNA clone IMAGE:35988 3'
1153	14195	27147	27.01	4.0E-03	AA099777.1	EST_HUMAN	RC3-BT0333-110100-012-f01 BT0333 Homo sapiens cDNA
1173	14214	27169	1.92	4.0E-03	AW794740.1	EST_HUMAN	281a08.r1 Stralagene colon (#937204) Homo sapiens cDNA clone IMAGE:510998 5'
1306	14342	27306	1.5	4.0E-03	AA284374.1	EST_HUMAN	RC6-UM0014-170400-023-G01 UM0014 Homo sapiens cDNA
1590	14622		1.64	4.0E-03	AV708305.1	EST_HUMAN	zs59a01.r1 NCI CGAP_GCB1 Homo sapiens cDNA clone IMAGE:701736 5'
1758	14787	27772	2.38	4.0E-03	U33472.1	NT	AV708305 ADC Homo sapiens cDNA clone ADCAKB06 5'
2034	15053	28070	11.42	4.0E-03	AA099777.1	EST_HUMAN	Rattus norvegicus type 1 astrocyte and olfactory-limbic associated protein AT1-48 mRNA, complete cds
							281a08.r1 Stralagene colon (#937204) Homo sapiens cDNA clone IMAGE:510998 5'

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Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2259	15273		1.66	4.0E-03	BE410556.1	EST_HUMAN	601304161F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3638510 5'
2286	15299	28323	1.53	4.0E-03	AW794740.1	EST_HUMAN	RC8-UM0014-170400-023-G01 UM0014 Homo sapiens cDNA
2579	15590	28598	1.75	4.0E-03	U52111.2	NT	Homo sapiens X28 region near ALD locus containing dual specificity phosphatase 9 (DUSP9), ribosomal protein L18a (RPL18a), Ca2+/Calmodulin-dependent protein kinase I (CAMKI), creatine transporter (CRTR), CDM protein (CDM), adrenoleukodystrophy protein >
2579	15590	28599	1.75	4.0E-03	U52111.2	NT	Homo sapiens X28 region near ALD locus containing dual specificity phosphatase 9 (DUSP9), ribosomal protein L18a (RPL18a), Ca2+/Calmodulin-dependent protein kinase I (CAMKI), creatine transporter (CRTR), CDM protein (CDM), adrenoleukodystrophy protein >
2701	15697	28712	3.92	4.0E-03	AJ277365.1	NT	CDM protein (CDM), adrenoleukodystrophy protein >
2701	15697	28713	3.92	4.0E-03	AJ277365.1	NT	Homo sapiens polyglutamine-containing C14ORF4 gene
2707	15702	28716	1.68	4.0E-03	AL163284.2	NT	Homo sapiens polyglutamine-containing C14ORF4 gene
3239	16294	29217	1.04	4.0E-03	BE154134.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C084
3239	16294	29218	1.04	4.0E-03	BE154134.1	EST_HUMAN	PM1-HT0340-151299-003-h08 HT0340 Homo sapiens cDNA
3541	16587	29510	0.8	4.0E-03	BE154134.1	EST_HUMAN	PM1-HT0340-151299-003-h08 HT0340 Homo sapiens cDNA
3541	16587	29511	0.8	4.0E-03	AW188426.1	EST_HUMAN	x99f04.x1 NCI_CGAP_C018 Homo sapiens cDNA clone IMAGE:2665278 3'
3639	16682	29597	0.84	4.0E-03	Q13606	SWISSPROT	x99f04.x1 NCI_CGAP_C018 Homo sapiens cDNA clone IMAGE:2665278 3'
4020	17058		2.14	4.0E-03	AJ011712.1	NT	OLFACTORY RECEPTOR 51 (OLFACTORY RECEPTOR-LIKE PROTEIN OLF1)
4643	17664	30553	1.1	4.0E-03	AI732754.1	EST_HUMAN	Homo sapiens TNNT1 gene, exons 1-11 (and joined CDS)
4805	17822	30717	3.73	4.0E-03	AL163284.2	NT	ab18a08.x5 Stratagene Lung (#937210) Homo sapiens cDNA clone IMAGE:841142 3' similar to contains Alu repetitive element;
5173	18182	31059	0.98	4.0E-03	AW103719.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C084
5220	18228	31102	0.93	4.0E-03	AA699995.1	EST_HUMAN	x83403.x1 NCI_CGAP_Brn35 Homo sapiens cDNA clone IMAGE:2614469 3' similar to contains L1.t1 L1
5272	18278	31142	0.93	4.0E-03	J02187.1	NT	L1 repetitive element;
5348	18453	31324	1.56	4.0E-03	AF003859.1	NT	z69b01.s1 Soares_fetal_liver_spleen_INFLS_S1 Homo sapiens cDNA clone IMAGE:436009 3'
5473	18574	31482	23.1	4.0E-03	AF169825.1	NT	Foot and mouth disease virus serotype A-12 119ab capsid protein VP3
5891	18979	32171	2.72	4.0E-03	P04196	SWISSPROT	Drosophila melanogaster anon207 (anon207) mRNA, complete cds
5895	18983	32173	1.63	4.0E-03	P21849	SWISSPROT	Rattus norvegicus beta-catenin binding protein mRNA, complete cds
5983	19068	32266	0.87	4.0E-03	AL133871.1	EST_HUMAN	MAJOR SURFACE-LABELLED TROPHOZOITE ANTIGEN PRECURSOR
6203	19277		3.56	4.0E-03	U22180.1	NT	DKFZp7611014_r1 761 (synonym: hary2) Homo sapiens cDNA clone DKFZp7611014 5'
6361	19430	32673	1	4.0E-03	AW590572.1	EST_HUMAN	Rattus norvegicus opsin gene, complete cds
6442	19607	32757	1.76	4.0E-03	BE548453.1	EST_HUMAN	hg46c07.x1 NCI_CGAP_G08 Homo sapiens cDNA clone IMAGE:2848652 3'
6827	19881	33172	0.87	4.0E-03	AA813222.1	EST_HUMAN	601076015F1 NIH_MGC_12 Homo sapiens cDNA clone IMAGE:3461954 5'
6942	20166	33489	1.5	4.0E-03	U76408.1	NT	a32111.s1 Soares_testis_NHT Homo sapiens cDNA clone 1392045 3'
							Lycopodium esculentum knotted 3 protein (TKn3) mRNA, complete cds

Table 4

Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7273	20008	33308	1.22	4.0E-03	AL163278.2	NT	Homo sapiens chromosome 21 segment HS21C078
7273	20008	33309	1.22	4.0E-03	AL163278.2	NT	Homo sapiens chromosome 21 segment HS21C078
7404	20372	33723	4.12	4.0E-03	Q02817	SWISSPROT	MUCIN 2 PRECURSOR (INTESTINAL MUCIN 2)
7665	20624	33988	0.99	4.0E-03	AI681483.1	EST_HUMAN	h37g12.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:2271814 3'
7667	20628	33990	0.72	4.0E-03	BE670170.1	EST_HUMAN	7e31b02.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3284043 3'
7767	20720		0.68	4.0E-03	X92109.1	NT	H. sapiens hcgX gene
8274	21243	34655	0.49	4.0E-03	Q9TT92	SWISSPROT	ADAM-TS 5 (A DISINTEGRIN AND METALLOPROTEINASE WITH THROMBOSPONDIN MOTIFS 5) (ADAMTS-5) (ADAM-TSS) (AGGRECANASE-2) (ADMP-2) (ADAM-TS 11)
8383	21352	34761	5.06	4.0E-03	AF111944.1	NT	Dicystostellium discoidium AX4 development protein DG1122 (DG1122) gene, partial cds
8845	21513	34930	1.92	4.0E-03	7682087	NT	Homo sapiens KIAA0345 gene product (KIAA0345), mRNA
9064	22030	35453	7.41	4.0E-03	AI559883.1	EST_HUMAN	te49b11.x1 Soares_NFL_I_GBC_S1 Homo sapiens cDNA clone IMAGE:2080013 3' similar to contains Alu repetitive element
9241	22207		4.72	4.0E-03	AL163209.2	NT	Homo sapiens chromosome 21 segment HS21C009
9250	22216	35646	3.66	4.0E-03	AL163278.2	NT	Homo sapiens chromosome 21 segment HS21C078
10287	23212	36695	0.57	4.0E-03	H30664.1	EST_HUMAN	jp42g12.r1 Soares retina N2b5HR Homo sapiens cDNA clone IMAGE:190150 5'
10742	23684	37159	0.79	4.0E-03	AL161555.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 65
11176	24133	37663	1.65	4.0E-03	AW513635.1	EST_HUMAN	xc47h04.x1 NCI_CGAP_UH1 Homo sapiens cDNA clone IMAGE:2707159 3'
11464	24407	37954	4.53	4.0E-03	AL163206.2	NT	Homo sapiens chromosome 21 segment HS21C006
12431	25956		1.52	4.0E-03	BE815173.1	EST_HUMAN	PM4-BN0138-180800-002-b08 BN0138 Homo sapiens cDNA
12454	25213		3.2	4.0E-03	BE298290.1	EST_HUMAN	601118164F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3028095 5'
12533	25259		2.13	4.0E-03	AW504273.1	EST_HUMAN	UH-HF-BN0-alp-g-04-o-UJ.r1 NIH_MGC_50 Homo sapiens cDNA clone IMAGE:3080822 5'
12755	25400		7.22	4.0E-03	BF224125.1	EST_HUMAN	7q74c09.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3' similar to contains Alu repetitive element; contains element MER31 repetitive element;
12801	25866		3.31	4.0E-03	AW614596.1	EST_HUMAN	hh02c07.x1 NCI_CGAP_K1d11 Homo sapiens cDNA clone IMAGE:2963932 3' similar to contains element LTR5 repetitive element;
12814	25437		2.73	4.0E-03	AW819141.1	EST_HUMAN	RC3-ST0281-240400-015-f03 ST0281 Homo sapiens cDNA
13093	25619	31675	6.48	4.0E-03	11436955	NT	Homo sapiens G1b2-associated binder 2 (KIAA0571), mRNA
371	13487	26387	1.69	3.0E-03	AF011920.1	NT	Homo sapiens protein kinase CK2 catalytic subunit alpha gene, exon 1
880	13935	26894	3.09	3.0E-03	AF011920.1	NT	Homo sapiens protein kinase CK2 catalytic subunit alpha gene, exon 1
1669	14701	27676	5.52	3.0E-03	AA468110.1	EST_HUMAN	nc73c05.s1 NCI_CGAP_P12 Homo sapiens cDNA clone IMAGE:782984 similar to contains Alu repetitive element;
2268	15281		1.58	3.0E-03	AF055066.1	NT	Homo sapiens MHC class 1 region
2302	15314		8.06	3.0E-03	Z32521.1	NT	S.cereale (cv. Halo) mRNA for triosephosphate isomerase
2303	15315	28334	1.3	3.0E-03	U46888.1	NT	Mus musculus intestinal trefol factor gene, partial cds

Single Exon Probes Expressed In Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2303	15315	28335	1.3	3.0E-03	U46858.1	NT	Mus musculus intestinal trefoil factor gene, partial cds
3006	16064		0.8	3.0E-03	Y09006.1	NT	Arabidopsis thaliana rpoMt gene
3099	16156	29069	4.09	3.0E-03	BE379296.1	EST_HUMAN	601237982F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3609933 5'
3166	16221	29136	2.54	3.0E-03	AW802687.1	EST_HUMAN	IL2JM0076-246300-056-D03 UM0076 Homo sapiens cDNA
3428	16476	29395	1.62	3.0E-03	U34806.1	NT	Mus musculus alpha-1(XVII) collagen (COL18A1) gene, exon 1 and 2
3439	16486		6.72	3.0E-03	Y12500.1	NT	C.elegans samdc gene
4002	17041	29949	7.18	3.0E-03	AV762392.1	EST_HUMAN	AV762392 MDS Homo sapiens cDNA clone MDSBSG01 5'
4002	17041	29950	7.18	3.0E-03	AV762392.1	EST_HUMAN	AV762392 MDS Homo sapiens cDNA clone MDSBSG01 5'
4067	17103	29995	1.47	3.0E-03	AI792278.1	EST_HUMAN	ah04f09.y6 Gessler Wilms tumor Homo sapiens cDNA clone IMAGE:1155689 5'
4177	17208		1.08	3.0E-03	Z32521.1	NT	S.cereale (cv. Halo) mRNA for triphosphate isomerase
4424	17451	30342	3.8	3.0E-03	AJ011432.1	NT	Rattus norvegicus gdnf gene
4546	17569	30458	5.58	3.0E-03	AI636141.1	EST_HUMAN	xu8.P10.H3 conorm Homo sapiens cDNA 3'
4871	17888	30776	1.74	3.0E-03	AI732754.1	EST_HUMAN	ab18a08.x6 Stragene lung (#837210) Homo sapiens cDNA clone IMAGE:841142 3' similar to contains Alu repetitive element
4890	17907	30796	5.49	3.0E-03	BE787945.1	EST_HUMAN	601482715F1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3885483 5'
5338	18443	31196	3.42	3.0E-03	8922489	NT	Homo sapiens hypothetical protein FLJ10539 (FLJ10539), mRNA
5635	18731	31893	1.22	3.0E-03	AJ249981.1	NT	Mus musculus mRNA for hypothetical protein (ORF2 ortholog)
5708	18903	31980	0.95	3.0E-03	U85323.1	NT	Mus musculus H2-M alpha chain (H2-Ma) gene, H2-M beta 2 chain (H2-Mb2) gene, H2-M beta 1 chain (H2-Mb1) gene, low molecular weight protein 2.Lmp2 (Lmp2) gene, complete cds
6705	19761	33040	10.04	3.0E-03	AA456701.1	EST_HUMAN	aat3f10.r1 Soares_NHMPu_ST Homo sapiens cDNA clone IMAGE:813163 5'
7224	20246	33590	0.85	3.0E-03	D37977.1	NT	Fugu rubripes mRNA for sodium channel alpha subunit, partial cds
7412	20379	33730	1.37	3.0E-03	AJ011418.1	NT	Kluyveromyces marxianus pcp3 gene for purine-cytosine permease
7765	20718	34091	3.16	3.0E-03	AB021736.1	NT	Oriza sativa gene for bZIP protein, complete cds
8145	21082	34481	0.49	3.0E-03	P26659	SWISSPROT	DNA REPAIR HELICASE RAD16 (RHP3)
8270	21239	34650	0.81	3.0E-03	BF33058.1	EST_HUMAN	RC0-BT0812-250900-032-e07 BT0812 Homo sapiens cDNA
8270	21239	34651	0.91	3.0E-03	BF33058.1	EST_HUMAN	RC0-BT0812-250900-032-e07 BT0812 Homo sapiens cDNA
8496	21464	34880	1.31	3.0E-03	N92580.1	EST_HUMAN	zb27b04.s1 Soares_parathyroid_tumor_NbHPA Homo sapiens cDNA clone IMAGE:304783 3'
8658	21626		0.77	3.0E-03	M63498.1	NT	S.cerevisiae UGA35 gene, complete cds
8804	21771	35197	1.16	3.0E-03	P51989	SWISSPROT	HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN A2 HOMOLOG 1 (HNRNP A2(A))
8827	21794	35217	1.34	3.0E-03	AL163268.2	NT	Homo sapiens chromosome 21 segment HS21C068
8833	21899		1.25	3.0E-03	Q9QIM81	SWISSPROT	NONSTRUCTURAL PROTEIN V
9343	22308		10.07	3.0E-03	AW613774.1	EST_HUMAN	hh80f10.x1 NCL_CGAP_GU1 Homo sapiens cDNA clone IMAGE:2969131 3' similar to contains L1.H1 L1 repetitive element
9400	22365	35797	4.01	3.0E-03	AL161589.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 85

Table 4

Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9424	22388	35827	4.74	3.0E-03	AI016731.1	EST_HUMAN	ov03d12.x1 NCL_CGAP_K143 Homo sapiens cDNA clone IMAGE:1636247 3' similar to gb:X57138_rna1
9434	22398	35836	0.83	3.0E-03	BF338078.1	EST_HUMAN	HISTONE H2B.2 (HUMAN);
9764	22705		0.95	3.0E-03	D90901.1	NT	Synedochysis sp. PCC6803 complete genome, 3/27, 271600-402289
9802	21125	34529	0.61	3.0E-03	BE154870.1	EST_HUMAN	PM3-HT0344-071299-003-407 HT0344 Homo sapiens cDNA
9894	22921		0.62	3.0E-03	P03355	SWISSPROT	POL POLYPOLYPROTEIN [CONTAINS: PROTEASE; REVERSE TRANSCRIPTASE; RIBONUCLEASE H]
10065	22992		5.33	3.0E-03	P08672	SWISSPROT	CIRCUMSPOROZOITE PROTEIN PRECURSOR (CS)
10255	23180	36667	1.56	3.0E-03	P11369	SWISSPROT	RETROVIRUS-RELATED POL POLYPOLYPROTEIN [CONTAINS: REVERSE TRANSCRIPTASE; ENDONUCLEASE]
10355	23279	36755	1.15	3.0E-03	P51989	SWISSPROT	HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN A2 HOMOLOG 1 (HNRNP A2(A))
10499	23421	36920	4.39	3.0E-03	AL163303.2	NT	Homo sapiens chromosome 21 segment HS21C103
11194	24149		1.62	3.0E-03	5803028	NT	Homo sapiens ATP/GTP-binding protein (HEAB), mRNA
11708	24673	38250	1.47	3.0E-03	AF009222.1	NT	Pneumocystis carinii kexin-like serine endoprotease mRNA, partial cds
11775	23930	37451	1.86	3.0E-03	AF266286.1	NT	Homo sapiens golgin-like protein (GLP) gene, complete cds
11810	24695	38275	2.27	3.0E-03	AF094481.1	NT	Homo sapiens trinucleotide repeat DNA binding protein p20-CGGBP (CGGBP) gene, complete cds
11810	24695	38276	2.27	3.0E-03	AF094481.1	NT	Homo sapiens trinucleotide repeat DNA binding protein p20-CGGBP (CGGBP) gene, complete cds
11881	24763	38348	1.47	3.0E-03	P11369	SWISSPROT	RETROVIRUS-RELATED POL POLYPOLYPROTEIN [CONTAINS: REVERSE TRANSCRIPTASE; ENDONUCLEASE]
12199	25765		4.08	3.0E-03	AI525056.1	EST_HUMAN	promna-5.E07.1 bvtumor Homo sapiens cDNA 5'
12232	25064	38162	1.83	3.0E-03	AA993154.1	EST_HUMAN	ci77b10.s1 Soares total_fetus Nb2HF8_9w Homo sapiens cDNA clone IMAGE:1622779 3' similar to contains L1.13 MER26 repetitive element ;
12478	25226	31794	2.42	3.0E-03	AB009668.1	NT	Homo sapiens gene for CMP-N-acetylneuraminic acid hydroxylase, partial cds
516	13587	26506	0.92	2.0E-03	AJ296282.1	SWISSPROT	Rattus norvegicus mRNA for connexin36 (cx36 gene)
516	13587	26507	0.92	2.0E-03	Q04652	SWISSPROT	RING CANAL PROTEIN (KELCH PROTEIN)
786	15851		12.64	2.0E-03	T70874.1	EST_HUMAN	RING CANAL PROTEIN (KELCH PROTEIN)
1365	14399	27370	1.9	2.0E-03	M20783.1	NT	yd15h03.r1 Soares fetal liver spleen TNFLS Homo sapiens cDNA clone IMAGE:108341 5'
1368	14402	27372	1.34	2.0E-03	AA661605.1	EST_HUMAN	Human alpha-2-plasmin inhibitor gene, exons 6 and 7
1376	14410	27380	12.34	2.0E-03	AF284446.1	NT	nu8601.s1 NCL_CGAP_A1v1 Homo sapiens cDNA clone IMAGE:1217593
1486	14519	27492	1.63	2.0E-03	P48609	SWISSPROT	Homo sapiens tumor-related protein DRC2 (DRC2) gene, complete cds
1519	14551	27522	3.03	2.0E-03	4557836	NT	PLATELET-ENDOTHELIAL TETRASPAN ANTIGEN 3 (PETA-3) (GP27) (MEMBRANE GLYCOPROTEIN SFA-1) (CD151 ANTIGEN)
							Homo sapiens procollagen-lysine, 2-oxoglutarate 5-dioxygenase (lysine hydroxylase, Ehlers-Danlos syndrome type VI) (PLOD) mRNA

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Table 4

Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1519	14551	27523	3.03	2.0E-03	4557838	NT	Homo sapiens procollagen-lysine, 2-oxoglutarate 5-dioxygenase (lysine hydroxylase, Ehlers-Danlos syndrome type VI) (PLOD) mRNA
1595	14627		8.7	2.0E-03	P29400	SWISSPROT	COLLAGEN ALPHA 5(V) CHAIN PRECURSOR
1786	14815	27800	1.26	2.0E-03	AA450138.1	EST_HUMAN	z42a10.1.1 Soares, total, fetus, Nb2HF8, 9w Homo sapiens cDNA clone IMAGE:789114 5'
2011	15032	28042	1.52	2.0E-03	AF302891.1	NT	Mus musculus myelin expression factor-3-like protein gene, partial cds
2261	15275	28299	1.02	2.0E-03	AL163022.2	NT	Homo sapiens chromosome 21 segment HS21C102
2584	15585		4.02	2.0E-03	AW137782.1	EST_HUMAN	UI-H-B11-adt-g-10-Q-UI.s1 NCI_CGAP_Sub8 Homo sapiens cDNA clone IMAGE:2717010 3'
3427	16475	29394	4.82	2.0E-03	AA450138.1	EST_HUMAN	z42a10.1.1 Soares, total, fetus, Nb2HF8, 9w Homo sapiens cDNA clone IMAGE:789114 5'
3434	16481	29400	0.8	2.0E-03	BF568955.1	EST_HUMAN	60218395011 NIH_MGC_42 Homo sapiens cDNA clone IMAGE:4300070 3'
3680	16723	29636	6.1	2.0E-03	X87344.1	NT	H. sapiens DMA, DMB, HLA-Z1, [P2, LMP2, TAP1, LMP7, TAP2, DOB, DQB2 and RING8, 9, 13 and 14 genes
3973	17013	29927	0.65	2.0E-03	AB040802.1	NT	Rattus norvegicus mRNA for SREB1, complete cds
4140	17171	30059	2.1	2.0E-03	P03374	SWISSPROT	ENV POLYPROTEIN [CONTAINS: COAT PROTEIN GP52, COAT PROTEIN GP36]
4203	17234	30122	1.29	2.0E-03	AA179693.1	EST_HUMAN	zp13h01.1 Stratagene fetal retina 937202 Homo sapiens cDNA clone IMAGE:603361 5'
4248	17277		9.31	2.0E-03	U68491.1	NT	Rattus norvegicus 5-hydroxytryptamine7 receptor gene, partial cds
4458	17484		1.01	2.0E-03	AW297390.1	EST_HUMAN	UI-H-BW0-ar-g-03-Q-UI.s1 NCI_CGAP_Sub8 Homo sapiens cDNA clone IMAGE:2730413 3'
4462	17488	30375	1.11	2.0E-03	A1084746.1	EST_HUMAN	HA0507 Human fetal liver cDNA library Homo sapiens cDNA
4577	17599	30493	1.99	2.0E-03	L42512.1	NT	Drosophila melanogaster shortighted class 2 (she) mRNA, complete cds
4577	17599	30494	1.99	2.0E-03	L42512.1	NT	Drosophila melanogaster shortighted class 2 (she) mRNA, complete cds
4735	17755	30849	1.09	2.0E-03	AF223391.1	NT	Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced
4740	17780		1.84	2.0E-03	R87773.1	EST_HUMAN	yc45602.s1 Soares adult brain N2b4HB55Y Homo sapiens cDNA clone IMAGE:160890 3'
5054	18086	30945	0.75	2.0E-03	AF003528.1	NT	Homo sapiens X-linked anhidrotic ectodermal dysplasia protein gene (EDA), exon 2 and flanking repeat regions
5163	18172	31051	1.02	2.0E-03	AF187974.1	NT	8 Homo sapiens concentrative nucleoside transporter (CNT1) gene, exon 12
5281	18287	31149	2.26	2.0E-03	D85606.1	NT	Homo sapiens gene for cholesterylkinin type-A receptor, complete cds
5564	18661	31607	1.33	2.0E-03	BF241410.1	EST_HUMAN	601876385F1 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:4104692 5'
5709	25643	31981	2.18	2.0E-03	AB014593.1	NT	Homo sapiens mRNA for KIAA0993 protein, partial cds
5795	18887	32088	0.61	2.0E-03	AW798111.1	EST_HUMAN	MP2-UM0025-300300-102-102 UM0025 Homo sapiens cDNA
5795	18887	32088	0.61	2.0E-03	AW798111.1	EST_HUMAN	MP2-UM0025-300300-102-102 UM0025 Homo sapiens cDNA
5797	18889	32071	1.73	2.0E-03	U63711.1	NT	Xenopus laevis xellin mRNA, complete cds
6231	19305	32536	3.79	2.0E-03	P23477	SWISSPROT	ATP-DEPENDENT NUCLEASE SUBUNIT B
6231	19305	32537	3.79	2.0E-03	P23477	SWISSPROT	ATP-DEPENDENT NUCLEASE SUBUNIT B
6480	19545	32793	15.10	2.0E-03	Q95203	SWISSPROT	CARBONIC ANHYDRASE-RELATED PROTEIN 2 PRECURSOR (CARP 2) (CA-RP II) (CA-XI)

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Table 4

Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6480	19545	32794	15.16	2.0E-03	Q95203	SWISSPROT	CARBONIC ANHYDRASE-RELATED PROTEIN 2 PRECURSOR (CARP 2) (CA-RP II) (CA-XI)
6492	19547	32796	7.38	2.0E-03	BF308187.1	EST_HUMAN	601867434F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4121408 5'
6521	19564	32842	2.28	2.0E-03	Q9UKP4	SWISSPROT	ADAM-TS 7 PRECURSOR (A DISINTEGRIN AND METALLOPROTEINASE WITH THROMBOSPONDIN MOTIFS 7) (ADAMTS-7) (ADAM-TS7)
6522	19585	32843	0.77	2.0E-03	AV709075.1	EST_HUMAN	AV709075 ADC Homo sapiens cDNA clone ADCAEF09 5'
6554	19614	32879	1.36	2.0E-03	X94451.1	NT	L. esculentum mRNA for lysyl-tRNA synthetase (LysRS)
6756	19810		1.25	2.0E-03	AI991089.1	EST_HUMAN	wu36h09.x1 Soares_Dieckgraefe_colon_NHCD Homo sapiens cDNA clone IMAGE:2522177 3' similar to SW:RL29_HUMAN P47914 90S RIBOSOMAL PROTEIN L29; contains element MSR1 repetitive element;
6794	19848	33133	0.71	2.0E-03	AA677831.1	EST_HUMAN	z13a11.s1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:430852 3'
7151	19383	31271	1.08	2.0E-03	AB038502.1	NT	Caenorhabditis elegans mRNA for galectin LEC-11, complete cds
7287	20064	33371	2.86	2.0E-03	BE087988.1	EST_HUMAN	CM4-BT0366-051299-054-401 BT0366 Homo sapiens cDNA
7351	20321	33668	0.64	2.0E-03	AI298883.1	EST_HUMAN	gm99d11.x1 NCI_OGAP_Lu5 Homo sapiens cDNA clone IMAGE:1896855 3'
7511	20476	33837	0.77	2.0E-03	T86659.1	EST_HUMAN	y477g10.t1 Soares_fetal_liver_spleen_1NFLS_Homo sapiens cDNA clone IMAGE:114308 5'
7877	20821	34198	1.55	2.0E-03	P07354	SWISSPROT	PROTEOGLYCAN LINK PROTEIN PRECURSOR (CARTILAGE LINK PROTEIN) (LP)
8386	21355	34763	1.95	2.0E-03	AW592004.1	EST_HUMAN	h37b06.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2834035 3' similar to TR:Q60978 Q60978 JERKY.;
8560	21528	34947	6.01	2.0E-03	N20287.1	EST_HUMAN	y42g06.s1 Soares_melanocyte_2NbHM_Homo sapiens cDNA clone IMAGE:264442 3' similar to contains L1.b2 L1 repetitive element;
8560	21528	34948	6.01	2.0E-03	N20287.1	EST_HUMAN	y42g06.s1 Soares_melanocyte_2NbHM_Homo sapiens cDNA clone IMAGE:264442 3' similar to contains L1.b2 L1 repetitive element;
8607	21575	34990	0.57	2.0E-03	Q92350	SWISSPROT	HYPOTHETICAL 328 KD PROTEIN C6G9.05 IN CHROMOSOME 1
8629	21597	35018	1.23	2.0E-03	P19137	SWISSPROT	LAMININ ALPHA-1 CHAIN PRECURSOR (LAMININ A CHAIN)
8684	21652	35074	0.77	2.0E-03	6005855	NT	Homo sapiens Retina-derived POU-domain factor-1 (RPF-1), mRNA
8684	21652	35075	0.77	2.0E-03	6005855	NT	Homo sapiens Retina-derived POU-domain factor-1 (RPF-1), mRNA
8709	21677	35102	0.81	2.0E-03	AU136879.1	EST_HUMAN	AU136879 PLACET1 Homo sapiens cDNA clone PLACE1004839 5'
8762	21729		0.87	2.0E-03	AJ400877.1	NT	Homo sapiens ASCL3 gene, CEGP1 gene, C11orf14 gene, C11orf15 gene, C11orf16 gene and C11orf17 gene
9550	18887	32068	0.66	2.0E-03	AW796111.1	EST_HUMAN	MR2-UM0025-300300-102-102 UM0025 Homo sapiens cDNA
9550	18887	32069	0.66	2.0E-03	AW796111.1	EST_HUMAN	MR2-UM0025-300300-102-102 UM0025 Homo sapiens cDNA
9595	22557	36007	0.66	2.0E-03	AF224669.1	NT	Homo sapiens mannosidase, beta A, lysosomal (MANBA) gene, and ubiquitin-conjugating enzyme E2D 3 (UBE2D3) genes, complete cds
9884	22837	36291	0.97	2.0E-03	H50832.1	EST_HUMAN	yp86a09.s1 Soares_fetal_liver_spleen_1NFLS_Homo sapiens cDNA clone IMAGE:194298 3'
9884	22837	36292	0.97	2.0E-03	H50832.1	EST_HUMAN	yp86a09.s1 Soares_fetal_liver_spleen_1NFLS_Homo sapiens cDNA clone IMAGE:194298 3'

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Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
							TENASCIN PRECURSOR (TN) (HEXABRACHION) (CYTOTACTIN) (NEURONECTIN) (GMEIN) (JI) (MIOTENDINOUS ANTIGEN) (GLIOMA-ASSOCIATED-EXTRACELLULAR MATRIX ANTIGEN) (GP 150- 225) (TENASCIN-C) (TN-C)
9816	22737	36190	3.31	2.0E-03	P24821	SWISSPROT	
10026	22953	36421	1.02	2.0E-03	P48982	SWISSPROT	BETA-GALACTOSIDASE PRECURSOR (LACTASE)
10026	22953	36422	1.02	2.0E-03	P48982	SWISSPROT	BETA-GALACTOSIDASE PRECURSOR (LACTASE)
10081	23008	36479	0.65	2.0E-03	AF097732.1	NT	Homo sapiens caspase recruitment domain-containing protein (BCL10) gene, complete cds
10081	23008	36480	0.65	2.0E-03	AF097732.1	NT	Homo sapiens caspase recruitment domain-containing protein (BCL10) gene, complete cds
10275	23200	36684	0.94	2.0E-03	AW884269.1	EST_HUMAN	QV3-OT0084-080400-144-e01 OT0084 Homo sapiens cDNA
10402	23324		6.44	2.0E-03	AA251376.1	EST_HUMAN	zs10a06.e1 NCL CGAP GCBI Homo sapiens cDNA clone IMAGE:684754 3'
10781	23702	37200	0.45	2.0E-03	BF367386.1	EST_HUMAN	MR2-GN0030-140800-001-e05 GN0030 Homo sapiens cDNA
10969	23889	37401	0.43	2.0E-03	AW361176.1	EST_HUMAN	RC1-CT0251-141099-012-d01 CT0251 Homo sapiens cDNA
10969	23889	37402	0.43	2.0E-03	AW361176.1	EST_HUMAN	RC1-CT0251-141099-012-d01 CT0251 Homo sapiens cDNA
11356	24306		2.4	2.0E-03	M86524.1	NT	Human dystrophin gene
11817	20821	34198	2.2	2.0E-03	P07354	SWISSPROT	PROTEOLYCAN LINK PROTEIN PRECURSOR (CARTILAGE LINK PROTEIN) (LP)
11870	24752		1.87	2.0E-03	BF330908.1	EST_HUMAN	RC3-BT0333-310800-115-g04 BT0333 Homo sapiens cDNA
11876	24758	38342	10.47	2.0E-03	Z11740.1	NT	H. sapiens variable number tandem repeat (VNTR) locus DNA
12180	25028		2.99	2.0E-03	AI625745.1	EST_HUMAN	ly65h03.x1 NCL CGAP Kid11 Homo sapiens cDNA clone IMAGE:2283989 3' similar to SW:VATG_MANSE
12197	25042	38623	2.41	2.0E-03	AF157516.2	NT	Q25532 VACUOLAR ATP SYNTHASE SUBUNIT G ; Homo sapiens SEL1L (SEL1L) gene, partial cds
12220	25057	38627	1.75	2.0E-03	AI084325.1	EST_HUMAN	oy43g06.e1 Soares_papillary thyroid tumor_NbHPA Homo sapiens cDNA clone IMAGE:1668634 3' similar to TR:P97535 P97535 PS-PLA1 PRECURSOR ;
12241	18349		11.57	2.0E-03	AJ245167.1	NT	Camelus dromedarius cwhp19 gene for immunoglobulin heavy chain variable region
12459	25932		2.03	2.0E-03	AV697966.1	EST_HUMAN	AV697966 GK Homo sapiens cDNA clone GKCGX005 5'
12550	25273	31777	1.93	2.0E-03	Y00508.1	NT	H. sapiens M1 gene for muscarinic acetylcholine receptor
12663	25341		1.33	2.0E-03	AL163203.2	NT	Homo sapiens chromosome 21 segment HS21C003
12710	25795		1.55	2.0E-03	AI375037.1	EST_HUMAN	ts66102.x1 Soares_totat_fetus_Nb2HF8_9w Homo sapiens cDNA clone IMAGE:2049051 3' similar to contains Alu repetitive element;
							Homo sapiens MSH55 gene, partial cds; and CLIC1, DDAH, G6b, G6c, G6d, G6e, G6f, BAT5, G5b, CSK2B, BAT4, G4, Apo M, BAT3, BAT2, AIF-1, 1C7, LST-1, LTB, TNF, and LTA genes, complete cds
12826	25445		1.6	2.0E-03	AF129756.1	NT	
13002	25745		1.95	2.0E-03	AV697966.1	EST_HUMAN	AV697966 GK Homo sapiens cDNA clone GKCGX005 5'
13095	25621		1.44	2.0E-03	P04797	SWISSPROT	GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE (GAPDH)
439	13513	26444	1.72	1.0E-03	H96471.1	EST_HUMAN	y68c08.r1 Soares_pineal_gland_N3HPG Homo sapiens cDNA clone IMAGE:232334 5'

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Table 4
Single Exon Probes Expressed In Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
830	13887	26842	2.09	1.0E-03	A1720283.1	EST_HUMAN	as70b08.x1 Barstead colon HPLRB7 Homo sapiens cDNA clone IMAGE:2334039 3' similar to TR:Q13825
830	13887	26843	2.09	1.0E-03	A1720283.1	EST_HUMAN	Q13825 AU-BINDING PROTEIN/ENOYL-COA HYDRATASE. ;
1097	14141	27091	3.37	1.0E-03	A1665788.1	EST_HUMAN	as70b08.x1 Barstead colon HPLRB7 Homo sapiens cDNA clone IMAGE:2334039 3' similar to TR:Q13825
1117	14161	27112	1.69	1.0E-03	A1954572.1	EST_HUMAN	Q13825 AU-BINDING PROTEIN/ENOYL-COA HYDRATASE. ;
							wk86a08.x1 NCI CGAP_Pan1 Homo sapiens cDNA clone IMAGE:2422258 3'
							wk86e10.x1 NCI CGAP_Mel15 Homo sapiens cDNA clone IMAGE:2551242 3'
1170	14211	27165	1.5	1.0E-03	A1692816.1	EST_HUMAN	wk86a01.x1 NCI CGAP_Lu24 Homo sapiens cDNA clone IMAGE:2338440 3' similar to contains Alu repetitive element
2042	15061	28082	3.08	1.0E-03	P47808	SWISSPROT	HIGH MOLECULAR WEIGHT FORM OF MYOSIN I (HMM/MI)
2163	15179	28199	9.01	1.0E-03	AJ131018.1	NT	Homo sapiens SCL gene locus
2993	16051	28972	1.42	1.0E-03	AB033117.1	NT	Homo sapiens mRNA for KIAA1291 protein, partial cds
3205	16260	29179	2.08	1.0E-03	P18915	SWISSPROT	CARBONIC ANHYDRASE VI PRECURSOR (CARBONATE DEHYDRATASE VI) (CA-VI) (SECRETED)
3205	16260	29180	2.08	1.0E-03	P18915	SWISSPROT	CARBONIC ANHYDRASE VI PRECURSOR (CARBONATE DEHYDRATASE VI) (CA-VI) (SECRETED)
3313	16366	29286	1.23	1.0E-03	P08647	SWISSPROT	CARBONIC ANHYDRASE (SALIVARY CARBONIC ANHYDRASE)
3553	16599	29524	0.92	1.0E-03	U68061.1	NT	CARBONIC ANHYDRASE VI PRECURSOR (CARBONATE DEHYDRATASE VI) (CA-VI) (SECRETED)
3553	16599	29525	0.92	1.0E-03	U68061.1	NT	CARBONIC ANHYDRASE VI PRECURSOR (CARBONATE DEHYDRATASE VI) (CA-VI) (SECRETED)
3678	16721		1.49	1.0E-03	AB044400.1	NT	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG
							Human MUC2 gene, promoter region
							Human MUC2 gene, promoter region
							Homo sapiens SVMT gene for synaptic vesicle monoamine transporter, exons 14, 15
3948	16986	29901	0.64	1.0E-03	AW170552.1	EST_HUMAN	xn63d07.x1 Soares_NH/CeC_cervical_tumor Homo sapiens cDNA clone IMAGE:2698381 3' similar to contains TAR1.1t TAR1 repetitive element ;
3954	16994	29910	1.11	1.0E-03	Z49649.1	NT	S. cerevisiae chromosome X reading frame ORF YJR149w
4464	17490	30377	2.27	1.0E-03	BE939162.1	EST_HUMAN	RC1-TN0128-160800-021-g01 TN0128 Homo sapiens cDNA
							TCBAP1D4909 Pediatric pre-B cell acute lymphoblastic leukemia Baylor-HGSC project=TCBAP Homo sapiens cDNA clone TCBAP4909
4502	17527	30412	4.39	1.0E-03	BE246536.1	EST_HUMAN	sapiens cDNA clone TCBAP4909
4692	17713	30608	0.79	1.0E-03	U29449.1	NT	Caenorhabditis elegans spliced leader RNA (SL3 alpha), (SL4), and (SL5) genes
4861	17878	30785	2.07	1.0E-03	A1073485.1	EST_HUMAN	o445c04.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1640262 3'
4861	17878	30786	2.07	1.0E-03	A1073485.1	EST_HUMAN	o445c04.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1640262 3'
4862	17879		4.33	1.0E-03	BE154087.1	EST_HUMAN	PMO-HT0339-200400-010-D02 HT0339 Homo sapiens cDNA
5113	18123	30998	9.53	1.0E-03	O46409	SWISSPROT	APOLIPOPROTEIN A-IV PRECURSOR (APO-AIV)
5202	18211	31085	1.03	1.0E-03	AV685870.1	EST_HUMAN	AV685870 GKC Homo sapiens cDNA clone GKCDME11 5'
5381	18485	31360	1.74	1.0E-03	AA290951.1	EST_HUMAN	zs44f01.1 NCI CGAP_GCBT Homo sapiens cDNA clone IMAGE:700345 5'
5476	18577	31498	2.98	1.0E-03	AJ008345.1	NT	Homo sapiens KVLQT1 gene
5531	18629	31585	1.77	1.0E-03	K03332.1	NT	Epstein-Barr virus (Ag876 isolate) U2-IR2 domain encoding nuclear protein EBNA2, complete cds

Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5531	18629	31566	1.77	1.0E-03	K03332.1	NT	Epstein-Barr virus (AG876 isolate) U2-IR2 domain encoding nuclear protein EBNA2, complete cds
5652	18748	31916	0.93	1.0E-03	BE796491.1	EST_HUMAN	601589841F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3943954 5'
5658	18754	31921	1.76	1.0E-03	Q02388	SWISSPROT	COLLAGEN ALPHA 1(VII) CHAIN PRECURSOR (LONG-CHAIN COLLAGEN) (LC COLLAGEN)
5716	18810	31988	0.7	1.0E-03	N41974.1	EST_HUMAN	y07h06.1 Soares melanocyte 2N6HM Homo sapiens cDNA clone IMAGE:270587 5' similar to contains element MER8 repetitive element ;
5716	18810	31989	0.7	1.0E-03	N41974.1	EST_HUMAN	y07h06.1 Soares melanocyte 2N6HM Homo sapiens cDNA clone IMAGE:270587 5' similar to contains element MER8 repetitive element ;
5995	19079	32276	0.56	1.0E-03	AA773352.1	EST_HUMAN	ab55g12.s1 Stratagene lung carcinoma 937218 Homo sapiens cDNA clone IMAGE:846734 3'
6018	19101		0.52	1.0E-03	BF541639.1	EST_HUMAN	602068042F1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:4066907 5'
6136	19213		2.57	1.0E-03	X07699.1	NT	Mouse nucleolin gene
6177	19252	32485	1.06	1.0E-03	BE963939.2	EST_HUMAN	601657519R1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3875683 3'
6316	19387		8.39	1.0E-03	11526176	NT	Homo sapiens T-cell lymphoma invasion and metastasis 1 (TIAM1), mRNA
6468	19533	32781	1.05	1.0E-03	T87761.1	EST_HUMAN	y053a1.1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:115772 5'
6549	19610		1.69	1.0E-03	AW902865.1	EST_HUMAN	QV3-NN1024-260400-171-g05 NN1024 Homo sapiens cDNA
6919	19970	33286	1.18	1.0E-03	L77570.1	NT	Homo sapiens DiGeorge syndrome critical region, centromeric end
7359	20329	33678	2.43	1.0E-03	D16826.1	NT	Human gene for fourth somatostatin receptor subtype
7729	20686		2.38	1.0E-03	AJ23042.1	NT	Homo sapiens 959 kb contig between AML1 and CBR1 on chromosome 21q22, segment 2/3
7901	20844	34228	1.71	1.0E-03	U52111.2	NT	Homo sapiens X28 region near ALD locus containing dual specificity phosphatase 9 (DUSP9), ribosomal protein L18a (RPL18a), Ca2+/Calmodulin-dependent protein kinase I (CAMKI), creatine transporter (CRTR), CDM protein (CDM), adrenoleukodystrophy protein >
7975	20914	34305	3.18	1.0E-03	M63376.1	NT	Human TRPM-2 protein gene, exons 1,2 and 3
8033	20970	34384	0.87	1.0E-03	BE880044.1	EST_HUMAN	601491081F1 NIH_MGC_69 Homo sapiens cDNA clone IMAGE:3893276 5'
8221	21190	34599	0.55	1.0E-03	AF274581.1	NT	Homo sapiens prolactin-releasing peptide receptor gene, 5' flanking region
8282	21251	34663	5.32	1.0E-03	AJ251973.1	NT	Homo sapiens partial steerin-1 gene
8483	21451	34869	1.01	1.0E-03	AA122270.1	EST_HUMAN	z097c09.s1 Soares_pregnant_uterus_NbHPU Homo sapiens cDNA clone IMAGE:490768 3' similar to contains L1, L1 repetitive element ;
8586	21554	34970	2.42	1.0E-03	AF153980.1	NT	Homo sapiens exostosin-like protein 1 (EXTL1) gene, exons 2 through 11, and complete cds
8773	21740	35161	0.7	1.0E-03	U28397.1	NT	Rattus norvegicus plasma membrane Ca2+ ATPase isoform 3 (PMCA3) gene, 5' flanking region
8941	21907	35331	0.53	1.0E-03	AA001613.1	EST_HUMAN	zh82c06.s1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:427810 3'
8941	21907	35332	0.53	1.0E-03	AA001613.1	EST_HUMAN	zh82c06.s1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:427810 3'
9295	22261		1.37	1.0E-03	Y11204.1	NT	V. carteri gene encoding volvoxopsin
9321	22288	35716	0.6	1.0E-03	AW840353.1	EST_HUMAN	CKM3-LT0079-170200-092-e07 LT0079 Homo sapiens cDNA

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Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9435	22399		0.65	1.0E-03	U52111.2	NT	Homo sapiens X28 region near ALD locus containing dual specificity phosphatase 9 (DUSP9), ribosomal protein L18a (RPL18a), Ca2+/Calmodulin-dependent protein kinase I (CAMKI1), creatine transporter (CRTTR), CDM protein (CDM), adrenoleukodystrophy protein >
9474	22438	35877	3.71	1.0E-03	M30471.1	NT	Human class III alcohol dehydrogenase (ADH5) chi subunit mRNA, complete cds
9474	22438	35878	3.71	1.0E-03	M30471.1	NT	Human class III alcohol dehydrogenase (ADH5) chi subunit mRNA, complete cds
9955	22882		0.45	1.0E-03	A1247482.1	EST_HUMAN	qh56d01.x1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:1848673 3' similar to gb:M87388 TATA-BINDING PROTEIN-ASSOCIATED PHOSPHOPROTEIN (HUMAN);
9966	22893	36354	1.77	1.0E-03	AF011400.1	NT	Thermotoga neapolitana alpha-1,6-galactosidase (aglA) gene, complete cds
9966	22893	36355	1.77	1.0E-03	AF011400.1	NT	Thermotoga neapolitana alpha-1,6-galactosidase (aglA) gene, complete cds
10179	23104	36585	0.8	1.0E-03	Q01129	SWISSPROT	BONE PROTEOGLYCAN II PRECURSOR (PG-S2) (DECORIN) (PG-40) (DERMATAN SULFATE PROTEOGLYCAN-II) (DSFG)
10324	23446	36944	1.55	1.0E-03	AF003529.1	NT	Homo sapiens glypican 3 (GPC3) gene, partial cds and flanking repeat regions
10529	23451		0.79	1.0E-03	AF097485.1	NT	Homo sapiens transducin beta-like 2 (TBL2) gene, complete cds
10679	23601	37096	1.12	1.0E-03	A1024350.1	EST_HUMAN	ov75f08.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1643175 3' similar to contains MER39.b1 MER39 MER39 repetitive element;
11025	23990	37516	1.65	1.0E-03	AW362393.1	EST_HUMAN	RC1-CT0279-181099-011-a09 CT0279 Homo sapiens cDNA
11025	23990	37517	1.65	1.0E-03	AW362393.1	EST_HUMAN	RC1-CT0279-181099-011-a09 CT0279 Homo sapiens cDNA
11102	24062	37585	2.91	1.0E-03	BE170859.1	EST_HUMAN	QV3-HT0543-220300-130-a03 HT0543 Homo sapiens cDNA
11172	24129		2.21	1.0E-03	A1583847.1	EST_HUMAN	tt73a12.x1 NCI_CGAP_HSC3 Homo sapiens cDNA clone IMAGE:2246446 3' similar to TR:Q26195 Q26195 PVA1 GENE.;
11491	24434		2.59	1.0E-03	AV759949.1	EST_HUMAN	AV759949 MDS Homo sapiens cDNA clone MDSDDF11 5'
11662	24598	38171	6.18	1.0E-03	AA122270.1	EST_HUMAN	z497c09.s1 Soares_pregnant_uterus_NbHPU Homo sapiens cDNA clone IMAGE:490768 3' similar to contains L1.1 L1 repetitive element;
12176	25024	38621	6.74	1.0E-03	BE894488.1	EST_HUMAN	601433087F1 NIH_MGC 72 Homo sapiens cDNA clone IMAGE:3918524 5'
12653	25915		1.53	1.0E-03	A1347355.1	EST_HUMAN	tc05h11.x1 NCI_CGAP_Cot16 Homo sapiens cDNA clone IMAGE:2063013 3' similar to contains Alu repetitive element;
12753	25936	31311	7.37	1.0E-03	BE780572.1	EST_HUMAN	301468878F1 NIH_MGC 67 Homo sapiens cDNA clone IMAGE:3872035 5'
5765	18857		1.76	9.0E-04	P06727	SWISSPROT	APOLIPOPROTEIN A-IV PRECURSOR (APO-AIV)
6388	19466		0.81	9.0E-04	AJ008345.1	NT	Homo sapiens KVLQ11 gene
6633	19691	32870	1.08	9.0E-04	P02381	SWISSPROT	MITOCHONDRIAL RIBOSOMAL PROTEIN VAR1
10001	22928		1.39	9.0E-04	AB037203.1	NT	Glycyrhiza glabra GgBAS1 mRNA for beta-amylin synthase, complete cds
1484	14517		1.04	8.0E-04	X96469.1	NT	X. laevis mRNA for C4SR protein
3939	15979	29894	0.84	8.0E-04	R07008.1	EST_HUMAN	y12h10.1 Soares_fetal_liver_spleen_1NFLS Homo sapiens cDNA clone IMAGE:126691 5'
4209	17238		4.49	8.0E-04	P08547	SWISSPROT	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG

Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4798	17815	30709	2.7	8.0E-04	U29185.1	NT	Homo sapiens prion protein (PrP) gene, complete cds
11480	24423		2.01	8.0E-04	AA77084.1	EST_HUMAN	z24c10.s1 Soares_fetal_heart_NbHH19W Homo sapiens cDNA clone IMAGE:377874 3'
11627	24565		2.02	8.0E-04	AI571099.1	EST_HUMAN	tr85a08.x1 NCL_CGAP_U2 Homo sapiens cDNA clone IMAGE:2176310 3'
1844	14870	27868	1.17	7.0E-04	L41825.1	NT	Homo sapiens CYP17 gene, 5' end
2408	15415	28439	1.01	7.0E-04	U29185.1	NT	Homo sapiens prion protein (PrP) gene, complete cds
2726	16720	28737	1.22	7.0E-04	AL163210.2	NT	Homo sapiens chromosome 21 segment HS21C010
3293	16346	29266	1.13	7.0E-04	4885170	NT	Homo sapiens chromosome X open reading frame 6 (CXORF6) mRNA
6215	19289	32522	1.02	7.0E-04	AA516212.1	EST_HUMAN	ng65g12.s1 NCL_CGAP_Lip2 Homo sapiens cDNA clone IMAGE:339718 similar to contains L1.b3 L1 L1
6662	19719		2.3	7.0E-04	AI769331.1	EST_HUMAN	repetitive element:
7438	20405		0.78	7.0E-04	AK024445.1	NT	wg36f09.x1 Soares_NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:2367209 3'
10163	23088	36565	0.48	7.0E-04	P13497	SWISSPROT	Homo sapiens mRNA for FLJ00035 protein, partial cds
10163	23088	36566	0.48	7.0E-04	P13497	SWISSPROT	Homo sapiens mRNA for FLJ00035 protein, partial cds
11892	24773		1.98	7.0E-04	U78027.1	NT	BONE MORPHOGENETIC PROTEIN 1 PRECURSOR (BMP-1)
11920	24801	38392	2.41	7.0E-04	Z40561.1	EST_HUMAN	BONE MORPHOGENETIC PROTEIN 1 PRECURSOR (BMP-1)
12921	25497		4.1	7.0E-04	R17336.1	EST_HUMAN	Homo sapiens Bruton's tyrosine kinase (BTK), alpha-D-galactosidase A (GLA), L44-like ribosomal protein (L44L) and FTP3 (FTP3) genes, complete cds
12952	25527		3.97	7.0E-04	6005855	NT	HSC28A072 normalized infant brain cDNA Homo sapiens cDNA clone alpha-28a07 3'
2706	15701		1.03	6.0E-04	BF341380.1	EST_HUMAN	y913c06.r1 Soares Infant brain 1N1B Homo sapiens cDNA clone IMAGE:32288 5'
3984	17024	29635	1.78	6.0E-04	AI862525.1	EST_HUMAN	Homo sapiens Relina-derived POU-domain factor-1 (RPF-1), mRNA
4214	17243	30128	3.15	6.0E-04	U45983.1	NT	602013339F1 NCL_CGAP_Brn64 Homo sapiens cDNA clone IMAGE:4149297 5'
7830	20778	34156	0.59	6.0E-04	Q15034	SWISSPROT	wj16a11.x1 NCL_CGAP_Kid12 Homo sapiens cDNA clone IMAGE:2402876 3'
8198	21168		3.16	6.0E-04	P46408	SWISSPROT	Homo sapiens COR8 chemokine receptor (CMKBR8) gene, complete cds
8349	21318		0.69	6.0E-04	H92947.1	EST_HUMAN	HYPOTHETICAL PROTEIN KIAA0032
10339	23263		3.99	6.0E-04	AL048507.2	EST_HUMAN	GLUCOSE TRANSPORTER TYPE 5, SMALL INTESTINE (FRUCTOSE TRANSPORTER)
10440	23362	36852	2.19	6.0E-04	BE005850.1	EST_HUMAN	GLUCOSE TRANSPORTER TYPE 5, SMALL INTESTINE (FRUCTOSE TRANSPORTER)
10704	23626		0.65	6.0E-04	AF287478.1	NT	y94c11.s1 Soares_pineal_gland_N3HPG Homo sapiens cDNA clone IMAGE:231956 3' similar to contains LOR1 repetitive element:
11814	24699	38280	2.11	6.0E-04	AJ229042.1	NT	LOR1 repetitive element:
11893	24774	38360	3.12	6.0E-04	AW013847.1	EST_HUMAN	DKFZp586M2024_r1 686 (synonym: hule1) Homo sapiens cDNA clone DKFZp586M2024
12364	25820		5.73	6.0E-04	AW380519.1	EST_HUMAN	RC2-BN0120-250400-012-h11 BN0120 Homo sapiens cDNA
562	13718	26640	8.71	5.0E-04	O10341	SWISSPROT	RC1-HT0269-261193-012-008 HT0269 Homo sapiens cDNA
1501	14534		1.88	5.0E-04	AW851844.1	EST_HUMAN	LYechinus variegatus embryonic blastocoele extracellular matrix protein precursor (ECM3) mRNA, complete cds
							UHH-BID-aab-09-0-UI.s1 NCL_CGAP_Sub1 Homo sapiens cDNA clone IMAGE:2708825 3'
							RC1-HT0269-261193-012-008 HT0269 Homo sapiens cDNA
							HYPOTHETICAL 29.3 KD PROTEIN (ORF92)
							QV0-CT0225-021099-030-a07 CT0225 Homo sapiens cDNA

Table 4

Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3424	16472	29391	1.28	5.0E-04 AA548931.1	EST_HUMAN		nk27e11.s1 NCI_CGAP_Cot11 Homo sapiens cDNA clone IMAGE:1014764 3' similar to contains Alu repetitive element
3728	16770	29682	0.95	5.0E-04 Q9UKP4	SWISSPROT		ADAM-TS 7 PRECURSOR (A DISINTEGRIN AND METALLOPROTEINASE WITH THROMBOSPONDIN MOTIFS 7) (ADAMTS-7) (ADAM-TS7)
5549	18646	31588	2.37	5.0E-04 AF248054.1	NT		Bos taurus micromolar calcium activated neutral protease 1 (CAPN1) gene, exons 11-20, and partial cds
6784	19939	33124	5.64	5.0E-04 AA156080.1	EST_HUMAN		zo33b08.r1 Stratagene cdon (#837204) Homo sapiens cDNA clone IMAGE:588663 5'
7602	20563	33924	10.72	5.0E-04 M23604.1	NT		Gorilla gorilla involucrin gene medium allele, complete cds
8289	21258	34669	4.95	5.0E-04 A1188382.1	EST_HUMAN		qd13f06.x1 Soares_placenta_8to9weeks_2NbHP869W Homo sapiens cDNA clone IMAGE:1723619 3' similar to gb:X51602.cds1 VASCULAR ENDOTHELIAL GROWTH FACTOR RECEPTOR 1 (HUMAN);contains Alu repetitive element;
8646	21614	35036	0.92	5.0E-04 AA814519.1	EST_HUMAN		ob96e02.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1339226 3' similar to contains element MER22 repetitive element;
9632	22576	36026	1.57	5.0E-04 AA846545.1	EST_HUMAN		aj55h03.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1394357 3'
9726	22754	36207	0.62	5.0E-04 N83765.1	EST_HUMAN		KK2745F Human fetal heart, Lambda ZAP Express Homo sapiens cDNA clone KK2745 5' similar to REPETITIVE ELEMENT
9876	22829	36283	0.54	5.0E-04 P29126	SWISSPROT		BIFUNCTIONAL ENDO-1,4-BETA-XYLANASE XYLA PRECURSOR
9968	22895	36358	4.55	5.0E-04 AW270938.1	EST_HUMAN		xs06e02.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2768858 3'
10640	23662		0.47	5.0E-04 U50871.1	NT		Human familial Alzheimer's disease (STM2) gene, complete cds
11320	24270		1.94	5.0E-04 AL048507.2	EST_HUMAN		DKFZp566M2024_r1 586 (synonym: hute1) Homo sapiens cDNA clone DKFZp566M2024
12022	18646	31588	10.61	5.0E-04 AF248054.1	NT		Bos taurus micromolar calcium activated neutral protease 1 (CAPN1) gene, exons 11-20, and partial cds
12296	25763		4.4	5.0E-04 AA568513.1	EST_HUMAN		nf15h02.s1 NCI_CGAP_P1 Homo sapiens cDNA clone IMAGE:913876
674	13738	26665	1.46	4.0E-04 U32748.1	NT		Haemophilus Influenzae Rd section 63 of 163 of the complete genome
848	13904	26862	1.6	4.0E-04 A1720263.1	EST_HUMAN		as70b08.x1 Barstead cdon HPLR87 Homo sapiens cDNA clone IMAGE:2334039 3' similar to TR:Q13825
848	13904	26863	1.6	4.0E-04 A1720263.1	EST_HUMAN		as70b08.x1 Barstead cdon HPLR87 Homo sapiens cDNA clone IMAGE:2334039 3' similar to TR:Q13825
1461	14494	27468	2.76	4.0E-04 AW763366.1	EST_HUMAN		Q13825 AU-BINDING PROTEIN/ENOYL-COA HYDRATASE. ;
2095	15112	28133	1.57	4.0E-04 AL163278.2	NT		RC3-CT0254-130100-023-f01 CT0254 Homo sapiens cDNA
2143	15160		0.99	4.0E-04 AL046704.1	EST_HUMAN		Homo sapiens chromosome 21 segment HS21C078
2635	15634	28658	1.66	4.0E-04 O96615	SWISSPROT		DKFZp434D059_r1 434 (synonym: htes3) Homo sapiens cDNA clone DKFZp434D059 5'
3178	16233	29150	1.8	4.0E-04 AF281074.1	NT		SERPIN-2 (SILK GUM PROTEIN 2)
							Homo sapiens neuropilin 2 (NRP2) gene, complete cds, alternatively spliced

Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4351	17378	30257	3.23	4.0E-04	AA576331.1	EST_HUMAN	h10a10.s1 NCI_CGAP_Cot1 Homo sapiens cDNA clone IMAGE:951930 3' similar to gb:M21121 T-CELL SPECIFIC RANTES PROTEIN PRECURSOR (HUMAN);
4351	17378	30258	3.23	4.0E-04	AA576331.1	EST_HUMAN	h10a10.s1 NCI_CGAP_Cot1 Homo sapiens cDNA clone IMAGE:951930 3' similar to gb:M21121 T-CELL SPECIFIC RANTES PROTEIN PRECURSOR (HUMAN);
4568	17591	30484	1.4	4.0E-04	AA086324.1	EST_HUMAN	SPECIFIC RANTES PROTEIN PRECURSOR (HUMAN);
5124	18133	31010	4.37	4.0E-04	BE560650.1	EST_HUMAN	zn61c08.s1 Stragene muscle 937209 Homo sapiens cDNA clone IMAGE:562670 3'
5288	16921		1.02	4.0E-04	AL163287.2	NT	601345895F1 NIH_MGC_8 Homo sapiens cDNA clone IMAGE:3678910 5'
7483	20449	33806	1.26	4.0E-04	P48442	SWISSPROT	EXTRACELLULAR CALCIUM-SENSING RECEPTOR PRECURSOR (CASR) (PARATHYROID CELL CALCIUM-SENSING RECEPTOR)
7780	20733		0.78	4.0E-04	AL161586.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 66
7987	20928	34321	0.56	4.0E-04	AU122078.1	EST_HUMAN	AU122078 MAMMA1 Homo sapiens cDNA clone MAMMA1001820 5'
8881	21848	35269	1.07	4.0E-04	BF240712.1	EST_HUMAN	601875985F1 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:4099700 5'
8889	21855	35275	1.56	4.0E-04	N25507.1	EST_HUMAN	yk39e12.1 Soares melanocyte 2NBHM Homo sapiens cDNA clone IMAGE:284142 5'
10049	22976	36442	3.11	4.0E-04	AI025699.1	EST_HUMAN	ov87n03.s1 Soares testis_NHT Homo sapiens cDNA clone IMAGE:1644341 3'
10200	23125		1.11	4.0E-04	AF022855.1	NT	Mus musculus neuropilin-2(al17) mRNA, alternatively spliced, complete cds
12664	25729		2.42	4.0E-04	AF254822.1	NT	Homo sapiens SMARCA4 isoform (SMARCA4) gene, complete cds, alternatively spliced
157	13280	26187	3.45	3.0E-04	AL119428.1	EST_HUMAN	DKFZp761J221.1 761 (synonym: hary2) Homo sapiens cDNA clone DKFZp761J221 5'
197	13298	26226	1.65	3.0E-04	P49259	SWISSPROT	180 KD SECRETORY PHOSPHOLIPASE A2 RECEPTOR PRECURSOR (PLA2-R)
881	13936	26895	1.84	3.0E-04	U83991.1	NT	Human short chain acyl CoA dehydrogenase gene, exons 1 and 2
1856	14882	27878	1.65	3.0E-04	AI282100.1	EST_HUMAN	qz28d03.y1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2028197 5'
1871	14896		1.43	3.0E-04	AI369874.1	EST_HUMAN	h23a02.x1 NCI_CGAP_Pt28 Homo sapiens cDNA clone IMAGE:2119082 3'
3319	16371	29291	3.17	3.0E-04	P25147	SWISSPROT	INTERNALIN B PRECURSOR
3987	17027	29938	2.72	3.0E-04	P49448	SWISSPROT	GLUTAMATE DEHYDROGENASE 2 PRECURSOR (GDH)
4086	17120		1.21	3.0E-04	AJ271735.1	NT	Homo sapiens Xq pseudautosomal region; segment 1/2
4120	17163		1.33	3.0E-04	BE140609.1	EST_HUMAN	RCO-HT0014-310599-028 HT0014 Homo sapiens cDNA
4854	17871		5.29	3.0E-04	BE153778.1	EST_HUMAN	PMO-HT0339-190200-007-g12 HT0339 Homo sapiens cDNA
5248	18256		1.02	3.0E-04	AJ271735.1	NT	Homo sapiens Xq pseudautosomal region; segment 1/2
6256	19339		5.73	3.0E-04	AL163281.2	NT	Homo sapiens chromosome 21 segment HS21C081
6993	20119	33432	1.62	3.0E-04	AL163278.2	NT	Homo sapiens chromosome 21 segment HS21C078
7183	18414	31216	0.71	3.0E-04	AW083981.1	EST_HUMAN	RCO-NN0027-060400-011-008 NN0027 Homo sapiens cDNA
7847	20794	34171	0.77	3.0E-04	P23468	SWISSPROT	PROTEIN-TYROSINE PHOSPHATASE DELTA PRECURSOR (R-PTP-DELTA)
8602	21570	34986	5.18	3.0E-04	P22607	SWISSPROT	FIBROBLAST GROWTH FACTOR RECEPTOR 3 PRECURSOR (FGFR-3)
10280	23205	36889	1.44	3.0E-04	AA454055.1	EST_HUMAN	zx48d08.1 Soares testis_NHT Homo sapiens cDNA clone IMAGE:795471 5' similar to gb:M62762 VACUOLAR ATP SYNTHASE 16 KD PROTEOLIPID SUBUNIT (HUMAN);

Table 4

Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10538	23460	36957	0.56	3.0E-04	AI992139.1	EST_HUMAN	wf75a11.x1 Soares_thymus_NHIFTh Homo sapiens cDNA clone IMAGE:2513278 3'
10825	23746	37247	7.72	3.0E-04	AA781201.1	EST_HUMAN	aj24g05.s1 Soares_testis_NHT Homo sapiens cDNA clone 1391288 3' similar to gb:M36072.60S RIBOSOMAL PROTEIN L7A (HUMAN);
12245	25957	31315	3.98	3.0E-04	AA228301.1	EST_HUMAN	nc38e04.r1 NCJ_CGAP_P12 Homo sapiens cDNA clone IMAGE:1010430 similar to contains L1.12 L1 repetitive element;
12623	28802	31525	5.33	3.0E-04	AB018292.1	NT	Homo sapiens mRNA for KIAA0749 protein, partial cds
13014	25564		4.33	3.0E-04	AL134483.1	EST_HUMAN	DKFZ547L185_r1 547 (synonym: hbr1) Homo sapiens cDNA clone DKFZp547L185 5'
177	13278	26204	1.29	2.0E-04	AF217796.1	NT	(Homo sapiens SCG10 like-protein, helicase-like protein NHL, M88, and ADP-ribosylation factor related protein 1 (ARFRP1) genes, complete cds
479	13551	26478	3.55	2.0E-04	AU146707.1	EST_HUMAN	AU146707 HEMBB1 Homo sapiens cDNA clone HEMBB1001253 3'
908	13963	26919	4.01	2.0E-04	M86524.1	NT	Human dystrophin gene
908	13963	26920	4.01	2.0E-04	M86524.1	NT	Human dystrophin gene
1183	14224		2.52	2.0E-04	AI286021.1	EST_HUMAN	qh98a11.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1855052 3' similar to contains MER3 b2 MER3 repetitive element;
1190	14230		2.5	2.0E-04	AL163203.2	NT	Homo sapiens chromosome 21 segment HS21C003
1849	14875		1.19	2.0E-04	AF224268.1	NT	Mus musculus 5' flanking region of Plb3 gene
2194	15209		1.03	2.0E-04	AA478980.1	EST_HUMAN	zu39b05.s1 Soares ovary tumor NbhOT Homo sapiens cDNA clone IMAGE:740337 3' similar to contains Alu repetitive element;
2581	15582	28601	4.05	2.0E-04	U68081.1	NT	Human germline T-cell receptor beta chain TCRBV17S1A1T, TCRBV2S1, TCRBV10S1P, TCRBV28S1P, TCRBV19S1P, TCRBV15S1, TCRBV11S1A1T, HVB relic, TCRBV28S1P, TCRBV34S1, TCRBV14S1, TCRBV3S1, TCRBV4S1A1T, TRY4, TRY5, TRY6, TRY8, TRY9, TRY10, TRY11, TRY12, TRY13, TRY14, TRY15, TRY16, TRY17, TRY18, TRY19, TRY20, TRY21, TRY22, TRY23, TRY24, TRY25, TRY26, TRY27, TRY28, TRY29, TRY30, TRY31, TRY32, TRY33, TRY34, TRY35, TRY36, TRY37, TRY38, TRY39, TRY40, TRY41, TRY42, TRY43, TRY44, TRY45, TRY46, TRY47, TRY48, TRY49, TRY50, TRY51, TRY52, TRY53, TRY54, TRY55, TRY56, TRY57, TRY58, TRY59, TRY60, TRY61, TRY62, TRY63, TRY64, TRY65, TRY66, TRY67, TRY68, TRY69, TRY70, TRY71, TRY72, TRY73, TRY74, TRY75, TRY76, TRY77, TRY78, TRY79, TRY80, TRY81, TRY82, TRY83, TRY84, TRY85, TRY86, TRY87, TRY88, TRY89, TRY90, TRY91, TRY92, TRY93, TRY94, TRY95, TRY96, TRY97, TRY98, TRY99, TRY100, TRY101, TRY102, TRY103, TRY104, TRY105, TRY106, TRY107, TRY108, TRY109, TRY110, TRY111, TRY112, TRY113, TRY114, TRY115, TRY116, TRY117, TRY118, TRY119, TRY120, TRY121, TRY122, TRY123, TRY124, TRY125, TRY126, TRY127, TRY128, TRY129, TRY130, TRY131, TRY132, TRY133, TRY134, TRY135, TRY136, TRY137, TRY138, TRY139, TRY140, TRY141, TRY142, TRY143, TRY144, TRY145, TRY146, TRY147, TRY148, TRY149, TRY150, TRY151, TRY152, TRY153, TRY154, TRY155, TRY156, TRY157, TRY158, TRY159, TRY160, TRY161, TRY162, TRY163, TRY164, TRY165, TRY166, TRY167, TRY168, TRY169, TRY170, TRY171, TRY172, TRY173, TRY174, TRY175, TRY176, TRY177, TRY178, TRY179, TRY180, TRY181, TRY182, TRY183, TRY184, TRY185, TRY186, TRY187, TRY188, TRY189, TRY190, TRY191, TRY192, TRY193, TRY194, TRY195, TRY196, TRY197, TRY198, TRY199, TRY200, TRY201, TRY202, TRY203, TRY204, TRY205, TRY206, TRY207, TRY208, TRY209, TRY210, TRY211, TRY212, TRY213, TRY214, TRY215, TRY216, TRY217, TRY218, TRY219, TRY220, TRY221, TRY222, TRY223, TRY224, TRY225, TRY226, TRY227, TRY228, TRY229, TRY230, TRY231, TRY232, TRY233, TRY234, TRY235, TRY236, TRY237, TRY238, TRY239, TRY240, TRY241, TRY242, TRY243, TRY244, TRY245, TRY246, TRY247, TRY248, TRY249, TRY250, TRY251, TRY252, TRY253, TRY254, TRY255, TRY256, TRY257, TRY258, TRY259, TRY260, TRY261, TRY262, TRY263, TRY264, TRY265, TRY266, TRY267, TRY268, TRY269, TRY270, TRY271, TRY272, TRY273, TRY274, TRY275, TRY276, TRY277, TRY278, TRY279, TRY280, TRY281, TRY282, TRY283, TRY284, TRY285, TRY286, TRY287, TRY288, TRY289, TRY290, TRY291, TRY292, TRY293, TRY294, TRY295, TRY296, TRY297, TRY298, TRY299, TRY300, TRY301, TRY302, TRY303, TRY304, TRY305, TRY306, TRY307, TRY308, TRY309, TRY310, TRY311, TRY312, TRY313, TRY314, TRY315, TRY316, TRY317, TRY318, TRY319, TRY320, TRY321, TRY322, TRY323, TRY324, TRY325, TRY326, TRY327, TRY328, TRY329, TRY330, TRY331, TRY332, TRY333, TRY334, TRY335, TRY336, TRY337, TRY338, TRY339, TRY340, TRY341, TRY342, TRY343, TRY344, TRY345, TRY346, TRY347, TRY348, TRY349, TRY350, TRY351, TRY352, TRY353, TRY354, TRY355, TRY356, TRY357, TRY358, TRY359, TRY360, TRY361, TRY362, TRY363, TRY364, TRY365, TRY366, TRY367, TRY368, TRY369, TRY370, TRY371, TRY372, TRY373, TRY374, TRY375, TRY376, TRY377, TRY378, TRY379, TRY380, TRY381, TRY382, TRY383, TRY384, TRY385, TRY386, TRY387, TRY388, TRY389, TRY390, TRY391, TRY392, TRY393, TRY394, TRY395, TRY396, TRY397, TRY398, TRY399, TRY400, TRY401, TRY402, TRY403, TRY404, TRY405, TRY406, TRY407, TRY408, TRY409, TRY410, TRY411, TRY412, TRY413, TRY414, TRY415, TRY416, TRY417, TRY418, TRY419, TRY420, TRY421, TRY422, TRY423, TRY424, TRY425, TRY426, TRY427, TRY428, TRY429, TRY430, TRY431, TRY432, TRY433, TRY434, TRY435, TRY436, TRY437, TRY438, TRY439, TRY440, TRY441, TRY442, TRY443, TRY444, TRY445, TRY446, TRY447, TRY448, TRY449, TRY450, TRY451, TRY452, TRY453, TRY454, TRY455, TRY456, TRY457, TRY458, TRY459, TRY460, TRY461, TRY462, TRY463, TRY464, TRY465, TRY466, TRY467, TRY468, TRY469, TRY470, TRY471, TRY472, TRY473, TRY474, TRY475, TRY476, TRY477, TRY478, TRY479, TRY480, TRY481, TRY482, TRY483, TRY484, TRY485, TRY486, TRY487, 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Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5843	18933	32117	1.15	2.0E-04	AA296652.1	EST_HUMAN	EST11191 Uterus Homo sapiens cDNA 5' end similar to EST containing O family repeat
6057	19138	32349	0.88	2.0E-04	4758179	NT	Homo sapiens cell cycle progression 3 protein (DNJ3) mRNA
6366	19435	32678	0.8	2.0E-04	AF140708.1	NT	Mus musculus G protein coupled receptor gene, complete cds; and unknown gene
7440	20407		2.54	2.0E-04	AU121712.1	EST_HUMAN	AU121712 MAMMA1 Homo sapiens cDNA clone MAMMA1000798 5'
7546	20509		0.61	2.0E-04	AW860963.1	EST_HUMAN	QVO-CT0387-180300-167-e10 CT0387 Homo sapiens cDNA
7882	20826		15.1	2.0E-04	P08548	SWISSPROT	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG
7892	20935	34215	1.21	2.0E-04	P54296	SWISSPROT	MYOMESIN 2 (M-PROTEIN) (165 KD TITIN-ASSOCIATED PROTEIN) (165 KD CONNECTIN-ASSOCIATED PROTEIN)
8170	21109	34508	0.53	2.0E-04	AL043272.2	EST_HUMAN	DKFZp434L2023.1 434 (synonym: hies3) Homo sapiens cDNA clone DKFZp434L2023 5'
8170	21109	34509	0.53	2.0E-04	AL043272.2	EST_HUMAN	DKFZp434L2023.1 434 (synonym: hies3) Homo sapiens cDNA clone DKFZp434L2023 5'
8288	21257	34657	2.13	2.0E-04	U32444.2	NT	Solanum lycopersicum phytochrome F (PHYF) gene, partial cds
8288	21257	34658	2.13	2.0E-04	U32444.2	NT	Solanum lycopersicum phytochrome F (PHYF) gene, partial cds
8627	21595	35015	1.21	2.0E-04	AB026898.1	NT	Homo sapiens DNA, DLEC1 to ORCTL4 gene region, section 1/2 (DLEC1, ORCTL3, ORCTL4 genes, complete cds)
8627	21595	35016	1.21	2.0E-04	AB026898.1	NT	Homo sapiens DNA, DLEC1 to ORCTL4 gene region, section 1/2 (DLEC1, ORCTL3, ORCTL4 genes, complete cds)
8911	21877	35303	1.9	2.0E-04	AF020503.1	NT	Homo sapiens FRA3B common fragile region, diadenosine triphosphate hydrolase (FHIT) gene, exon 5
9095	22061	35486	0.56	2.0E-04	X67331.1	NT	Human immunoglobulin C(mu) and C(delta) heavy chain genes (constant regions)
9689	22642	36100	0.51	2.0E-04	AA725700.1	EST_HUMAN	ai22a12.s1 Soares_testis_NHT Homo sapiens cDNA clone 1343518 3'
9774	22715	36170	0.65	2.0E-04	P18715	SWISSPROT	GASTRULA ZINC FINGER PROTEIN XLG26.1
10334	23258	36735	1.21	2.0E-04	BE149303.1	EST_HUMAN	RC3-HT0254-151099-011-b05 HT0254 Homo sapiens cDNA
10377	23300	36776	2.74	2.0E-04	AA405777.1	EST_HUMAN	zu66c11.1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:742964 5'
11197	24152	37683	3.56	2.0E-04	AV730373.1	EST_HUMAN	AV730373 HTF Homo sapiens cDNA clone HTFAAA01 5'
11510	24451		2.59	2.0E-04	AJ243213.1	NT	Homo sapiens partial 5-HT4 receptor gene, exons 2 to 6
11635	24572	38136	2.95	2.0E-04	AI440282.1	EST_HUMAN	tt01f11.x1 NCL_CGAP_Gas4 Homo sapiens cDNA clone IMAGE:2140269 3' similar to contains Alu repetitive element;
11755	24683	38262	2.49	2.0E-04	AW136740.1	EST_HUMAN	UJ-H-B11-adm-c-04-Q-U1.s1 NCL_CGAP_Sub3 Homo sapiens cDNA clone IMAGE:2717190 3'
768	13827	26771	0.81	1.0E-04	H99646.1	EST_HUMAN	yz26c09.s1 Soares_melanocyte_2NbhM Homo sapiens cDNA clone IMAGE:262864 3' similar to contains L1 11 L1 repetitive element ;
951	14004	26956	2.03	1.0E-04	P48725	SWISSPROT	PERICENTRIN
1076	14121	27072	2.61	1.0E-04	P11369	SWISSPROT	RETROVIRUS-RELATED POLYPROTEIN [CONTAINS: REVERSE TRANSCRIPTASE ; ENDONUCLEASE]
1116	14160	27110	4.21	1.0E-04	AW013847.1	EST_HUMAN	UI-H-B10-aab-e-09-Q-U1.s1 NCL_CGAP_Sub1 Homo sapiens cDNA clone IMAGE:2708825 3'

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Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1118	14180	27111	4.21	1.0E-04	AW013847.1	EST_HUMAN	U1-H-B10-eab-e-09-0-U1.s1 NCI_CGAP_Sub1 Homo sapiens cDNA clone IMAGE:2708825 3'
1335	14369		3.08	1.0E-04	U62918.1	NT	Anguilla anguilla dopamine D1A1 receptor (d1A1) gene, complete cds
1632	14665	27640	3.19	1.0E-04	AF148805.1	NT	Kaposi's sarcoma-associated herpesvirus ORF 68 gene, partial cds; and ORF 69, kaposin, v-FLIP, v-cyclin, latent nuclear antigen, ORF K14, v-GPCR, putative phosphoribosylglycinamide synthase, and LAMP (LAMP) genes, complete cds
1632	14665	27641	3.19	1.0E-04	AF148805.1	NT	Kaposi's sarcoma-associated herpesvirus ORF 68 gene, partial cds; and ORF 69, kaposin, v-FLIP, v-cyclin, latent nuclear antigen, ORF K14, v-GPCR, putative phosphoribosylglycinamide synthase, and LAMP (LAMP) genes, complete cds
1878	14903	27903	2.37	1.0E-04	AB048342.1	NT	Equus caballus DNA, chromosome 24q14, microsatellite TKY36
2698	15694	28710	1.05	1.0E-04	BE218833.1	EST_HUMAN	h45c08.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3176366 3'
2698	15694	28711	1.05	1.0E-04	BE218833.1	EST_HUMAN	h45c08.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3176366 3'
3297	16350	29270	1.14	1.0E-04	Q62203	SWISSPROT	SPICEOSOME ASSOCIATED PROTEIN 92 (SAP 92) (SPLICING FACTOR 3A SUBUNIT 2) (SF3A66)
3748	16780	28702	0.93	1.0E-04	AI440282.1	EST_HUMAN	j01f11.x1 NCI_CGAP_Gas4 Homo sapiens cDNA clone IMAGE:2140289 3' similar to contains Alu repetitive element;
4089	17123	30017	2.07	1.0E-04	M14042.1	NT	Mouse alpha 1 type-IV collagen mRNA
4109	17143	30037	1.04	1.0E-04	AV647727.1	EST_HUMAN	AV647727 GLC Homo sapiens cDNA clone GLCBB04 3'
5132	18141	31019	1.87	1.0E-04	7662015	NT	Homo sapiens KIAA0237 gene product (KIAA0237), mRNA
5132	18141	31020	1.87	1.0E-04	7662015	NT	Homo sapiens KIAA0237 gene product (KIAA0237), mRNA
5137	18146	31026	0.92	1.0E-04	AI357156.1	EST_HUMAN	q62h04.x1 NCI_CGAP_GC4 Homo sapiens cDNA clone IMAGE:2006975 3'
5990	19045	32244	1.19	1.0E-04	P08547	SWISSPROT	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG
6033	19116	32319	0.52	1.0E-04	T19615.1	EST_HUMAN	753F Heart Homo sapiens cDNA clone 753
6033	19116	32320	0.52	1.0E-04	T19615.1	EST_HUMAN	753F Heart Homo sapiens cDNA clone 753
6579	19639	32905	0.9	1.0E-04	AA177111.1	EST_HUMAN	nc02e12.s1 NCI_CGAP_P38 Homo sapiens cDNA clone IMAGE:252
7012	20138	33455	0.86	1.0E-04	AA564561.1	EST_HUMAN	h25a04.s1 NCI_CGAP_AA1 Homo sapiens cDNA clone IMAGE:993486 3' similar to gb:U97252
7392	20361	33713	12.86	1.0E-04	AI251980.1	EST_HUMAN	KALLMANN SYNDROME PROTEIN PRECURSOR (HUMAN); contains Alu repetitive element;
7821	20361	33713	12.73	1.0E-04	AI251980.1	EST_HUMAN	q67d10.x1 NCI_CGAP_Ov32 Homo sapiens cDNA clone IMAGE:1985683 3'
8328	21297	34712	0.89	1.0E-04	AA630453.1	EST_HUMAN	ab04g08.s1 Stragene lung (h937210) Homo sapiens cDNA clone IMAGE:854654 3'
9692	22645	36102	2.18	1.0E-04	AI806220.1	EST_HUMAN	wf26e08.x1 Soares NFL_T_GBC S1 Homo sapiens cDNA clone IMAGE:2356742 3'
9703	22856	36111	1.47	1.0E-04	O88969	SWISSPROT	CYSTATIN-RELATED EPIDIDYMAL SPERMATOGENIC PROTEIN PRECURSOR (CYSTATIN 8)
9780	22721		0.63	1.0E-04	T77153.1	EST_HUMAN	yd72c08.r1 Soares fetal liver spleen 1NfLS Homo sapiens cDNA clone IMAGE:113774 5'
10004	22931	36394	1.89	1.0E-04	P08547	SWISSPROT	Homo sapiens phospholipid scramblase 1 (PLSCR1), mRNA
10539	23461		9.91	1.0E-04	P08547	SWISSPROT	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG
10578	23498	36990	0.91	1.0E-04	P08547	SWISSPROT	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
11867	24603		1.74	1.0E-04	M28587.1	NT	Mouse alpha leukocyte interferon gene, complete cds
11961	24840	38433	1.5	1.0E-04	AB032988.1	NT	Homo sapiens mRNA for KIAA1142 protein, partial cds
11999	24878	38472	1.46	1.0E-04	AW269061.1	EST_HUMAN	xv49g12.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2816518 3'
12032	24908	38502	1.81	1.0E-04	Q03696	SWISSPROT	NEURONAL-GLIAL CELL ADHESION MOLECULE PRECURSOR (NG-CAM)
12032	24908	38503	1.81	1.0E-04	Q03696	SWISSPROT	NEURONAL-GLIAL CELL ADHESION MOLECULE PRECURSOR (NG-CAM)
12413	25770		2.4	1.0E-04	BE676399.1	EST_HUMAN	722a10.x1 NCL_CGAP_CLL1 Homo sapiens cDNA clone IMAGE:3296058 3' similar to contains L1.13 L1
13061	25597		1.38	1.0E-04	BE700353.1	EST_HUMAN	repetitive element
699	13761	26693	2.39	9.0E-05	AA718933.1	EST_HUMAN	PM4-NN0091-190700-004-f11 NN0091 Homo sapiens cDNA
2020	15041	28052	1.09	9.0E-05	AW866218.1	EST_HUMAN	ah45c11.s1 Soares_testis NHT Homo sapiens cDNA clone 1292488 3'
6074	19155	32367	1.58	9.0E-05	Q60716	SWISSPROT	QV4-SN0023-070400-166-b04 SN0023 Homo sapiens cDNA
7828	20776	34153	0.67	9.0E-05	AW204958.1	EST_HUMAN	PROLYL 4-HYDROXYLASE ALPHA-2 SUBUNIT PRECURSOR
7828	20776	34154	0.67	9.0E-05	AW204958.1	EST_HUMAN	UI-H-B11-aer-4-05-0-U1.s1 NCL_CGAP_Sub3 Homo sapiens cDNA clone IMAGE:2720289 3'
9831	22680		2.69	9.0E-05	D85606.1	NT	UI-H-B11-aer-4-05-0-U1.s1 NCL_CGAP_Sub3 Homo sapiens cDNA clone IMAGE:2720289 3'
9833	22682	36137	3.13	9.0E-05	AF120982.1	NT	Homo sapiens gene for cholesterylkinin type-A receptor, complete cds
11472	24415	37994	2.03	9.0E-05	AW073078.1	EST_HUMAN	Homo sapiens methyl-CpG binding protein 1 (MBD1) gene, exon 15b
11938	19155	32367	3.21	9.0E-05	Q60716	SWISSPROT	xa34g05.x1 NCL_CGAP_Br18 Homo sapiens cDNA clone IMAGE:2566728 3' similar to contains L1.12 L1
12465	25832		3.02	9.0E-05	AF129786.1	NT	repetitive element
822	13860	26831	1.79	8.0E-05	AJ251646.1	NT	PROLYL 4-HYDROXYLASE ALPHA-2 SUBUNIT PRECURSOR
865	13921		7.38	8.0E-05	AJ251646.1	NT	Homo sapiens MSH55 gene, partial cds; and CLIC1, DDAH, G6b, G6c, G6d, G6e, G6f, BAT5, G5b, CSK2B, BAT4, G4, Apo M, BAT3, BAT2, AIF-1, 1C7, LST-1, LTB, TNF, and LTA genes, complete cds
2981	18019		0.91	8.0E-05	M83575.1	NT	Pisum sativum mRNA for beta-1,3 glucanase (gns2 gene)
4507	17532	30415	0.87	8.0E-05	AW044605.1	EST_HUMAN	Pisum sativum mRNA for beta-1,3 glucanase (gns2 gene)
9701	22067	35493	0.48	8.0E-05	Y11686.1	NT	Human platelet-derived growth factor A chain (PDGFA) gene, exons only
11485	24428	37979	3.06	8.0E-05	M69197.1	NT	Human platelet-derived growth factor A chain (PDGFA) gene, exons only
13050	25815		2.74	8.0E-05	AA279333.1	EST_HUMAN	Myo myosin gene for hexokinase II, exon 1 (and joined CDS)
347	13436	26358	6.11	7.0E-05	AW847445.1	EST_HUMAN	Human haptoglobin and haptoglobin-related protein (HP and HPR) genes, complete cds
347	13436	26359	6.11	7.0E-05	AW847445.1	EST_HUMAN	zs88h01.s1 NCL_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:704593 3' similar to contains Alu
569	13639	26553	1	7.0E-05	L49075.1	EST_HUMAN	repetitive element/contains element MSR1 repetitive element
569	13639	26554	1	7.0E-05	L49075.1	EST_HUMAN	RC3-CT0208-220999-011-E04 CT0208 Homo sapiens cDNA
							RC3-CT0208-220999-011-E04 CT0208 Homo sapiens cDNA
							HUM072014F Human fovea cDNA Homo sapiens cDNA clone EST HFD072014
							HUM072014F Human fovea cDNA Homo sapiens cDNA clone EST HFD072014

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1058	14104	27055	1.47	7.0E-05	Q22949	SWISSPROT	PROBABLE GLYCEROL-3-PHOSPHATE ACYLTRANSFERASE, MITOCHONDRIAL PRECURSOR (GPAT)
2730	15724	28740	4.26	7.0E-05	AL163276.2	NT	Homo sapiens chromosome 21 segment HS21C078
3172	16227	29143	4.21	7.0E-05	AB009080.1	NT	Dichytellium discoidium gene for TRFA, complete cds
3714	16757		0.9	7.0E-05	AI432413.1	EST_HUMAN	g73c09.x1 Soares_NHMPu_S1 Homo sapiens cDNA clone IMAGE:21144163
4400	17428	30313	1.53	7.0E-05	AL163201.2	NT	Homo sapiens chromosome 21 segment HS21C001
4982	17977	30887	0.89	7.0E-05	9845300	NT	Rat cytomegalovirus Maastricht, complete genome
8567	21535	34955	1.27	7.0E-05	AA505582.1	EST_HUMAN	h83g01.s1 NCL_CGAP_Br2 Homo sapiens cDNA clone IMAGE:966096 3'
9911	22732	36187	3.34	7.0E-05	T07095.1	EST_HUMAN	EST04984 Fetal brain, Stragene (cat#935206) Homo sapiens cDNA clone HFBED60
10982	23902	37415	0.44	7.0E-05	AL163249.2	NT	Homo sapiens chromosome 21 segment HS21C049
10982	23902	37416	0.44	7.0E-05	AL163249.2	NT	Homo sapiens chromosome 21 segment HS21C049
11495	24438		9	7.0E-05	10835046	NT	Homo sapiens sarcoglycan, epsilon (SGCE), mRNA
2041	15060	28080	1.6	6.0E-05	4885170	NT	Homo sapiens chromosome X open reading frame 6 (CXORF6) mRNA
2041	15060	28081	1.6	6.0E-05	4885170	NT	Homo sapiens chromosome X open reading frame 6 (CXORF6) mRNA
2594	15595	28613	1.05	6.0E-05	AI655241.1	EST_HUMAN	wb54h06.x1 NCL_CGAP_GC6 Homo sapiens cDNA clone IMAGE:2309531 3' similar to gb.J03250 DNA TOPOISOMERASE I (HUMAN);
2694	15690	28707	1.3	6.0E-05	Z84506.1	NT	H.sapiens flow-sorted chromosome 6 HindIII fragment, SC6pA28B10
2694	15690	28708	1.3	6.0E-05	Z84506.1	NT	H.sapiens flow-sorted chromosome 6 HindIII fragment, SC6pA28B10
2825	13743	26689	3.23	6.0E-05	AF053630.1	NT	Homo sapiens monocyte/neutrophil elastase inhibitor gene, complete cds
5107	18117	30890	0.93	6.0E-05	AV722942.1	EST_HUMAN	AV722942 HTB Homo sapiens cDNA clone HTBBED12 5'
5107	18117	30891	0.93	6.0E-05	AV722942.1	EST_HUMAN	AV722942 HTB Homo sapiens cDNA clone HTBBED12 5'
6019	19102	32303	3.06	6.0E-05	Q12860	SWISSPROT	CONTACTIN PRECURSOR (GLYCOPROTEIN GP135)
6019	19102	32304	3.06	6.0E-05	Q12860	SWISSPROT	CONTACTIN PRECURSOR (GLYCOPROTEIN GP135)
6543	19605	32867	1.45	6.0E-05	N72829.1	EST_HUMAN	w50g11.r1 Soares fetal liver spleen 1NLS Homo sapiens cDNA clone IMAGE:246212 5'
7119	20053	33357	0.77	6.0E-05	AA897680.1	EST_HUMAN	q80e03.s1 Soares_NFL_T_GBC_ST Homo sapiens cDNA clone IMAGE:1504588 3'
8421	21390	34800	0.71	6.0E-05	BE064410.1	EST_HUMAN	RC4-BT0311-141199-011-h06 BT0311 Homo sapiens cDNA
8421	21390	34801	0.71	6.0E-05	BE064410.1	EST_HUMAN	RC4-BT0311-141199-011-h06 BT0311 Homo sapiens cDNA
8786	21793	35175	0.88	6.0E-05	AA150482.1	EST_HUMAN	z08e08.s1 Soares_pregnant_uterus_NbHPu Homo sapiens cDNA clone IMAGE:491726 3' similar to contains element MER28 repetitive element;
8791	21758	35180	2.37	6.0E-05	AW896829.1	EST_HUMAN	PM4-NN0050-310300-001-f10 NN0050 Homo sapiens cDNA
8927	21893	35321	0.61	6.0E-05	Q80401	SWISSPROT	COMPLEMENT DECAY-ACCELERATING FACTOR PRECURSOR
9607	22611	36063	1.11	6.0E-05	P08607	SWISSPROT	C4B-BINDING PROTEIN PRECURSOR (C4BP)
9607	22611	36064	1.11	6.0E-05	P08607	SWISSPROT	C4B-BINDING PROTEIN PRECURSOR (C4BP)
9879	22832	36286	1.05	6.0E-05	T94149.1	EST_HUMAN	ye28c12.t1 Stragene lung (#837210) Homo sapiens cDNA clone IMAGE:119062 5'

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10079	23006	36477	0.71	6.0E-05	AW627985.1	EST_HUMAN	h37a03.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2974444 3'
11100	24060	37584	2.27	6.0E-05	R75639.1	EST_HUMAN	y59d08.s1 Soares placenta N52HP Homo sapiens cDNA clone IMAGE:143535 3' similar to contains Alu repetitive element; contains LTR repetitive element;
11847	24730	38316	2.71	6.0E-05	AA044015.1	EST_HUMAN	2458f02.r1 Soares_pregnant uterus_NbHPU Homo sapiens cDNA clone IMAGE:487035 5'
12670	25813	31529	16.08	6.0E-05	AW890110.1	EST_HUMAN	MF0-NT0038-250400-001-099 NT0038 Homo sapiens cDNA
1403	14436	27404	16.34	5.0E-05	AW392088.1	EST_HUMAN	QV4-ST0234-241199-040-h11 ST0234 Homo sapiens cDNA
1880	14905		1.15	5.0E-05	8923891	NT	Homo sapiens 22kDa peroxisomal membrane protein-like (LOC55895), mRNA
4004	17043	29951	3.54	5.0E-05	AJ251884.1	NT	Homo sapiens partial SLC22A3 gene for extraneuronal monoamine transporter (EMT), exon 1
5803	18899	31670	11.74	5.0E-05	X58855.1	NT	Human MLG1emb gene for embryonic myosin alkaline light chain, 3'UTR
6107	19186	32405	3.22	5.0E-05	AV653544.1	EST_HUMAN	AY653544 GLC Homo sapiens cDNA clone GLODMA06 3'
6292	19384	32603	0.84	5.0E-05	AF260225.1	NT	Homo sapiens TESTIN 2 and TESTIN 3 genes, complete cds, alternatively spliced
7553	20516		1.18	5.0E-05	AB037964.1	NT	Mus musculus gene for calretinin, exon 1
12462	25371		5.88	5.0E-05	P49193	SWISSPROT	RETINAL-BINDING PROTEIN (RALBP)
12717	25371		4.8	5.0E-05	P49193	SWISSPROT	RETINAL-BINDING PROTEIN (RALBP)
2818	13329		4.95	4.0E-05	U12821.1	NT	Human renin (REN) gene, 5' flanking region
4508	17533	30416	1.68	4.0E-05	P49193	SWISSPROT	RETINAL-BINDING PROTEIN (RALBP)
4508	17533	30417	1.68	4.0E-05	P49193	SWISSPROT	RETINAL-BINDING PROTEIN (RALBP)
4910	17927		0.99	4.0E-05	AF164488.1	NT	Cryptosporidium parvum isolate Zaire 15 kDa glycoprotein gp15 gene, partial cds
7127	20060	33366	0.71	4.0E-05	U01947.1	NT	Macaca mulatta lactoglobulin (HP) gene, 5' region
9881	22834		8.43	4.0E-05	AF202635.1	NT	Homo sapiens PP1200 mRNA, complete cds
							RETROVIRUS-RELATED POLYPROTEIN [CONTAINS: REVERSE TRANSCRIPTASE ;
							ENDONUCLEASE]
10360	23283	36780	0.51	4.0E-05	P11369	SWISSPROT	BETA-GALACTOSIDASE PRECURSOR (LACTASE) (ACID BETA-GALACTOSIDASE)
10771	23692	37189	0.66	4.0E-05	P23780	SWISSPROT	BETA-GALACTOSIDASE PRECURSOR (LACTASE) (ACID BETA-GALACTOSIDASE)
11120	24080	37604	3.91	4.0E-05	AW627946.1	EST_HUMAN	h36c07.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2805192 3'
12423	25192		2.46	4.0E-05	AW117580.1	EST_HUMAN	x483a09.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:748252 3'
13081	25612		2.29	4.0E-05	AA417566.1	EST_HUMAN	z071e11.s1 NCI CGAP GCBT Homo sapiens cDNA clone IMAGE:748252 3'
							qf64c10.x1 Soares_fetal_liver_spleen_NFLS_S1 Homo sapiens cDNA clone IMAGE:1849458 3' similar to contains Alu repetitive element; contains element KER repetitive element;
681	13744	26871	0.78	3.0E-05	AL248061.1	EST_HUMAN	contains Alu repetitive element; contains element KER repetitive element;
1081	14107	27057	1.89	3.0E-05	AW273851.1	EST_HUMAN	x224g05.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2814100 3'
1133	14176	27125	0.82	3.0E-05	BF037898.1	EST_HUMAN	601461463F1 NIH_MGC 66 Homo sapiens cDNA clone IMAGE:3865142 5'
1133	14176	27126	0.82	3.0E-05	BF037898.1	EST_HUMAN	601461463F1 NIH_MGC 66 Homo sapiens cDNA clone IMAGE:3865142 5'
4409	17437	30324	8.15	3.0E-05	BE169211.1	EST_HUMAN	PM1-HT0521-120200-001-e10 HT0521 Homo sapiens cDNA
4409	17437	30325	8.15	3.0E-05	BE169211.1	EST_HUMAN	PM1-HT0521-120200-001-e10 HT0521 Homo sapiens cDNA

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Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4493	17518	30405	2.41	3.0E-05	AA368679.1	EST_HUMAN	EST179998 Placenta 1 Homo sapiens cDNA similar to p53-associated protein
4493	17518	30406	2.41	3.0E-05	AA368679.1	EST_HUMAN	EST179998 Placenta 1 Homo sapiens cDNA similar to p53-associated protein
4620	17641		0.7	3.0E-05	AL163302.2	NT	Homo sapiens chromosome 21 segment HS21C102
5637	18733	31895	1.76	3.0E-05	11072102	NT	Mus musculus myosin light chain 2, precursor lymphocyte-specific (Mylc2p), mRNA
6921	19971	33287	1.18	3.0E-05	AJ225782.1	NT	Homo sapiens SYBL1 gene, exons 6-8
6921	19971	33288	1.18	3.0E-05	AJ225782.1	NT	Homo sapiens SYBL1 gene, exons 6-8
8230	21198	34606	2.46	3.0E-05	BE733157.1	EST_HUMAN	601567451F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3842292 5'
8695	21663	35087	1.68	3.0E-05	AA284049.1	EST_HUMAN	zs60b05.s1 Stratagene schizo brain S11 Homo sapiens cDNA clone IMAGE:701841 3'
9244	22210	35641	1.54	3.0E-05	AW770882.1	EST_HUMAN	h18408.x1 NCL_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3008638 3'
9248	22214	35644	1.37	3.0E-05	6912431	NT	Homo sapiens interleukin-1 receptor antagonist homolog 1 (IL1HY1), mRNA
9252	22218	35649	0.59	3.0E-05	P43361	SWISSPROT	MELANOMA-ASSOCIATED ANTIGEN 8 (MAGE-8 ANTIGEN)
9486	22450		0.51	3.0E-05	X03273.1	NT	Human Alu-family cluster 5' of alpha(1)-acid glycoprotein gene
9675	22828	36081	1.2	3.0E-05	AA372582.1	EST_HUMAN	EST84475 Colon adenocarcinoma IV Homo sapiens cDNA 5' end
10021	22948		3.24	3.0E-05	AI769331.1	EST_HUMAN	wg36109.x1 Soares_NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:2367209 3'
10801	23821	37330	0.89	3.0E-05	Q62918	SWISSPROT	PROTEIN KINASE C-BINDING PROTEIN NELL2 PRECURSOR (NELL-LIKE PROTEIN 2)
10801	23821	37331	0.89	3.0E-05	Q62918	SWISSPROT	PROTEIN KINASE C-BINDING PROTEIN NELL2 PRECURSOR (NELL-LIKE PROTEIN 2)
12353	25147		1.49	3.0E-05	L77570.1	NT	Homo sapiens DiGeorge syndrome critical region, centromeric end
2332	15343	28365	1.32	2.0E-05	AI286021.1	EST_HUMAN	q198e11.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1855052 3' similar to contains MER3.b2 MER3 repetitive element;
2587	15588	28605	2.2	2.0E-05	M13792.1	NT	Human adenosine deaminase (ADA) gene, complete cds
2725	15719		7.98	2.0E-05	AA160582.1	EST_HUMAN	zq46a12.r1 Stratagene hNT neuron (#937233) Homo sapiens cDNA clone IMAGE:632734 5' similar to contains Alu repetitive element; contains element L1 repetitive element;
3154	16211	29128	1.15	2.0E-05	BE066036.1	EST_HUMAN	RC3-BT0319-120200-014-h08 BT0319 Homo sapiens cDNA
3359	16409	29331	0.88	2.0E-05	AF184614.1	NT	Homo sapiens p47-phox (NCF1) gene, complete cds
3382	16431	29359	1.35	2.0E-05	X89211.1	NT	H. sapiens DNA for endogenous retroviral like element
3505	16552		0.7	2.0E-05	X95465.1	NT	S. cerevisiae 12.8 Kbp fragment of the left arm of chromosome XV
3820	16860		0.69	2.0E-05	AL039107.1	EST_HUMAN	DKFZp566i064.r1 566 (synonym: hfkd2) Homo sapiens cDNA clone DKFZp566i064 5'
4720	17740		1	2.0E-05	BE378471.1	EST_HUMAN	601236455F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3608653 5'
5852	18943	32128	1.57	2.0E-05	AJ011712.1	NT	Homo sapiens TNNT1 gene, exons 1-11 (and joined CDS)
6024	19107		0.65	2.0E-05	AF028308.1	NT	Homo sapiens chromosome 9 duplication of the T cell receptor beta locus and trypsinogen gene families
6082	19162	32373	0.86	2.0E-05	Q13183	SWISSPROT	RENAL SODIUM/DICARBOXYLATE COTRANSPORTER (NA(+)/DICARBOXYLATE COTRANSPORTER)

Table 4

Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6092	19162	32374	0.86	2.0E-05	Q13183	SWISSPROT	RENAL SODIUM/DICARBOXYLATE COTRANSPORTER (NA(+)/DICARBOXYLATE COTRANSPORTER)
6281	19353	32589	0.68	2.0E-05	A149272.1	EST_HUMAN	qc72a02.x1 Soares_placenta_8to9weeks_2NbHP8to9W Homo sapiens cDNA clone IMAGE:1715114 3'
6356	19425	32667	0.49	2.0E-05	P35085	SWISSPROT	similar to contains L1, L3 L1 repetitive element:
6778	19833	33116	2.32	2.0E-05	AA714330.1	EST_HUMAN	CALCIUM-BINDING PROTEIN
7086	20020	33322	1.52	2.0E-05	V08926.1	NT	my06d12.s1 NCI_CGAP_SS1 Homo sapiens cDNA clone IMAGE:1238519 3'
7099	20033	33336	0.94	2.0E-05	A1492960.1	EST_HUMAN	P_falciptum mRNA for AARP1 protein, partial
7108	20042		8.62	2.0E-05	A1991025.1	EST_HUMAN	q247b08.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2030003 3' similar to TR:O02711
							O02711 PRO-POL-DUTPASE POLYPROTEIN :
7360	20330	33679	2.22	2.0E-05	AF224262.1	NT	wu35h07.x1 Soares_Dieckgraefe_colon_NHCD Homo sapiens cDNA clone IMAGE:2522077 3'
							Heterodontus francisci HoxA10 (HoxA10), HoxA9 (HoxA9), HoxA7 (HoxA7), HoxA6 (HoxA6), HoxA5 (HoxA5), HoxA4 (HoxA4), HoxA3 (HoxA3), HoxA2 (HoxA2), and HoxA1 (HoxA1) genes, complete cds
7360	20330	33680	2.22	2.0E-05	AF224262.1	NT	Heterodontus francisci HoxA10 (HoxA10), HoxA9 (HoxA9), HoxA7 (HoxA7), HoxA6 (HoxA6), HoxA5 (HoxA5), HoxA4 (HoxA4), HoxA3 (HoxA3), HoxA2 (HoxA2), and HoxA1 (HoxA1) genes, complete cds
7592	20553		0.81	2.0E-05	AF128847.1	NT	Homo sapiens indolethylamine N-methyltransferase (INMT) mRNA, INMT-2 allele, complete cds
							Human germ-line T-cell receptor beta chain TCRBV17S1A1T, TCRBV2S1, TCRBV10S1P, TCRBV28S1P, TCRBV19S1P, TCRBV15S1, TCRBV11S1A1T, HVB relic, TCRBV28S1P, TCRBV34S1, TCRBV14S1, TCRBV3S1, TCRBV4S1A1T, TRY4, TRY6, TRY8, TRY7, TRY8, TCRBD1, TCRBJ1S1, TCRBJ1S2>
8157	21095	34494	0.5	2.0E-05	U66091.1	NT	ig20h05.x1 NCI_CGAP_CLL1 Homo sapiens cDNA clone IMAGE:2109369 3'
8217	21186	34506	1.25	2.0E-05	A381040.1	EST_HUMAN	TCBAP2E1500 Pediatric pre-B cell acute lymphoblastic leukemia Baylor-HGSC project=TCBA Homo sapiens cDNA clone TCBAP1590
9477	22441	35981	0.52	2.0E-05	BE244840.1	EST_HUMAN	TCBAP2E1500 Pediatric pre-B cell acute lymphoblastic leukemia Baylor-HGSC project=TCBA Homo sapiens cDNA clone TCBAP1590
9477	22441	35982	0.52	2.0E-05	BE244840.1	EST_HUMAN	TCBAP2E1500 Pediatric pre-B cell acute lymphoblastic leukemia Baylor-HGSC project=TCBA Homo sapiens cDNA clone TCBAP1590
9622	22566	36015	0.57	2.0E-05	P49457	SWISSPROT	COMPLEMENT DECAY-ACCELERATING FACTOR (CD55)
9622	22566	36016	0.57	2.0E-05	P49457	SWISSPROT	COMPLEMENT DECAY-ACCELERATING FACTOR (CD55)
10283	23208	36693	0.57	2.0E-05	AL169207.2	NT	Homo sapiens chromosome 21 segment HS21C007
10494	23416	36914	0.87	2.0E-05	BF056939.1	EST_HUMAN	7175g09.y1 NCI_CGAP_Bm20 Homo sapiens cDNA clone IMAGE:3340576 5'
10954	23874	37387	2.1	2.0E-05	N41761.1	EST_HUMAN	yw91a06.r1 Soares_placenta_8to9weeks_2NbHP8to9W Homo sapiens cDNA clone IMAGE:259570 5'
10954	23874	37388	2.1	2.0E-05	N41761.1	EST_HUMAN	yw91a06.r1 Soares_placenta_8to9weeks_2NbHP8to9W Homo sapiens cDNA clone IMAGE:259570 5'

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
11006	20042		2.01	2.0E-05	AI991025.1	EST_HUMAN	wu35h07.x1 Soares_Dieckgraefe_colon_NHCD Homo sapiens cDNA clone IMAGE:2522077 3'
11781	23936	37457	1.8	2.0E-05	BE175801.1	EST_HUMAN	RC5-HT0582:280300-012-E12 HT0582 Homo sapiens cDNA
12473	25740		6.5	2.0E-05	BE348229.1	EST_HUMAN	hw21a03.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:3183532 3' similar to TR:Q12832
12626	25727		1.54	2.0E-05	AF275948.1	NT	Q12832 GLYCOPHORIN HEP2;
12768	25409	31759	1.49	2.0E-05	AU131513.1	EST_HUMAN	Homo sapiens ABCA1 (ABCA1) gene, complete cds
2705	15902	28715	3.2	1.0E-05	AL163282.2	NT	AU131513 NT2RP3 Homo sapiens cDNA clone NT2RP3002707 5'
3663	16706	29821	1.86	1.0E-05	AF088273.1	NT	Homo sapiens chromosome 21 segment HS21C082
3826	16866		1.17	1.0E-05	AF223391.1	NT	Drosophila melanogaster strain Lamto T20 Suppressor of Hairless (Su(H)) gene, partial cds
3991	17031	25940	10.43	1.0E-05	P81274	SWISSPROT	Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced
4201	17232	30119	1.82	1.0E-05	AL168203.2	NT	MOSAIC PROTEIN LGN
4306	17335	30213	1.77	1.0E-05	AA431118.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C0303
4887	17904	30793	1.82	1.0E-05	AW419134.1	EST_HUMAN	zw68g04.r1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:781494 5'
5005	18019	30907	0.94	1.0E-05	Z18943.1	NT	xy49g11.x1 NCI_CGAP_Lu34.1 Homo sapiens cDNA clone IMAGE:2855548 3'
6815	19987	33262	1.03	1.0E-05	AJ246003.1	NT	H. sapiens repeat region
7028	18360	31281	0.52	1.0E-05	P08548	SWISSPROT	Homo sapiens Spast gene for spastin protein
7286	20063	33370	3.02	1.0E-05	AA541848.1	EST_HUMAN	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG
7288	20260	33594	8.81	1.0E-05	4505844	NT	ns19g02.s1 NCI_CGAP_GC081 Homo sapiens cDNA clone IMAGE:1184114 3' similar to contains L1.1 L1
7921	20864	34252	0.66	1.0E-05	BF222646.1	EST_HUMAN	Homo sapiens phospholipase A2, group X (PLA2G10) mRNA, and translated products
8057	20984		1.5	1.0E-05	P19474	SWISSPROT	MER10 repetitive element;
9266	22232		2.45	1.0E-05	AL163227.2	NT	62 KD RO PROTEIN (SJOJOREN SYNDROME TYPE A ANTIGEN (SS-A)) (RO(SS-A))
9415	22380	35818	2.22	1.0E-05	AA452578.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C027
9642	22596	36035	14.03	1.0E-05	AA238110.1	EST_HUMAN	z335h12.s1 Soares_total_fetus_Nb2Hf8_9w Homo sapiens cDNA clone IMAGE:788519 3' similar to gb1.02332 PEROXISOME PROLIFERATOR ACTIVATED RECEPTOR ALPHA (HUMAN);
9721	22749	36201	0.82	1.0E-05	AV732190.1	EST_HUMAN	z305e11.r1 NCI_CGAP_GC081 Homo sapiens cDNA clone IMAGE:684332 5' similar to contains Alu repetitive element; contains element TAR1 repetitive element;
10186	23123	36609	0.79	1.0E-05	AW510902.1	EST_HUMAN	AV732190 HTF Homo sapiens cDNA clone HTFBIH01 5'
10198	23123	36610	0.79	1.0E-05	AW510902.1	EST_HUMAN	hd41b02.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2912043 3' similar to contains OFR.t1 OFR repetitive element;
10276	23201	36685	1.11	1.0E-05	AW291521.1	EST_HUMAN	hd41b02.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2912043 3' similar to contains OFR.t1 OFR repetitive element;
							UJH-BI2-agk-a-08-0-UJ.s1 NCI_CGAP_Sub4 Homo sapiens cDNA clone IMAGE:2724398 3'

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10276	23201	36686	1.11	1.0E-05	AW291521.1	EST_HUMAN	U-H-BI2-agk-a-08-0-J1.s1 NCI_CGAP_Sub4 Homo sapiens cDNA clone IMAGE:2724398 3'
10544	23466		1.95	1.0E-05	AW466995.1	EST_HUMAN	ha07c10.x1 NCI_CGAP_Ki612 Homo sapiens cDNA clone IMAGE:2873010 3' similar to contains L1.12 L1 repetitive element;
11264	24216	37740	1.79	1.0E-05	U91328.1	NT	Human hereditary haemochromatosis region, histone 2A-like protein gene, hereditary haemochromatosis (HLA-H) gene, RoRet gene, and sodium phosphate transporter (NPT3) gene, complete cds
11264	24216	37741	1.79	1.0E-05	U91328.1	NT	Human hereditary haemochromatosis region, histone 2A-like protein gene, hereditary haemochromatosis (HLA-H) gene, RoRet gene, and sodium phosphate transporter (NPT3) gene, complete cds
12941	25900	31421	1.43	1.0E-05	AL163303.2	NT	Homo sapiens chromosome 21 segment HS21C103
2680	15676	28697	5.9	9.0E-06	AI583811.1	EST_HUMAN	h73a06.x1 NCI_CGAP_HSC3 Homo sapiens cDNA clone IMAGE:2246386 3'
3112	16169	28079	4.25	9.0E-06	AI218983.1	EST_HUMAN	qg11b08.x1 Soares_placenta_8tc9weeks_2Nbl-P8tc9W Homo sapiens cDNA clone IMAGE:1759191 3'
3624	16667		2.82	9.0E-06	M61755.1	NT	Human alanine:glyoxylate aminotransferase (AGXT) gene, exons 1 and 2
6008	19091	32291	2.31	9.0E-06	L23416.1	NT	Homo sapiens differentiation antigen CD20 gene, exons 5, 6
7047	20069	33375	0.73	9.0E-06	BE06042.1	EST_HUMAN	RC1-BT0313-110500-017-a07 BT0313 Homo sapiens cDNA
7674	20632	33996	0.94	9.0E-06	P08647	SWISSPROT	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG
8053	20990	34388	11.84	9.0E-06	AI034370.1	EST_HUMAN	α20g01.x1 Soares_fetal_liver_spleen_INFLS_S1 Homo sapiens cDNA clone IMAGE:1656912 3' similar to contains Alu repetitive element;
8807	21774	38200	1.18	9.0E-06	AL163209.2	NT	Homo sapiens chromosome 21 segment HS21C009
9334	22299	35728	2.51	9.0E-06	Q63769	SWISSPROT	SUSHI REPEAT-CONTAINING PROTEIN SRPX PRECURSOR (DRS PROTEIN) (DOWN-REGULATED BY V-SRC)
9334	22299	35729	2.51	9.0E-06	Q63769	SWISSPROT	SUSHI REPEAT-CONTAINING PROTEIN SRPX PRECURSOR (DRS PROTEIN) (DOWN-REGULATED BY V-SRC)
9577	22539	35990	4.44	9.0E-06	U35114.1	NT	Human apolipoprotein E (APOE) gene, hepatic control region HCR-2
11286	24236	37783	3.65	9.0E-06	Q10364	SWISSPROT	PUTATIVE SERINE/THREONINE-PROTEIN KINASE C22E12.14C
2535	15896	28559	2.23	8.0E-06	AW362539.1	EST_HUMAN	RC3-CT0283-201189-011-111 CT0283 Homo sapiens cDNA
10898	23818	37326	0.64	8.0E-06	P34083	SWISSPROT	FASCICLIN II, PHOSPHATIDYLINOSITOL-LINKED ISOFORM PRECURSOR (FAS II)
10898	23818	37327	0.64	8.0E-06	P34083	SWISSPROT	FASCICLIN II, PHOSPHATIDYLINOSITOL-LINKED ISOFORM PRECURSOR (FAS II)
980	14031		2.14	7.0E-06	AA669729.1	EST_HUMAN	ab90f10.s1 Stratagene lung (#937210) Homo sapiens cDNA clone IMAGE:854251 3' similar to contains MER20.11 MER20 repetitive element;
1433	14467	27444	3.06	7.0E-06	7682177	NT	Homo sapiens KIAA0555 gene product (KIAA0555), mRNA
2884	15943		7.94	7.0E-06	AI368252.1	EST_HUMAN	qwt16g09.x1 NCI_CGAP_U13 Homo sapiens cDNA clone IMAGE:1991296 3' similar to contains Alu repetitive element;

Single Exon Probes Expressed in Bone Marrow

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3578	16821		0.78	7.0E-06	AA385642.1	EST_HUMAN	EST93205 Thyroid Homo sapiens cDNA 5' end similar to EST containing L1 repeat
5780	18872		5.16	7.0E-06	AW883141.1	EST_HUMAN	QV2-OT0062-260400-173-h01 OT0062 Homo sapiens cDNA
5902	18989	32179	0.81	7.0E-06	N98945.1	EST_HUMAN	y65c07.r1 Soares_multiple_sclerosis_2NbHMSHP Homo sapiens cDNA clone IMAGE:278412 5'
9141	22107	35533	0.7	7.0E-06	11420709	NT	Homo sapiens DNA segment, numerous copies, expressed probes (GS1 gene) (DXF68S1E). mRNA
10280	23185		0.54	7.0E-06	Q61147	SWISSPROT	CERULOPLASMIN PRECURSOR (FERROXIDASE)
12202	25927	31307	2.83	7.0E-06	BF215972.1	EST_HUMAN	601881522F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4093972 5'
2928	15886	28907	1.27	6.0E-06	BE099189.1	EST_HUMAN	QV3-BT0379-010300-105-d11 BT0379 Homo sapiens cDNA
3706	16749	29664	1.08	6.0E-06	BE069189.1	EST_HUMAN	QV3-BT0379-010300-105-d11 BT0379 Homo sapiens cDNA
4785	16010	28938	2.35	6.0E-06	Q01466	SWISSPROT	OVARIAN ABUNDANT MESSAGE PROTEIN (OAM PROTEIN)
4794	17811	30703	2.54	6.0E-06	AI040099.1	EST_HUMAN	ox08e02.x1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:1655738 3' similar to contains MER8.12 MER8 repetitive element:
5422	18525	31403	1.41	6.0E-06	AF167441.1	NT	Mus musculus E-cadherin binding protein E7 mRNA, complete cds
5483	18583	31495	1.05	6.0E-06	Q02040	SWISSPROT	PROTEIN XE7
10215	23140		1.52	6.0E-06	AW801912.1	EST_HUMAN	IL5-UM0070-110400-083-g02 UM0070 Homo sapiens cDNA
13041	25582	31700	1.74	6.0E-06	11418157	NT	Homo sapiens calcium channel, voltage-dependent, alpha 11 subunit (CACNA11), mRNA
6179	19254	32487	3.86	5.0E-06	AL183248.2	NT	Homo sapiens chromosome 21 segment HS21C046
6471	19536	32784	3.96	5.0E-06	U07581.1	NT	Human ABL gene, exon 1b and intron 1b, and putative M8604 Met protein (M8604 Met) gene, complete cds
7444	20410	33762	1.14	5.0E-06	AB007546.1	NT	Homo sapiens gene for LECT2, complete cds
8803	21770	35195	0.49	5.0E-06	AW856972.1	EST_HUMAN	RC1-CT0302-120200-013-h02 CT0302 Homo sapiens cDNA
8803	21770	35196	0.49	5.0E-06	AW856972.1	EST_HUMAN	RC1-CT0302-120200-013-h02 CT0302 Homo sapiens cDNA
10482	23384	36877	7.1	5.0E-06	AA313820.1	EST_HUMAN	EST185498 Colon carcinoma (HCC) cell line Homo sapiens cDNA 5' end
12101	24972	38569	2	5.0E-06	Q28039	SWISSPROT	SODIUM- AND CHLORIDE-DEPENDENT GLYCINE TRANSPORTER 1 (GLYT-1)
12928	25512	31709	2.14	5.0E-06	AI065045.1	EST_HUMAN	HA0877 Human fetal liver cDNA library Homo sapiens cDNA
648	13714	28635	6.59	4.0E-06	R16267.1	EST_HUMAN	ya48c03.r1 Soares infant brain 1N1B Homo sapiens cDNA clone IMAGE:53254 5' similar to contains Alu repetitive element; contains L1 repetitive element:
847	13903	28861	6.33	4.0E-06	AW103354.1	EST_HUMAN	xc09g12.x1 NCI_CGAP_Eso2 Homo sapiens cDNA clone IMAGE:2889574 3' similar to contains Alu repetitive element; contains element MER21 repetitive element:
1337	14371	27340	4.22	4.0E-06	AI334928.1	EST_HUMAN	ts33c09.x1 NCI_CGAP_HSC2 Homo sapiens cDNA clone IMAGE:2056168 3'
1337	14371	27341	4.22	4.0E-06	AI334928.1	EST_HUMAN	ts33c09.x1 NCI_CGAP_HSC2 Homo sapiens cDNA clone IMAGE:2056168 3'
1470	14503	27477	2.58	4.0E-06	BF365612.1	EST_HUMAN	QV2-NT0046-200800-250-h07 NT0046 Homo sapiens cDNA
2274	15287	28313	3.05	4.0E-06	AW015401.1	EST_HUMAN	UHH-B10-aat4-f05-0.UJ.s1 NCI_CGAP_Sub1 Homo sapiens cDNA clone IMAGE:2710425 3'
3078	16133	29048	0.94	4.0E-06	AF189349.1	NT	Gallus gallus Dach2 protein (Dach2) mRNA, complete cds

Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3909	16949	29860	1.1	4.0E-06	AW848295.1	EST_HUMAN	IL3-CT0214-150200-074-B03 CT0214 Homo sapiens cDNA
4846	17863	30756	2.18	4.0E-06	AI886939.1	EST_HUMAN	W194C10.X1 NCI_CGAP_Brn25 Homo sapiens cDNA clone IMAGE:2432562 3' similar to contains element
8844	21811	35230	0.56	4.0E-06	O15393	SWISSPROT	MER22 repetitive element:
9152	22118	35545	3.6	4.0E-06	AF009660.1	NT	TRANSMEMBRANE PROTEASE, SERINE 2
10066	22893	38462	1.14	4.0E-06	AJ272265.1	NT	Homo sapiens T cell receptor beta locus, TCRBV7S3A2 to TCRBV12S2 region
11778	23933	37454	2.91	4.0E-06	AB007855.1	NT	Homo sapiens SPP2 gene for secreted phosphoprotein 24 precursor, exons 1-8
2173	15189	28209	1.9	3.0E-06	AA700562.1	EST_HUMAN	Homo sapiens mRNA, chromosome 1 specific transcript KIAA0486
2173	15189	28210	1.9	3.0E-06	AA700562.1	EST_HUMAN	z34b08.s1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:432663 3' similar to
2275	15288		1.89	3.0E-06	AF202635.1	NT	contains L1.11 L1 repetitive element;
2833	15991	28911	0.95	3.0E-06	AA868218.1	EST_HUMAN	z34b08.s1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:432663 3' similar to
3279	16333		2.32	3.0E-06	AI857779.1	EST_HUMAN	contains L1.11 L1 repetitive element;
3797	16837	29743	1.12	3.0E-06	BE047094.1	EST_HUMAN	ak48g11.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1409252 3' similar to contains LTR1 t3
3797	16837	29744	1.12	3.0E-06	BE047094.1	EST_HUMAN	LTR1 repetitive element;
4501	17526	30411	0.87	3.0E-06	T50266.1	EST_HUMAN	W122a05.x1 NCI_CGAP_U11 Homo sapiens cDNA clone IMAGE:2425516 3' similar to TR:O60734 O60734
4594	17615	30509	4.02	3.0E-06	X54816.1	NT	LINE-1 LIKE PROTEIN :contains L1.2 L1 repetitive element;
6284	19356	32592	0.74	3.0E-06	AU169412.1	EST_HUMAN	h94412.x1 NCI_CGAP_HN13 Homo sapiens cDNA clone IMAGE:3124151 3'
6974	20197	33525	0.56	3.0E-06	Z79478.1	NT	h94412.x1 NCI_CGAP_HN13 Homo sapiens cDNA clone IMAGE:3124151 3'
6974	20197	33526	0.56	3.0E-06	Z79478.1	NT	y678b10.r1 Strategene ovary (#637217) Homo sapiens cDNA clone IMAGE:77275 5' similar to contains L1
7439	20406		1.9	3.0E-06	P08548	SWISSPROT	repetitive element
8419	21388	34798	0.76	3.0E-06	BE562964.1	EST_HUMAN	Homo sapiens gene for alpha-1-microglobulin-bikunin, exons 1-5 (encoding alpha-1-microglobulin, N-terminus.)
9032	21998	35417	0.84	3.0E-06	P07743	SWISSPROT	AU159412 THYROT1 Homo sapiens cDNA clone THYROT1001602 3'
12631	26317		6.4	3.0E-06	AW385262.1	EST_HUMAN	H sapiens flow-sorted chromosome 6 TaqI fragment, SC9pA9E5
203	13304		3.24	2.0E-06	P54366	SWISSPROT	H sapiens flow-sorted chromosome 6 TaqI fragment, SC9pA9E5
1572	14605		5.6	2.0E-06	P21414	SWISSPROT	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG
2387	15395	28420	2.64	2.0E-06	AI672138.1	EST_HUMAN	601336213F1 NIH_MGC 44 Homo sapiens cDNA clone IMAGE:3690314 5'
2474	16478	28501	2.73	2.0E-06	P04929	SWISSPROT	PAROTID SECRETORY PROTEIN PRECURSOR (PSP)
							RCOL10001-261199-011-A03 L70001 Homo sapiens cDNA
							HOMEOBOX PROTEIN GOOSECOID
							POL POLYPROTEIN [CONTAINS: PROTEASE ; REVERSE TRANSCRIPTASE ; ENDONUCLEASE]
							wa04a03.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2297088 3' similar to contains MER30.b1
							MER30 repetitive element:
							HISTIDINE-RICH GLYCOPROTEIN PRECURSOR

Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2573	15574	28594	1.94	2.0E-06	P06719	SWISSPROT	KNOB-ASSOCIATED HISTIDINE-RICH PROTEIN PRECURSOR (KAHRP)
3531	16577	29500	1.29	2.0E-06	AV657655.1	EST_HUMAN	AV657555 GLC Homo sapiens cDNA clone GLCFDB05 3'
3774	16816	29725	1.56	2.0E-06	AA173518.1	EST_HUMAN	z02e05.t1 Stratagene ovarian cancer (#937219) Homo sapiens cDNA clone IMAGE:595232 5'
3783	16824	29732	0.67	2.0E-06	AW450215.1	EST_HUMAN	UHF-B13-aky-g-05-Q-U1.s1 NCI CGAP Sub5 Homo sapiens cDNA clone IMAGE:2736176 3'
3789	16830	29736	1.74	2.0E-06	AB030896.1	NT	Mus musculus gene for odorant receptor A16, complete cds
6208	19282		0.9	2.0E-06	AA974932.1	EST_HUMAN	or34h01.s1 NCI CGAP Lu5 Homo sapiens cDNA clone IMAGE:1558609 3' similar to contains Alu repetitive element
6241	19314	32544	0.93	2.0E-06	AI539448.1	EST_HUMAN	le51f05.x1 Soares NFL T_GBC S1 Homo sapiens cDNA clone IMAGE:2090241 3' similar to TR:Q13537
6581	19641	32908	5.37	2.0E-06	AI819424.1	EST_HUMAN	Q13537 MER37 TRANSPOSABLE ELEMENT, COMPLETE CONSENSUS SEQUENCE. ;
8250	21219		0.81	2.0E-06	AW869223.1	EST_HUMAN	w90b04.x1 NCI CGAP Lym12 Homo sapiens cDNA clone IMAGE:2410063 3'
8426	21395	34806	0.63	2.0E-06	T12238.1	EST_HUMAN	MR3-SN0067-12040-002-02 SN0067 Homo sapiens cDNA
9188	22154		0.61	2.0E-06	AA772497.1	EST_HUMAN	A447R Heart Homo sapiens cDNA clone A447
9200	22166	35596	1.83	2.0E-06	H62051.1	EST_HUMAN	z127c11.s1 Soares pineal gland N3HPG Homo sapiens cDNA clone IMAGE:413300 3' similar to
9571	22533	35983	0.87	2.0E-06	AF003529.1	NT	TR:P70467 P70467 REVERSE TRANSCRIPTASE ;
9571	22533	35984	0.87	2.0E-06	AF003529.1	NT	Y437d04.r1 Soares ovary tumor N3HOT Homo sapiens cDNA clone IMAGE:235974 5' similar to gb:X74929
9591	22553		0.48	2.0E-06	AI473450.1	EST_HUMAN	KERATIN, TYPE II CYTOSKELETAL 8 (HUMAN);
10059	22986	36454	0.92	2.0E-06	N30576.1	EST_HUMAN	Homo sapiens glypican 3 (GPC3) gene, partial cds and flanking repeat regions
10279	23204		0.61	2.0E-06	AV748969.1	EST_HUMAN	Homo sapiens glypican 3 (GPC3) gene, partial cds and flanking repeat regions
12111	24981	38581	2.21	2.0E-06	O15553	SWISSPROT	y16g10.x1 NCI CGAP Gas4 Homo sapiens cDNA clone IMAGE:2141730 3'
12111	24981	38582	2.21	2.0E-06	O15553	SWISSPROT	
12540	25928	31308	2.97	2.0E-06	P23249	SWISSPROT	PROTEIN MOV-10
36	13156	28057	3.02	1.0E-06	O76092	SWISSPROT	ORGANIC CATION/CARNITINE TRANSPORTER 2 (SOLUTE CARRIER FAMILY 22, MEMBER 5) (HIGH AFFINITY SODIUM-DEPENDENT CARNITINE CO TRANSPORTER)
658	13724	26649	1.96	1.0E-06	AF084364.1	NT	Mus musculus D6M5E protein (D6M5e) mRNA, complete cds
1445	14478	27454	1.61	1.0E-06	P09126	SWISSPROT	MEROZOITE SURFACE PROTEIN CMZ-8
1527	14560	27531	1.87	1.0E-06	AL163278.2	NT	Homo sapiens chromosome 21 segment HS21C078
1576	14609	27582	1.22	1.0E-06	AA034141.1	EST_HUMAN	z106a12.s1 Soares_fetal_liver_spleen_INFLS_S1 Homo sapiens cDNA clone IMAGE:429982 3' similar to contains Alu repetitive element
1576	14609	27583	1.22	1.0E-06	AA034141.1	EST_HUMAN	z106a12.s1 Soares_fetal_liver_spleen_INFLS_S1 Homo sapiens cDNA clone IMAGE:429982 3' similar to contains Alu repetitive element

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1587	14920		1.36	1.0E-06	P27625	SWISSPROT	DNA-DIRECTED RNA POLYMERASE III LARGEST SUBUNIT
2010	15031	28040	5.53	1.0E-06	AF184614.1	NT	Homo sapiens p47-phox (NCF1) gene, complete cds
2010	15031	28041	5.53	1.0E-06	AF184614.1	NT	Homo sapiens p47-phox (NCF1) gene, complete cds
4397	17425	30309	13.21	1.0E-06	U07561.1	NT	Human ABL gene, exon 1b and intron 1b, and putative M8604 Met protein (M8604 Met) gene, complete cds
5146	18155	31034	1.23	1.0E-06	AL163285.2	NT	Homo sapiens chromosome 21 segment HS21C085
5146	18155	31035	1.23	1.0E-06	AL163285.2	NT	Homo sapiens chromosome 21 segment HS21C085
5363	18468	31339	4.63	1.0E-06	BF333015.1	EST_HUMAN	MR1-BT0800-030700-002-c06 BT0800 Homo sapiens cDNA
5368	18491	31367	1.01	1.0E-06	BE834518.1	EST_HUMAN	MR3-FN0004-090600-001-s04 FN0004 Homo sapiens cDNA
5388	18491	31368	1.01	1.0E-06	BE834518.1	EST_HUMAN	MR3-FN0004-090600-001-s04 FN0004 Homo sapiens cDNA
5552	18649	31592	1.24	1.0E-06	O60613	SWISSPROT	15 KDA SELENOPROTEIN PRECURSOR
5892	18980		0.64	1.0E-06	BE063527.1	EST_HUMAN	CM0-BT0281-031199-087-h04 BT0281 Homo sapiens cDNA
7056	20078	33387	6.4	1.0E-06	P02671	SWISSPROT	FIBRINOGEN ALPHA1(A) CHAIN PRECURSOR
8018	26005		0.56	1.0E-06	BE165330.1	EST_HUMAN	IL5-HT0730-020500-074-g01 HT0730 Homo sapiens cDNA
8334	21303		0.75	1.0E-06	AA912623.1	EST_HUMAN	cl29c08.s1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA IMAGE:1524878 3'
8616	21594	35000	1.05	1.0E-06	A1347010.1	EST_HUMAN	qp54602.x1 NCI_CGAP_C06 Homo sapiens cDNA clone IMAGE:1926842 3'
8833	21800	35219	1.26	1.0E-06	A1287878.1	EST_HUMAN	q2306.x1 NCI_CGAP_Lym6 Homo sapiens cDNA clone IMAGE:1982435 3' similar to contains element
9659	22816	36270	1.15	1.0E-06	N74635.1	EST_HUMAN	MIR repetitive element
9734	22762	36217	0.56	1.0E-06	Q39575	SWISSPROT	z555e01.s1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:296472 3'
10041	22968	36434	3.97	1.0E-06	U82668.1	NT	DYNEIN GAMMA CHAIN, FLAGELLAR OUTER ARM
10041	22968	36435	3.97	1.0E-06	U82668.1	NT	Homo sapiens shox gene, alternatively spliced products, complete cds
10085	23012	36485	4.9	1.0E-06	AA132611.1	EST_HUMAN	Homo sapiens shox gene, alternatively spliced products, complete cds
10147	23073		3.88	1.0E-06	AA449257.1	EST_HUMAN	z04411.s1 Soares_tet_fetus_Nb2HF8_9w Homo sapiens cDNA clone IMAGE:587174 5'
10854	23774		2.02	1.0E-06	AL163203.2	NT	z017603.r1 Stratagene colon (#637204) Homo sapiens cDNA clone IMAGE:587174 5'
11960	24839		3.14	1.0E-06	AW890941.1	EST_HUMAN	gb/D26129 RIBONUCLEASE PANCREATIC PRECURSOR (HUMAN);
12672	15031	28040	1.71	1.0E-06	AF184614.1	NT	Homo sapiens chromosome 21 segment HS21C003
12672	15031	28041	1.71	1.0E-06	AF184614.1	NT	Homo sapiens p47-phox (NCF1) gene, complete cds
360	13447	26374	1.95	9.0E-07	AF003529.1	NT	Homo sapiens p47-phox (NCF1) gene, complete cds
360	13447	26375	1.95	9.0E-07	AF003529.1	NT	Homo sapiens glypican 3 (GPC3) gene, partial cds and flanking repeat regions
8750	21718		0.59	9.0E-07	AL163280.2	NT	Homo sapiens glypican 3 (GPC3) gene, partial cds and flanking repeat regions
8898	21864		0.43	9.0E-07	AA448276.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C080
11577	24515	38070	4.11	9.0E-07	AL163281.2	NT	z063h01.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:782833 3'
						NT	Homo sapiens chromosome 21 segment HS21C081

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4804	17821	30715	3.87	8.0E-07	A1288596.1	EST_HUMAN	q182g07.x1 Soares_NHIMPu_S1 Homo sapiens cDNA clone IMAGE:1878876 3'
4804	17821	30716	3.87	8.0E-07	A1288596.1	EST_HUMAN	q182g07.x1 Soares_NHIMPu_S1 Homo sapiens cDNA clone IMAGE:1878876 3'
5988	19073		8.55	8.0E-07	P21414	SWISSPROT	POLYPROTEIN [CONTAINS: PROTEASE; REVERSE TRANSCRIPTASE; ENDONUCLEASE]
8335	21304		11.24	8.0E-07	AF135416.1	NT	Homo sapiens UDP-glucuronosyltransferase gene, complete cds
11943	24823		5.78	8.0E-07	T07770.1	EST_HUMAN	EST05660 Fetal brain, Stragene (cat#938206) Homo sapiens cDNA clone HFBEN89
12183	25031		9.17	8.0E-07	AL163280.2	NT	Homo sapiens chromosome 21 segment HS21C080
5597	18693	31663	0.73	7.0E-07	6005700	NT	Homo sapiens ATP-binding cassette, sub-family A (ABC1), member 8 (ABCA8), mRNA
5597	18693	31664	0.73	7.0E-07	6005700	NT	Homo sapiens ATP-binding cassette, sub-family A (ABC1), member 8 (ABCA8), mRNA
1928	14952	27948	4.99	6.0E-07	AW855558.1	EST_HUMAN	CM3-CT0277-221099-024-e11 CT0277 Homo sapiens cDNA
							Homo sapiens HLA class III region containing tenascin X (tenascin-X) gene, partial cds; cytochrome P450 21-hydroxylase (CYP21B), complement component C4 (C4B) G11, heilcase (SKI2W), RD, complement factor B (Bf), and complement component C2 (C2) genes; >
2500	15503	28530	5.38	6.0E-07	AF019413.1	NT	HYPOTHETICAL 24.1 KD PROTEIN IN LEF4-F33 INTERGENIC REGION
3996	17036		2.25	6.0E-07	P41479	SWISSPROT	7g94f07.x1 NCL_CGAP_C016 Homo sapiens cDNA clone IMAGE:3314149 3' similar to TR:O75920 O75920 4F5L
9487	22461	35902	2.17	6.0E-07	BF001867.1	EST_HUMAN	CM4-NN1029-250300-121-h12 NN1029 Homo sapiens cDNA
12442	25880		3.45	6.0E-07	AW903222.1	EST_HUMAN	wh84f10.x1 NCL_CGAP_K1d11 Homo sapiens cDNA clone IMAGE:2385547 3'
328	13417		0.99	6.0E-07	A1831893.1	EST_HUMAN	EST193615 Supt cells Homo sapiens cDNA 5' end
1060	14106		2.45	6.0E-07	AA380630.1	EST_HUMAN	wh84f10.x1 NCL_CGAP_K1d11 Homo sapiens cDNA clone IMAGE:2385547 3'
3044	16101		0.66	6.0E-07	A1831893.1	EST_HUMAN	Homo sapiens NOD1 protein (NOD1) gene, exons 4 through 14 and complete cds
4676	17697	30584	1.16	6.0E-07	AF149774.1	NT	Mus musculus OG-2 homeodomain protein (OG-2) gene, partial cds
6242	19315	32545	1.23	6.0E-07	U65067.1	NT	ig06b05.x1 NCL_CGAP_CLL1 Homo sapiens cDNA clone IMAGE:2107953 3' similar to contains Alu repetitive element; contains element A3R, repetitive element
7266	20001	33300	1.68	6.0E-07	AI333981.1	EST_HUMAN	ig06b05.x1 NCL_CGAP_CLL1 Homo sapiens cDNA clone IMAGE:2107953 3' similar to contains Alu repetitive element; contains element A3R, repetitive element
7266	20001	33301	1.68	6.0E-07	AI333981.1	EST_HUMAN	ig06b05.x1 NCL_CGAP_CLL1 Homo sapiens cDNA clone IMAGE:2107953 3' similar to contains Alu repetitive element; contains element A3R, repetitive element
7571	20534	33982	15.74	6.0E-07	AW070885.1	EST_HUMAN	xc31a02.x1 NCL_CGAP_B18 Homo sapiens cDNA clone IMAGE:2568362 3' similar to gb:U15341 CYTOCHROME C OXIDASE POLYPEPTIDE VIA-LIVER (HUMAN);
8618	21586	35002	0.87	6.0E-07	Q9WUQ1	SWISSPROT	ADAM-TS1 PRECURSOR (A DISINTEGRIN AND METALLOPROTEINASE WITH THROMBOSPONDIN MOTIFS 1) (ADAMTS-1) (ADAM-TS1)
8835	21802		1.86	6.0E-07	P09583	SWISSPROT	S-ANTIGEN PROTEIN PRECURSOR
10732	23654	37147	5.39	6.0E-07	A1908587.1	EST_HUMAN	CM-BT178-220499-014 BT178 Homo sapiens cDNA
11845	24728	38314	3.52	6.0E-07	P11087	SWISSPROT	COLLAGEN ALPHA 1(I) CHAIN PRECURSOR
11906	24787		2.12	6.0E-07	AJ271795.1	NT	Homo sapiens Xq pseudocentromeric region; segment 1/2
12842	25780		4.14	6.0E-07	AW862537.1	EST_HUMAN	QV0-CT0383-210400-204-b12 CT0383 Homo sapiens cDNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4024	17062	29984	1.81	4.0E-07	AW009602.1	EST_HUMAN	we84h05.x1 NCL CGAP_C03 Homo sapiens cDNA clone IMAGE:2504697 3'
7384	20354		0.81	4.0E-07	AJ272265.1	NT	Homo sapiens SPP2 gene for secreted phosphoprotein 24 precursor, exons 1-8
7482	20448	33804	1.3	4.0E-07	Q8ZZV6	SWISSPROT	HISTONE DEACETYLASE 5 (HD5) (HISTONE DEACETYLASE MHDA1)
7482	20448	33805	1.3	4.0E-07	Q8ZZV6	SWISSPROT	HISTONE DEACETYLASE 5 (HD5) (HISTONE DEACETYLASE MHDA1)
8255	21224	34634	0.53	4.0E-07	AL163207.2	NT	Homo sapiens chromosome 21 segment HS21C007
9408	22371	35806	5.52	4.0E-07	AW419134.1	EST_HUMAN	xy49g11.x1 NCL CGAP_Lu34.1 Homo sapiens cDNA clone IMAGE:2856548 3'
10486	23408	36904	0.46	4.0E-07	BE901975.1	EST_HUMAN	601676748F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3959651 5'
10488	23408	36905	0.46	4.0E-07	BE901975.1	EST_HUMAN	601676748F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3959651 5'
10888	23610	37105	0.47	4.0E-07	AL163218.2	NT	Homo sapiens chromosome 21 segment HS21C018
11284	24234	37760	2.6	4.0E-07	AI765528.1	EST_HUMAN	wi81b08.x1 NCL CGAP_Kid12 Homo sapiens cDNA clone IMAGE:2399703 3'
11284	24234	37761	2.6	4.0E-07	AI765528.1	EST_HUMAN	wi81b08.x1 NCL CGAP_Kid12 Homo sapiens cDNA clone IMAGE:2399703 3'
11555	24495		2.72	4.0E-07	BE001828.1	EST_HUMAN	PM1-BN0083-030300-003-e12 BN0083 Homo sapiens cDNA
441	13515	28446	4.77	3.0E-07	U19719.1	NT	Human microfilament-associated glycoprotein (MIFAP2) gene, putative promoter region and alternatively spliced untranslated exons
585	13653	26567	3.11	3.0E-07	AJ271735.1	NT	Homo sapiens Xq pseudautosomal region; segment 1/2
1375	14409	27379	2.82	3.0E-07	M89149.1	NT	Human polymorphic microsatellite DNA
1630	14863		2.45	3.0E-07	M84857.1	NT	Human Igk subgroup 1 germline gene, exons 1 and 2, V-region 018 allele
2082	15080		1.01	3.0E-07	AA526763.1	EST_HUMAN	n156b08.s1 NCL CGAP_Ov2 Homo sapiens cDNA clone IMAGE:980825 similar to contains Alu repetitive element; contains L1.3 L1 repetitive element ;
2296	15308	28330	2.58	3.0E-07	M89149.1	NT	Human polymorphic microsatellite DNA
2477	15481	28505	6.03	3.0E-07	BE005077.1	EST_HUMAN	MRO-BN0115-020300-001-f11 BN0115 Homo sapiens cDNA
2477	15481	28506	6.03	3.0E-07	BE005077.1	EST_HUMAN	MRO-BN0115-020300-001-f11 BN0115 Homo sapiens cDNA
3047	16104	29018	0.8	3.0E-07	T84704.1	EST_HUMAN	yl50f12.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:11695 5'
3173	16228	29144	1.71	3.0E-07	P38739	SWISSPROT	HYPOTHETICAL 63.8 KD PROTEIN IN GUT1-RIM1 INTERGENIC REGION PRECURSOR
4706	17727		0.74	3.0E-07	P20740	SWISSPROT	OVOSTATIN PRECURSOR (OVOMACROGLOBULIN)
4758	17778	30673	8.86	3.0E-07	AV650201.1	EST_HUMAN	AV650201 GLC Homo sapiens cDNA clone GLCCDD01 3'
4798	17813	30706	0.81	3.0E-07	AI797238.1	EST_HUMAN	we86b12.x1 Soares NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2347967 3'
5103	18113	30985	2.02	3.0E-07	T57850.1	EST_HUMAN	yc14h09.s1 Stralagene lung (#937210) Homo sapiens cDNA clone IMAGE:80705 3' similar to similar to gb:U62982 ARACHIDONATE 12-LIPOXYGENASE (HUMAN)
5103	18113	30986	2.02	3.0E-07	T57850.1	EST_HUMAN	yc14h09.s1 Stralagene lung (#937210) Homo sapiens cDNA clone IMAGE:80705 3' similar to similar to gb:U62982 ARACHIDONATE 12-LIPOXYGENASE (HUMAN)
5749	18843	32026	9.02	3.0E-07	O88807	SWISSPROT	PROTEIN-ARGININE DEIMINASE TYPE IV (PEPTIDYLARGININE DEIMINASE IV) (PAD-R4)
6085	19165	32377	0.73	3.0E-07	O42280	SWISSPROT	WNT-14 PROTEIN PRECURSOR

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6861	19914		5.12	3.0E-07	AA816175.1	EST_HUMAN	cc04c10.s1 NCL_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1339890 3'
7752	20705	34074	3.26	3.0E-07	AW787188.1	EST_HUMAN	QV1-UM0036-200300-115-g02 UM0036 Homo sapiens cDNA
7825	20888		1.09	3.0E-07	AI691066.1	EST_HUMAN	hw28f11.x1 NCL_CGAP_Ov35 Homo sapiens cDNA clone IMAGE:2261037 3' similar to contains Alu repetitive element; contains element MSR1 MSR1 repetitive element ;
13083	26814		7.27	3.0E-07	AJ132382.1	NT	Rattus norvegicus mRNA for 45 kDa secretory protein, partial
31	13151	26051	4.19	2.0E-07	AF262988.1	NT	Homo sapiens TRF2-interacting telomeric RAP1 protein (RAP1) mRNA, complete cds
155	13258	26186	6.64	2.0E-07	L77569.1	NT	Homo sapiens DGeorge syndrome critical region, telomeric end
155	13258	26186	6.64	2.0E-07	L77569.1	NT	Homo sapiens DGeorge syndrome critical region, telomeric end
183	13283	26209	152.51	2.0E-07	U38849.1	NT	Fugu rubripes beta-cytoplasmic(vascular) actin gene, complete cds
749	13810	26751	1.29	2.0E-07	AF003530.1	NT	Homo sapiens homeobox protein CDX4 (CDX4) gene, complete cds and flanking repeat regions
749	13810	26752	1.29	2.0E-07	AF003530.1	NT	Homo sapiens homeobox protein CDX4 (CDX4) gene, complete cds and flanking repeat regions
760	13820		0.87	2.0E-07	P11369	SWISSPROT	RETROVIRUS-RELATED POL POLYPROTEIN [CONTAINS: REVERSE TRANSCRIPTASE ; ENDONUCLEASE]
942	13995	26947	3.12	2.0E-07	AA223260.1	EST_HUMAN	zr08b07.s1 Stragene NT2 neuronal precursor 937230 Homo sapiens cDNA clone IMAGE:650889 3' similar to gbL131860 GLYCOPHORIN A PRECURSOR (HUMAN); contains Alu repetitive element;
943	13996	26948	7.18	2.0E-07	T63042.1	EST_HUMAN	yc1f604.s1 Stragene lung (#937210) Homo sapiens cDNA clone IMAGE:80790 3' similar to contains L1 repetitive element ;
1167	14208	27162	1.16	2.0E-07	Q26768	SWISSPROT	I/6 AUTOANTIGEN
1604	14636	27613	2.35	2.0E-07	Q09701	SWISSPROT	HYPOTHETICAL 72.5 KD PROTEIN C2F7.10 IN CHROMOSOME I
3633	16676		0.86	2.0E-07	BF131397.1	EST_HUMAN	601818976.F1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:4044891 5'
3700	16743	29656	17.94	2.0E-07	AF126348.1	NT	Homo sapiens caveolin 1 (CAV1) gene, exon 3 and partial cds
4195	17228	30115	1.42	2.0E-07	AI873563.1	EST_HUMAN	wk20h04.x1 NCL_CGAP_Lym12 Homo sapiens cDNA clone IMAGE:2412918 3'
5417	18520	31397	1.71	2.0E-07	AW898066.1	EST_HUMAN	RC3-NN0066-260400-021-g11 NN0066 Homo sapiens cDNA
6702	25655	33037	0.9	2.0E-07	AW448968.1	EST_HUMAN	U1H-B13-ake-b-01-Q-U1.s1 NCL_CGAP_Sub5 Homo sapiens cDNA clone IMAGE:2734008 3'
6820	19874	33163	1.93	2.0E-07	AI208716.1	EST_HUMAN	qg56405.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1839177 3'
6832	19895	33178	0.81	2.0E-07	AA572953.1	EST_HUMAN	nrm33a06.s1 NCL_CGAP_Lip2 Homo sapiens cDNA clone IMAGE:1061938 similar to contains Alu repetitive element;
8813	21780		4.23	2.0E-07	AV728390.1	EST_HUMAN	AV728390 HTC Homo sapiens cDNA clone HTCAEG02 5'
9043	22093	35430	0.99	2.0E-07	AA035198.1	EST_HUMAN	zk27g09.s1 Soares_pregnant_uterus_NbHPU Homo sapiens cDNA clone IMAGE:471808 3'
10119	23045		1.8	2.0E-07	AL163303.2	NT	Homo sapiens chromosome 21 segment HS21C103
10630	23552	37052	6.11	2.0E-07	AW892507.1	EST_HUMAN	GM4-NN003-280300-124-e06 NN003 Homo sapiens cDNA
10855	23775	37272	0.92	2.0E-07	P00751	SWISSPROT	COMPLEMENT FACTOR B PRECURSOR (C3/C5 CONVERTASE) (PROPERDIN FACTOR B) (GLYCINE-RICH BETA GLYCOPROTEIN) (GBG) (PBF2)

Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10855	23775	37273	0.92	2.0E-07	P00751	SWISSPROT	COMPLEMENT FACTOR B PRECURSOR (C3/C5 CONVERTASE) (PROPERDIN FACTOR B)
12138	25503		2.86	2.0E-07	BE153717.1	EST_HUMAN	(GLYCINE-RICH BETA GLYCOPROTEIN) (GBG) (PBF2)
12224	25781		1.86	2.0E-07	AI732462.1	EST_HUMAN	PM0-HT0339-260100-006-H07 HT0339 Homo sapiens cDNA
1104	14148		1.46	1.0E-07	AL163282.2	NT	zr85n11.x6 Stralagene lung carcinoma 937218 Homo sapiens cDNA clone IMAGE:565029 3' similar to contains THR.b2 THR repetitive element ;
2838	14558	27529	2.95	1.0E-07	P09256	SWISSPROT	Homo sapiens chromosome 21 segment HS21C082
3757	14148		1.25	1.0E-07	AL163282.2	NT	GLYCOPROTEIN GPV
4321	17350	30234	3.01	1.0E-07	AV718662.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C082
4321	17350	30235	3.01	1.0E-07	AV718662.1	EST_HUMAN	AV718662 GLC Homo sapiens cDNA clone GLCFNF04 5'
6652	19709	32986	0.82	1.0E-07	U82671.2	NT	AV718662 GLC Homo sapiens cDNA clone GLCFNF04 5'
7050	20072	33378	4.44	1.0E-07	BE047871.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C081
7050	20072	33379	4.44	1.0E-07	BE047871.1	EST_HUMAN	z43406.y1 NCI_CGAP_Brm52 Homo sapiens cDNA clone IMAGE:2291339 5'
7735	20690	34054	9.42	1.0E-07	N55081.1	EST_HUMAN	z43406.y1 NCI_CGAP_Brm52 Homo sapiens cDNA clone IMAGE:2291339 5'
7910	20853	34240	0.89	1.0E-07	BF375909.1	EST_HUMAN	y43c07.s1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:246484 3'
7910	20853	34241	0.89	1.0E-07	BF375909.1	EST_HUMAN	PM4-TN0024-030800-002-b05 TN0024 Homo sapiens cDNA
7940	20882	34272	1.27	1.0E-07	AL163281.2	NT	PM4-TN0024-030800-002-b05 TN0024 Homo sapiens cDNA
8558	21526	34944	2.28	1.0E-07	P97435	SWISSPROT	Homo sapiens chromosome 21 segment HS21C081
8558	21526	34945	2.28	1.0E-07	P97435	SWISSPROT	ENTEROPEPTIDASE (ENTEROKINASE)
9306	22271	35702	2.83	1.0E-07	AA693576.1	EST_HUMAN	ENTEROPEPTIDASE (ENTEROKINASE)
9625	22569	36018	0.96	1.0E-07	P57110	SWISSPROT	251e10.s1 Soares fetal liver spleen 1NFLS_S1 Homo sapiens cDNA clone IMAGE:434346 3'
9975	22902	36366	0.53	1.0E-07	BE327843.1	EST_HUMAN	ADAM-TS 8 PRECURSOR (A DISINTEGRIN AND METALLOPROTEINASE WITH THROMBOSPONDIN
10296	23221	36705	2.5	1.0E-07	BF674524.1	EST_HUMAN	MOTIFS 8 (ADAMTS-8) (ADAM-TS8) (METH-2)
10304	23229	36712	1.26	1.0E-07	AA366311.1	EST_HUMAN	MOTIFS 8 (ADAMTS-8) (ADAM-TS8) (METH-2)
10831	23752		2.53	1.0E-07	AL163282.2	NT	h28h06.x1 NCI_CGAP_Maf15 Homo sapiens cDNA clone IMAGE:3171419 3' similar to contains MER18.13
12500	25756	31517	4.03	1.0E-07	BE048770.1	EST_HUMAN	h28h06.x1 NCI_CGAP_Maf15 Homo sapiens cDNA clone IMAGE:3171419 3' similar to contains MER18.13
12634	25320		1.59	1.0E-07	X64467.1	NT	h28h06.x1 NCI_CGAP_Maf15 Homo sapiens cDNA clone IMAGE:3171419 3' similar to contains MER18.13
12783	25423		1.89	1.0E-07	X51755.1	NT	h28h06.x1 NCI_CGAP_Maf15 Homo sapiens cDNA clone IMAGE:3171419 3' similar to contains MER18.13
7498	20463	33823	0.84	9.0E-08	AI539362.1	EST_HUMAN	h28h06.x1 NCI_CGAP_Maf15 Homo sapiens cDNA clone IMAGE:3171419 3' similar to contains MER18.13

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10247	23172	36651	2.18	9.0E-08	AV734819.1	EST_HUMAN	AV734819 cDNA Homo sapiens cDNA clone cdABFB06 5'
11515	24456	38006	1.46	9.0E-08	AI891052.1	EST_HUMAN	wn30a07.x1 NC1_OGAP_Gas4 Homo sapiens cDNA clone IMAGE:2446832 3' similar to contains OFR.12
11977	24854	38452	2.32	9.0E-08	AL163301.2	NT	OFR repetitive element;
12453	25212		3.51	9.0E-08	AJ251973.1	NT	Homo sapiens chromosome 21 segment HS21C101
609	15845		2.97	8.0E-08	AI911352.1	EST_HUMAN	Homo sapiens partial steirin-1 gene
1052	14098		0.77	8.0E-08	BE798469.1	EST_HUMAN	wd16b05.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2328273 3'
3555	16601		2.07	8.0E-08	BE798469.1	EST_HUMAN	601560133F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3943976 5'
							601560133F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3943976 5'
9091	22057	35482	3.38	8.0E-08	AI752367.1	EST_HUMAN	cn15c02.x1 Normal Human Trabecular Bone Cells Homo sapiens cDNA clone NHTBC_cn15c02 random
9091	22057	35483	3.38	8.0E-08	AI752367.1	EST_HUMAN	cn15c02.x1 Normal Human Trabecular Bone Cells Homo sapiens cDNA clone NHTBC_cn15c02 random
9885	22912	36377	2.8	8.0E-08	AW970693.1	EST_HUMAN	EST382776 IMAGE resequences, MAGK Homo sapiens cDNA
10928	23848	37363	0.46	8.0E-08	AF111167.2	NT	Homo sapiens jun dimerization protein gene, partial cds; cfos gene, complete cds; and unknown gene
11575	24513		2.53	8.0E-08	AF253417.1	NT	Homo sapiens mitochondrial epoxide hydrolase (EPHX1) gene, complete cds
81	13197	26121	4.07	7.0E-08	Q02357	SWISSPROT	ANKYRIN 1 (ERYTHROCYTE ANKYRIN)
1363	14397	27368	17.17	7.0E-08	X04809.1	NT	Rat mRNA for ribosomal protein L31
3589	16634	29553	0.7	7.0E-08	P15305	SWISSPROT	DYNEIN HEAVY CHAIN (DYHC)
3589	16634	29554	0.7	7.0E-08	P15305	SWISSPROT	DYNEIN HEAVY CHAIN (DYHC)
3949	16989	29904	0.9	7.0E-08	P01606	SWISSPROT	IG KAPPA CHAIN V-J REGION OU
3949	16989	29905	0.9	7.0E-08	P01606	SWISSPROT	IG KAPPA CHAIN V-J REGION OU
11165	24123		2.33	7.0E-08	AI535743.1	EST_HUMAN	cong3.P11.A5 cona1m Homo sapiens cDNA 3'
11982	24859	38454	4.32	7.0E-08	U24070.1	NT	Rattus norvegicus Munc13-1 mRNA, complete cds
12899	16634	29553	1.55	7.0E-08	P15305	SWISSPROT	DYNEIN HEAVY CHAIN (DYHC)
12899	16634	29554	1.55	7.0E-08	P15305	SWISSPROT	DYNEIN HEAVY CHAIN (DYHC)
12978	25541		1.9	7.0E-08	AJ131016.1	NT	Homo sapiens SCL gene locus
818	13876	26824	4.23	6.0E-08	AL163248.2	NT	Homo sapiens chromosome 21 segment HS21C048
818	13876	26825	4.23	6.0E-08	AL163248.2	NT	Homo sapiens chromosome 21 segment HS21C048
2371	15379	28403	2.72	6.0E-08	BE144398.1	EST_HUMAN	MR0-HT0166-197199-004-g09 HT0166 Homo sapiens cDNA
4276	17305	30184	1.28	6.0E-08	AL163248.2	NT	Homo sapiens chromosome 21 segment HS21C048
							Homo sapiens chromosome X region from filamin (FLN) gene to glucose-6-phosphate dehydrogenase
8162	21100	34499	0.49	6.0E-08	L44140.1	NT	(G8PD) gene, complete cds's
8283	21252		0.74	6.0E-08	P08547	SWISSPROT	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9683	22636		0.54	6.0E-08	AA827075.1	EST_HUMAN	q556c05.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1353368 3' similar to contains MER12.b3 MER12 repetitive element ;
11744	24629	38208	1.91	6.0E-08	P11369	SWISSPROT	RETROVIRUS-RELATED POLYPROTEIN [CONTAINS: REVERSE TRANSCRIPTASE ;
86	13201	26125	3.22	5.0E-08	AL163303.2	NT	ENDONUCLEASE]
2245	15259	28286	1.95	5.0E-08	AA493851.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C103 element;
12185	25032		10.16	5.0E-08	P06681	SWISSPROT	COMPLEMENT C2 PRECURSOR (C3/C5 CONVERTASE)
12382	25162	31814	1.63	5.0E-08	AW851878.1	EST_HUMAN	QV0-CT0225-131099-034-a12 CT0225 Homo sapiens cDNA
1775	14804	27789	1.07	4.0E-08	P25723	SWISSPROT	DORSAL-VENTRAL PATTERNING TOLLOID PROTEIN PRECURSOR
1776	14804	27790	1.07	4.0E-08	P25723	SWISSPROT	DORSAL-VENTRAL PATTERNING TOLLOID PROTEIN PRECURSOR
3077	16134		0.95	4.0E-08	AI078417.1	EST_HUMAN	oz05602.x1 Soares_fetal_liver_spleen_infls_S1 Homo sapiens cDNA clone IMAGE:1674458 3' similar to contains Alu repetitive element;
3934	16974	28888	0.76	4.0E-08	U82668.1	NT	Homo sapiens shox gene, alternatively spliced products, complete cds
6545	19606	32868	0.91	4.0E-08	P52624	SWISSPROT	URIDINE PHOSPHORYLASE (UDRPASE)
9150	22116	35542	0.6	4.0E-08	O15393	SWISSPROT	TRANSMEMBRANE PROTEASE, SERINE 2
9494	22458	35898	1.32	4.0E-08	L42571.1	NT	Citellus griseus ribosomal transcription factor (UBF2) mRNA, complete cds
10003	22930		0.82	4.0E-08	P08547	SWISSPROT	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG
10693	23615		0.65	4.0E-08	AI016342.1	EST_HUMAN	q78412.s1 Soares_total_fetus_Nb2HF8_9w Homo sapiens cDNA clone IMAGE:1622903 3' an22d10.x1 Gessler Wilms Tumor Homo sapiens cDNA clone IMAGE:1699411 3' similar to contains Alu repetitive element; contains element MER22 repetitive element ;
10752	23674	37171	3.67	4.0E-08	AI050027.1	EST_HUMAN	repetitive element; contains element MER22 repetitive element ;
11411	24355	37889	1.51	4.0E-08	AA393627.1	EST_HUMAN	z176b08.r1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:728247 5' similar to TR:G505579
11411	24355	37890	1.51	4.0E-08	AA393627.1	EST_HUMAN	G505579 NA/CA,K-EXCHANGER ;
11426	24370	37907	3.11	4.0E-08	BF692493.1	EST_HUMAN	G505579 NA/CA,K-EXCHANGER ;
11426	24370	37908	3.11	4.0E-08	BF692493.1	EST_HUMAN	602248024FT NIH_MGC_62 Homo sapiens cDNA clone IMAGE:4333300 5'
12190	25907		4.96	4.0E-08	W76159.1	EST_HUMAN	602248024FT NIH_MGC_62 Homo sapiens cDNA clone IMAGE:4333300 5'
12830	25448		1.84	4.0E-08	AI343353.1	EST_HUMAN	z165g03.r1 Soares_fetal_heart_NbHH19W Homo sapiens cDNA clone IMAGE:345556 5' similar to contains L1.1 L1 repetitive element ;
3438	16485	29404	0.94	3.0E-08	MB3242.1	NT	L1.1 L1 repetitive element ;
5692	18787	31956	3.06	3.0E-08	BE018948.1	EST_HUMAN	ts55a11.x1 NCI_CGAP_Co16 Homo sapiens cDNA clone IMAGE:2062076 3' similar to contains MER18.b3 MER18 MER18 repetitive element ;
							Macaca fascicularis apolipoprotein A-1 gene, complete cds
							bb79a10.y1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3048570 5' similar to TR:Q9Z158 Q9Z158 SYNTAXIN 17 ;

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Database Source	Top Hit Descriptor
7168	18399	31245	4.23	3.0E-08	AL192737.1	q376f1.1, y6 NCL_CGAP_P128 Homo sapiens cDNA clone IMAGE:1944045 5'
7787	20740	34113	1.41	3.0E-08	AL163246.2	Homo sapiens chromosome 21 segment HS21C046
8025	20962		3.85	3.0E-08	AI436352.1	th93h09.x1 Soares NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:2126273 3' similar to TR:Q13537 Q13537 MER37 TRANSPORTABLE ELEMENT, COMPLETE CONSENSUS SEQUENCE. ;
10258	23183		0.57	3.0E-08	AF065066.1	Homo sapiens MHC class 1 region
12157	25013		2.76	3.0E-08	R18420.1	yg0204.r1 Soares Infant brain 1N1B Homo sapiens cDNA clone IMAGE:30948 5' similar to contains Alu repetitive element
207	13308		10.54	2.0E-08	AW302996.1	xs8706.x1 NCL_CGAP_L28 Homo sapiens cDNA clone IMAGE:2787139 3'
230	13330		8.83	2.0E-08	AA425598.1	zw48f07.1 Soares_fetus_Nb2HF8_9w Homo sapiens cDNA clone IMAGE:773317 5' similar to contains Alu repetitive element; contains element MER15 repetitive element ;
497	13569	26492	1.3	2.0E-08	AF198349.1	Gallus gallus Dach2 protein (Dach2) mRNA, complete cds
681	13727	26651	9.73	2.0E-08	AW886438.1	MR0-OT0080-240200-001-g08 OT0080 Homo sapiens cDNA
681	13727	26652	9.73	2.0E-08	AW886438.1	MR0-OT0080-240200-001-g08 OT0080 Homo sapiens cDNA
992	14044		17	2.0E-08	BE280477.1	601155321F1 NIH_MGC 21 Homo sapiens cDNA clone IMAGE:3138893 5'
1346	14381	27350	1.93	2.0E-08	AL163247.2	Homo sapiens chromosome 21 segment HS21C047
1755	14784		1.87	2.0E-08	BE734871.1	601570463F1 NIH_MGC 21 Homo sapiens cDNA clone IMAGE:3845169 5'
1872	14897		3.57	2.0E-08	AW270271.1	xs43f11.x1 NCL_CGAP_HN11 Homo sapiens cDNA clone IMAGE:2743149 3'
2550	15552		1.7	2.0E-08	K00218.1	Sheep His-rRNA-GUG
3221	16276	29200	8.15	2.0E-08	O42280	WNT-14 PROTEIN PRECURSOR
3221	16276	29201	8.15	2.0E-08	O42280	WNT-14 PROTEIN PRECURSOR
3873	16912		1.62	2.0E-08	AW813620.1	RC3-ST0197-161099-012-603 ST0197 Homo sapiens cDNA
4104	17138	30033	0.68	2.0E-08	U82968.1	Homo sapiens shox gene, alternatively spliced products, complete cds
4434	17461		1.2	2.0E-08	AA459040.1	aa26c07.r1 NCL_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:814380 5' similar to contains L1.12 L1 repetitive element ;
4994	18009		2.97	2.0E-08	AW572881.1	he17h08.x2 NCL_CGAP_CML1 Homo sapiens cDNA clone IMAGE:2919327 3' similar to contains Alu repetitive element ;
5719	18813	31992	1.26	2.0E-08	AA813204.1	ab00h11.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1377189 3'
5932	19018	32213	0.99	2.0E-08	AW089924.1	xs82c04.x1 NCL_CGAP_Ov23 Homo sapiens cDNA clone IMAGE:2595462 3' similar to contains MER18.b3
8337	21306	34721	1.89	2.0E-08	P10272	MER18 MER18 repetitive element ;
8447	21416	34829	1.47	2.0E-08	AA490121.1	POL POLYPOLYMERIN [CONTAINS: PROTEASE; REVERSE TRANSCRIPTASE; ENDONUCLEASE]
9440	22404		0.77	2.0E-08	AU139978.1	ab02g05.g1 StrataGene fetal refina g37202 Homo sapiens cDNA clone IMAGE:839674 3'
						AU139978 PLACE1 Homo sapiens cDNA clone PLACE1011719 5'

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Table 4

Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10886	23806	37310	0.8	2.0E-08	N78097.1	EST_HUMAN	yw7202.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:248283 5' similar to contains LTR1.b3 LTR1 repetitive element;
10886	23806	37311	0.8	2.0E-08	N78097.1	EST_HUMAN	yw7202.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:248283 5' similar to contains LTR1.b3 LTR1 repetitive element;
12472	25221		1.88	2.0E-08	AL163284.2	NT	Homo sapiens chromosome 21 segment HS21C084
12982	25953		1.4	2.0E-08	11431676	NT	Homo sapiens hypodermal protein FLJ11342 (FLJ11342), mRNA
1510	15870	27513	1.42	1.0E-08	P31792	SWISSPROT	POL POLYPROTEIN [CONTAINS: REVERSE TRANSCRIPTASE; ENDONUCLEASE]
1790	14819	27804	2.12	1.0E-08	AF125348.1	NT	Homo sapiens caveolin 1 (CAV1) gene, exon 3 and partial cds
2067	15084		2.49	1.0E-08	BE141959.1	EST_HUMAN	PM2-HT0130-150999-001-f12 HT0130 Homo sapiens cDNA
3206	18261	29181	1.19	1.0E-08	BE246844.1	EST_HUMAN	TCBAP1D5232 Pediatric pre-B cell acute lymphoblastic leukemia Baylor-HGSC project=TCBA Homo sapiens cDNA clone TCBAP-5232
3206	18261	29182	1.19	1.0E-08	BE246844.1	EST_HUMAN	TCBAP1D5232 Pediatric pre-B cell acute lymphoblastic leukemia Baylor-HGSC project=TCBA Homo sapiens cDNA clone TCBAP-5232
5680	18775	31947	4.5	1.0E-08	AJ010770.1	NT	Homo sapiens tyrosin gene, exons 1-50
8046	20983	34380	0.98	1.0E-08	P19474	SWISSPROT	52 KD RO PROTEIN (SJOGREN SYNDROME TYPE A ANTIGEN (SS-A)) (RO(SS-A))
8369	21338	34749	0.47	1.0E-08	AL163302.2	NT	Homo sapiens chromosome 21 segment HS21C102
8466	21435	34852	0.56	1.0E-08	AF224869.1	NT	Homo sapiens mannosidase, beta A, lysosomal (MANBA) gene, and ubiquitin-conjugating enzyme E2D 3 (UBE2D3) genes, complete cds
8466	21435	34853	0.56	1.0E-08	AF224869.1	NT	Homo sapiens mannosidase, beta A, lysosomal (MANBA) gene, and ubiquitin-conjugating enzyme E2D 3 (UBE2D3) genes, complete cds
8892	21858	35280	1.89	1.0E-08	AJ015304.1	EST_HUMAN	cd35a05.s1 Soares testis_NHT Homo sapiens cDNA clone IMAGE:1618736 3'
9559	22521		0.46	1.0E-08	P09593	SWISSPROT	S-ANTIGEN PROTEIN PRECURSOR
9560	22522	35970	0.68	1.0E-08	BE072572.1	EST_HUMAN	PM2-BT0546-210100-004-402 BT0546 Homo sapiens cDNA
10325	23249	36728	0.81	1.0E-08	P79110	SWISSPROT	TRICARBOXYLATE TRANSPORT PROTEIN PRECURSOR (CITRATE TRANSPORT PROTEIN) (CTP)
10921	23841	37357	0.67	1.0E-08	P98063	SWISSPROT	TRICARBOXYLATE CARRIER PROTEIN
11644	24581	38149	3.4	1.0E-08	AF044083.1	NT	BONE MORPHOGENETIC PROTEIN 1 PRECURSOR (BMP-1)
12129	24998	38602	1.5	1.0E-08	P29315	SWISSPROT	Homo sapiens major histocompatibility locus class III region
12129	24998	38603	1.5	1.0E-08	P29315	SWISSPROT	RIBONUCLEASE INHIBITOR
12569	25281		3.12	1.0E-08	X51755.1	NT	RIBONUCLEASE INHIBITOR
12940	25520		1.68	1.0E-08	X51755.1	NT	Human lambda-immunoglobulin constant region complex (germline)
4271	17300	30179	4.15	9.0E-09	AL163279.2	NT	Human lambda-immunoglobulin constant region complex (germline)
4271	17300	30180	4.15	9.0E-09	AL163279.2	NT	Homo sapiens chromosome 21 segment HS21C079
10422	23344		0.53	9.0E-09	T97950.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C079
							y558a12.s1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:121918 3'

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Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6628	19686		1.59	8.0E-09	AI270615.1	EST_HUMAN	qu86c11.x1 NCL_CGAP_Gas4 Homo sapiens cDNA clone IMAGE:1978964 3' similar to contains L1.13 L1 repetitive element ;
7479	20445	33801	7.91	8.0E-09	AI183500.1	EST_HUMAN	qq42s07.x1 Soares_fetal_heart_NbHH19W Homo sapiens cDNA clone IMAGE:1732164 3' similar to contains MSR1.1t MSR1 repetitive element ;
8333	21302	34719	3.04	8.0E-09	AW900159.1	EST_HUMAN	GM0-N11004-100300-273-e08 NN1004 Homo sapiens cDNA
9340	22305		2.64	8.0E-09	AA938892.1	EST_HUMAN	op74d08.s1 Soares_NFL_T_GBC S1 Homo sapiens cDNA clone IMAGE:1582575 3'
3621	16664		1.91	7.0E-09	D86942.1	NT	Homo sapiens DNA for 3-ketacyl-CoA thiolase beta-subunit of mitochondrial trifunctional protein, exon 2, 3
4034	17072		1.22	7.0E-09	U50871.1	NT	Human familial Alzheimer's disease (STM2) gene, complete cds
8234	21203		0.58	7.0E-09	BF108755.1	EST_HUMAN	7145e10.x1 Soares_NSF_F8_gw_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:3524443 3' similar to contains MER29.b2 MER29 repetitive element ;
8382	21351		0.91	7.0E-09	AA256200.1	EST_HUMAN	zr80c05.r1 Soares_NhHMPu_S1 Homo sapiens cDNA clone IMAGE:681892 5' similar to contains L1.12 L1 repetitive element ;
9615	22559	36008	3.06	7.0E-09	L09709.1	NT	Human lysosomal membrane glycoprotein-2 (LAMP2) gene, 5' end and flanking region
10543	23465	36960	1.17	7.0E-09	BE254850.1	EST_HUMAN	60111173F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3351834 5'
10711	23633		0.59	7.0E-09	AA058628.1	EST_HUMAN	zf58e07.s1 Soares retina N2b4HR Homo sapiens cDNA clone IMAGE:381156 3' similar to contains L1.12 L1 repetitive element ;
11032	23966		3.65	7.0E-09	T97950.1	EST_HUMAN	ye58e12.s1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:121918 3'
2162	15178		0.98	6.0E-09	AL040439.1	EST_HUMAN	DKFZp434C0514.1 434 (synonym: htes3) Homo sapiens cDNA clone DKFZp434C0514 5'
4059	17095	29960	0.96	6.0E-09	AA557940.1	EST_HUMAN	n117a11.s1 NCL_CGAP_HSC1 Homo sapiens cDNA clone IMAGE:1040924 similar to contains L1.12 L1 repetitive element ;
5017	18031	30917	5.44	6.0E-09	BE169421.1	EST_HUMAN	PM1-HT0527-160200-001-h05 HT0527 Homo sapiens cDNA
5464	18566	31467	9.55	6.0E-09	AW195784.1	EST_HUMAN	xn85h08.x1 Soares_NFL_T_GBC S1 Homo sapiens cDNA clone IMAGE:2701311 3'
8922	21888	35315	0.88	6.0E-09	BE161653.1	EST_HUMAN	MR3-HT0446-260300-201-h12 HT0446 Homo sapiens cDNA
9531	22494	35942	2.12	6.0E-09	4503710	NT	Homo sapiens fibroblast growth factor receptor 3 (achondroplasia, thanatophoric dwarfism) (FGFR3) mRNA
10639	23561		4.42	6.0E-09	AF200923.2	NT	Homo sapiens testis-specific kinase substrate (TSKS) gene, complete cds
1413	14446	27418	4.43	5.0E-09	BE149284.1	EST_HUMAN	RC2-HT0252-120200-014-h10 HT0252 Homo sapiens cDNA
1870	14855	27894	1.02	5.0E-09	AL163284.2	NT	Homo sapiens chromosome 21 segment HS21C084
6550	19811	32872	2.31	5.0E-09	AA359454.1	EST_HUMAN	EST68746 Fetal lung II Homo sapiens cDNA 5' end
7025	18357	31277	0.59	5.0E-09	U66059.1	NT	Human gemline T-cell receptor beta chain Dopamine-beta-hydroxylase-like, TRY1, TRY2, TRY3, TCRBV27S1P, TCRBV22S1A2N1T, TCRBV9S1A1T, TCRBV7S1A1N2T, TCRBV5S1A1T, TCRBV13S3, TCRBV6S7P, TCRBV7S3A2T, TCRBV13S2A1T, TCRBV9S2A2P1, TCRBV7S2A1N4T, TCRBV13S9/13S>

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Table 4
Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8932	21898	35326	0.5	5.0E-09	P37071	SWISSPROT	OLFACTORY RECEPTOR-LIKE PROTEIN COR5
10455	23377	36870	2.53	5.0E-09	AW799667.1	EST_HUMAN	PM2-UM0053-240300-005-c09 UM0053 Homo sapiens cDNA
522	13593		1.81	4.0E-09	AL163282.2	NT	Homo sapiens chromosome 21 segment HS21C082
966	14018		2.79	4.0E-09	AL163285.2	NT	Homo sapiens chromosome 21 segment HS21C085
1465	14498	27472	2.79	4.0E-09	9558718	NT	Homo sapiens hypothalamic protein (AF038169), mRNA
2038	15057	28075	1.63	4.0E-09	AF175325.1	NT	Homo sapiens eukaryotic initiation factor 4A1 (EIF4A1) gene, partial cds
2038	15057	28076	1.63	4.0E-09	AF175325.1	NT	Homo sapiens eukaryotic initiation factor 4A1 (EIF4A1) gene, partial cds
2436	15443	28461	2.87	4.0E-09	AA350678.1	EST_HUMAN	EST58385 Infant brain Homo sapiens cDNA 5' end similar to similar to heat shock protein, 90 kDa
8179	21149	34556	0.66	4.0E-09	AA495747.1	EST_HUMAN	z04c06.t1 Soares_NhHMPu_S1 Homo sapiens cDNA clone IMAGE:768298 5'
8867	21834	35255	0.66	4.0E-09	T64942.1	EST_HUMAN	yc11a07.s1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:36804 3'
							hu09e09.x1 NCL_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3166120 3' similar to contains MER18.13
							MER18 repetitive element;
2359	15367	28389	4.28	3.0E-09	BE222239.1	EST_HUMAN	hu09e09.x1 NCL_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3166120 3' similar to contains MER18.13
2560	15561	28579	1.39	3.0E-09	BE222239.1	EST_HUMAN	MER18 repetitive element;
2659	15656	28674	1.03	3.0E-09	P23249	SWISSPROT	PROTEIN MOV-10
3340	16391	29312	1.15	3.0E-09	BE222239.1	EST_HUMAN	hu09e09.x1 NCL_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3166120 3' similar to contains MER18.13
3388	16437		0.79	3.0E-09	AA442272.1	EST_HUMAN	MER18 repetitive element;
4124	17157		0.69	3.0E-09	X16674.1	NT	z064e04.t1 Soares testis_NHT Homo sapiens cDNA clone IMAGE:757422 5'
4457	17483	30371	3.77	3.0E-09	AF175325.1	NT	H. sapiens PADPRP-1 gene for NAD(+) ADP-ribosyltransferase
4540	17563	30450	3.44	3.0E-09	Q9Y3R5	SWISSPROT	Homo sapiens eukaryotic initiation factor 4A1 (EIF4A1) gene, partial cds
							258.1 KDA PROTEIN C21ORF5 (KIAA0933)
5225	18233		0.99	3.0E-09	D86942.1	NT	Homo sapiens DNA for 3-ketoacyl-CoA thiolase beta-subunit of mitochondrial trifunctional protein, exon 2, 3
							hu09e02.x1 NCL_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:3194090 3' similar to TR:O55091
8232	21201	34607	1.08	3.0E-09	BE465780.1	EST_HUMAN	O55091 IMPACT PROTEIN.;
10609	23331	37026	1.84	3.0E-09	AL163247.2	NT	Homo sapiens chromosome 21 segment HS21C047
11361	24310	37836	3.06	3.0E-09	BF109943.1	EST_HUMAN	7172c08.x1 Soares_NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:3527030 3'
11361	24310	37837	3.06	3.0E-09	BF109943.1	EST_HUMAN	7172c08.x1 Soares_NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:3527030 3'
813	13871		10.64	2.0E-09	X16674.1	NT	H. sapiens PADPRP-1 gene for NAD(+) ADP-ribosyltransferase
1283	14298	27261	5.84	2.0E-09	AL163284.2	NT	Homo sapiens chromosome 21 segment HS21C084
1667	14699		9.53	2.0E-09	AL118573.1	EST_HUMAN	DKFZp761B1710.1 761 (synonym: hamy2) Homo sapiens cDNA clone DKFZp761B1710 5'
2334	15345	28363	2.58	2.0E-09	Q9Y3R5	SWISSPROT	258.1 KDA PROTEIN C21ORF5 (KIAA0933)
3958	16998	28913	3.67	2.0E-09	O60241	SWISSPROT	BRAIN-SPECIFIC ANGIOGENESIS INHIBITOR 2 PRECURSOR
4039	17077	29977	1.65	2.0E-09	AL263479.1	EST_HUMAN	q107d09.x1 Soares_NHMPu_S1 Homo sapiens cDNA clone IMAGE:1855793 3'

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Single Exon Probes Expressed In Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5198	18207	31081	0.66	2.0E-09	M23161.1	NT	Human transposon-like element mRNA
5808	18998	32081	0.69	2.0E-09	AI004062.1	EST_HUMAN	047009.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1618897 3'
6273	18346		0.65	2.0E-09	AL163248.2	NT	Homo sapiens chromosome 21 segment HS21C049
6947	20171		0.8	2.0E-09	AA357407.1	EST_HUMAN	EST66142 Kidney IX Homo sapiens cDNA 5' end similar to EST containing L1 repeat
7684	20642	34006	7.6	2.0E-09	AA461430.1	EST_HUMAN	263106.r1 Soares_total_testis_Nb2HF8_9w Homo sapiens cDNA clone IMAGE:796187 5' similar to contains Alu repetitive element;
7766	20719	34082	0.63	2.0E-09	W28834.1	EST_HUMAN	52d11 Human retina cDNA randomly primed sublibrary Homo sapiens cDNA
8126	21063	34461	0.82	2.0E-09	AW862126.1	EST_HUMAN	MR1-CT0352-240200-105-506 GT0352 Homo sapiens cDNA
9062	22028	35452	2.25	2.0E-09	AJ271735.1	NT	Homo sapiens Xq pseudautosomal region, segment 1/2
12705	13871		22.38	2.0E-09	X16674.1	NT	H. sapiens PADPRP-1 gene for NAD(+) ADP-ribosyltransferase
12772	25975		1.67	2.0E-09	AA226070.1	EST_HUMAN	nc11602.r1 NCI_CGAP_P1 Homo sapiens cDNA clone IMAGE:1007810 similar to contains Alu repetitive element;
12778	25828		1.47	2.0E-09	AW301637.1	EST_HUMAN	xs98a02.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2768234 3'
12913	25492		1.98	2.0E-09	U82668.1	NT	Homo sapiens shox gene, alternatively spliced products, complete cds
1111	14155	27105	1.1	1.0E-09	5031624	NT	Homo sapiens CCAAT-box-binding transcription factor (CBF2) mRNA
1111	14155	27106	1.1	1.0E-09	5031624	NT	Homo sapiens CCAAT-box-binding transcription factor (CBF2) mRNA
1638	14670		0.91	1.0E-09	AJ228041.1	NT	Homo sapiens 959 kb contig between AML1 and CBR1 on chromosome 21q22; segment 1/3
2510	15513		1.16	1.0E-09	AI356086.1	EST_HUMAN	qy4e11.x1 NCI_CGAP_Bim25 Homo sapiens cDNA clone IMAGE:2016812 3' similar to contains MER12.12 MER12 repetitive element;
2900	15959	28878	1.83	1.0E-09	U80017.1	NT	Homo sapiens basic transcription factor 2 p44 (btf2p44) gene, partial cds, neuronal apoptosis inhibitory protein (nalp) and survival motor neuron protein (smn) genes, complete cds
2937	15995	28915	4.07	1.0E-09	M28699.1	NT	Homo sapiens nucleolar phosphoprotein B23 (NPM1) mRNA, complete cds
2937	15995	28916	4.07	1.0E-09	M28699.1	NT	Homo sapiens nucleolar phosphoprotein B23 (NPM1) mRNA, complete cds
3051	16108	28022	0.89	1.0E-09	BE535440.1	EST_HUMAN	607058602.F1 NIH_JMGC_10 Homo sapiens cDNA clone IMAGE:3445177 5'
4838	17853		5.63	1.0E-09	AA719297.1	EST_HUMAN	2h35b03.s1 Soares_pineal_gland_N8HPG Homo sapiens cDNA clone IMAGE:3445177 5'
5162	18171	31050	0.84	1.0E-09	T60216.1	EST_HUMAN	Alu repetitive element; contains element MER28 repetitive element;
5581	18677	31640	0.82	1.0E-09	AL163283.2	NT	yc22c09.r1 Stratagene lung (#837210) Homo sapiens cDNA clone IMAGE:81424 5' similar to contains Alu repetitive element; contains MER28 repetitive element;
5930	19016	32211	1.35	1.0E-09	U07000.1	NT	Homo sapiens chromosome 21 segment HS21C083
6267	19340	32572	3.11	1.0E-09	P26694	SWISSPROT	Human breakpoint cluster region (BCR) gene, complete cds
8113	21050	34449	0.63	1.0E-09	AV728645.1	EST_HUMAN	CIRCUMSPOROZOTE PROTEIN PRECURSOR (CS)
8733	21701	35127	0.87	1.0E-09	AI698474.1	EST_HUMAN	AV728645 HTC Homo sapiens cDNA clone HTCBIG07 5'
							wd39b05.x1 Soares_NFL_T_OBC_S1 Homo sapiens cDNA clone IMAGE:2330481 3' similar to contains MER25.11 MER25 repetitive element;

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Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10877	23599		2.87	1.0E-09	AL163283.2	NT	Homo sapiens chromosome 21 segment HS21C083
12081	24963		1.53	1.0E-09	AL163283.2	NT	Homo sapiens chromosome 21 segment HS21C083
12618	25916	31425	2.01	1.0E-08	11418127	NT	Homo sapiens GTP binding protein 1 (GTPBP1), mRNA
12781	25416		1.6	1.0E-09	T93176.1	EST_HUMAN	ye24e05.11 Stralagene lung (#837210) Homo sapiens cDNA clone IMAGE:118688 5'
1312	14348	27314	2.49	9.0E-10	AW887740.1	EST_HUMAN	MRO-SN0040-050500-002-c07 SN0040 Homo sapiens cDNA
2845	15905	28830	6.64	9.0E-10	AI870071.1	EST_HUMAN	we78h03.x1 Soares Dieckgraefe colon NHCD Homo sapiens cDNA clone IMAGE:2347253 3' similar to SW:RL29 HUMAN P47914.60S RIBOSOMAL PROTEIN L29 contains element PTR5 repetitive element ; U46b09.x1 Soares NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:2144537 3' similar to TR:O00372 O00372 PUTATIVE P160 ; Homo sapiens MCM4 (MCM4) and DNA-PKcs (PRKDC) genes, partial cds
7008	20134	33449	4.22	9.0E-10	AI452982.1	EST_HUMAN	QV1-BT0631-150200-071-01 BT0631 Homo sapiens cDNA
148	13251	28180	12.13	8.0E-10	U63630.2	NT	EST89564 Small intestine I Homo sapiens cDNA 5' end
3363	16404	29325	0.76	8.0E-10	BE080748.1	EST_HUMAN	EST89564 Small intestine I Homo sapiens cDNA 5' end
4229	17258	30142	3.69	8.0E-10	AA376832.1	EST_HUMAN	Homo sapiens lens major intrinsic protein (MIP) gene, complete cds
10324	23248		2.46	8.0E-10	U36308.2	NT	Homo sapiens TPA inducible protein (LOC51586), mRNA
702	13784	26598	32.88	7.0E-10	7706225	NT	Homo sapiens TPA inducible protein (LOC51586), mRNA
702	13784	26599	32.88	7.0E-10	7706225	NT	LYSP100 PROTEIN (LYMPHOID-RESTRICTED HOMOLOG OF SP100)
1626	14659	27636	2.48	7.0E-10	Q13342	SWISSPROT	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG
2566	15687		21.84	7.0E-10	P08547	SWISSPROT	H.sapiens DHFR gene, exon 3
3104	16161	29072	2.86	7.0E-10	X00856.1	NT	EST51247 Gall bladder II Homo sapiens cDNA 5' end
6309	19380	32619	3.72	7.0E-10	AA345220.1	EST_HUMAN	IL3-HT0619-110700-209-D12 HT0619 Homo sapiens cDNA
7647	20607	33973	1.2	7.0E-10	BF352883.1	EST_HUMAN	DNA-DIRECTED RNA POLYMERASE II LARGEST SUBUNIT
7918	20861		1.46	7.0E-10	P35084	SWISSPROT	Homo sapiens presentin-1 gene, exons 1 and 2
8308	21277	34688	1.29	7.0E-10	AF029701.2	NT	Homo sapiens presentin-1 gene, exons 1 and 2
8308	21277	34689	1.29	7.0E-10	AF029701.2	NT	Homo sapiens MADSMIF2-family transcription factor (MEF2C) mRNA, complete cds
10673	23595	37092	0.68	7.0E-10	L08895.1	NT	Homo sapiens ASCL3 gene, C11orf14 gene, C11orf15 gene and C11orf17 gene
914	13969	26922	2.67	6.0E-10	AI400877.1	NT	rc02d07.x1 NCL CGAP_P128 Homo sapiens cDNA clone IMAGE:2085021 3'
2686	15882	28700	1.37	6.0E-10	AI424405.1	EST_HUMAN	RC3-CT0254-031069-012-g12 CT0254 Homo sapiens cDNA
4768	17788		2.72	6.0E-10	AW653719.1	EST_HUMAN	E-SELECTIN PRECURSOR (ENDOTHELIAL LEUKOCYTE ADHESION MOLECULE 1) (ELAM-1)
9135	22101	35527	0.89	6.0E-10	P33730	SWISSPROT	(LEUKOCYTE-ENDOTHELIAL CELL ADHESION MOLECULE 2) (LECAM2) (CD62E)
9135	22101	35528	0.89	6.0E-10	P33730	SWISSPROT	E-SELECTIN PRECURSOR (ENDOTHELIAL LEUKOCYTE ADHESION MOLECULE 1) (ELAM-1)
9992	22819	36386	0.43	6.0E-10	P68073	SWISSPROT	(LEUKOCYTE-ENDOTHELIAL CELL ADHESION MOLECULE 2) (LECAM2) (CD62E)

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Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
12221	25058		1.84	6.0E-10	AW971923.1	EST_HUMAN	EST384012 IMAGE: ressequences, MAGI, Homo sapiens cDNA
761	13821		5.01	5.0E-10	AL046804.1	EST_HUMAN	DKFZ434N219.1 434 (synonym: htes3) Homo sapiens cDNA clone DKFZ434N219 5'
3489	16335	29490	1.53	5.0E-10	Q07033	SWISSPROT	HYPOTHETICAL GENE 48 PROTEIN
5026	18040	30923	1.1	5.0E-10	AF181897.1	NT	Homo sapiens WRN (WRN) gene, complete cds
7544	20507		1.74	5.0E-10	BF105159.1	EST_HUMAN	607822184F1 NIH_MGC_75 Homo sapiens cDNA clone IMAGE:4042413 5'
9894	22847	36303	1.95	5.0E-10	P34678	SWISSPROT	HYPOTHETICAL 67.9 KD PROTEIN ZK688.8 IN CHROMOSOME III
9894	22847	36304	1.95	5.0E-10	P34678	SWISSPROT	HYPOTHETICAL 67.9 KD PROTEIN ZK688.8 IN CHROMOSOME III
111	13222		1.27	4.0E-10	AJ221083.1	EST_HUMAN	qg09f09.x1 Soares_placenta_8tc9weeks_2NbhP8tc9w Homo sapiens cDNA clone IMAGE:1759049 3'
583	13651	26565	0.75	4.0E-10	AA515260.1	EST_HUMAN	similar to contains LTR8.b2 LTR8 repetitive element ;
2012	15033	28043	1.4	4.0E-10	AW594709.1	EST_HUMAN	nt64a01.s1 NCI_CGAP_Co3 Homo sapiens cDNA clone IMAGE:924648 3'
2580	15581	28600	5.49	4.0E-10	AL163303.2	EST_HUMAN	hg58g03.s1 NCI_CGAP_GC6 Homo sapiens cDNA clone IMAGE:2949844 3' similar to contains Alu repetitive element;
7382	20352	33703	17.71	4.0E-10	AF224689.1	NT	Homo sapiens chromosome 21 segment HS21C103
10555	23477	36971	0.53	4.0E-10	AW293243.1	EST_HUMAN	(UBE2D3) genes, complete cds
10812	23733	37235	0.87	4.0E-10	AI287342.1	EST_HUMAN	UI-H-B12-ah1-a-07-Q-UI.s1 NCI_CGAP_Sub4 Homo sapiens cDNA clone IMAGE:2727061 3'
10933	23853	37368	0.45	4.0E-10	BE169208.1	EST_HUMAN	aq63h11.x1 Stanley Frontal SN pool 2 Homo sapiens cDNA clone IMAGE:2035653
10933	23853	37369	0.45	4.0E-10	BE169208.1	EST_HUMAN	PM1-HT0521-120200-001-f08 HT0521 Homo sapiens cDNA
916	13970	26924	1.8	3.0E-10	N36113.1	EST_HUMAN	PM1-HT0521-120200-001-f08 HT0521 Homo sapiens cDNA
1353	14398		4.8	3.0E-10	AY005150.1	NT	Y3206.s1 Soares melanocyte 2NbhM Homo sapiens cDNA clone IMAGE:272963 3' similar to contains L1.1 L1 repetitive element ;
4566	17589	30480	1.04	3.0E-10	AY005150.1	NT	Homo sapiens extracellular glycoprotein lactin precursor, gene, complete cds
4566	17589	30481	1.04	3.0E-10	AL163203.2	NT	Homo sapiens chromosome 21 segment HS21C003
5530	18628	31564	1.06	3.0E-10	N50109.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C003
6327	19397	32639	4.03	3.0E-10	P20350	SWISSPROT	Y271908.s1 Soares_multiple_sclerosis_2NbhMSP Homo sapiens cDNA clone IMAGE:282782 3'
6486	19551	32801	3.08	3.0E-10	BE302970.1	EST_HUMAN	RHOMBOD PROTEIN (VEINLET PROTEIN)
8036	20973	34367	1.42	3.0E-10	AV743302.1	EST_HUMAN	ba76d08.y1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:2906319 5'
8036	20973	34368	1.42	3.0E-10	AV743302.1	EST_HUMAN	AV743302 CB Homo sapiens cDNA clone CBFBG008 5'
9082	22048	35471	1.04	3.0E-10	H87208.1	EST_HUMAN	AV743302 CB Homo sapiens cDNA clone CBFBG008 5'
9404	22369	35803	1.8	3.0E-10	AW850731.1	EST_HUMAN	ys74b12.s1 Soares retina N2b-4HR Homo sapiens cDNA clone IMAGE:220511 3' similar to contains MER29 repetitive element ;
9404	22369	35804	1.8	3.0E-10	AW850731.1	EST_HUMAN	IL3-CT0219-160200-064-B06 CT0219 Homo sapiens cDNA

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Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9696	22649		0.73	3.0E-10	AF20503.1	NT	Homo sapiens FRA3B common fragile region, diadenosine triphosphate hydrolase (FHT) gene, exon 5
10828	23749		2.05	3.0E-10	T65891.1	EST_HUMAN	yc11e12.11 Stratagene lung (#637210) Homo sapiens cDNA clone IMAGE:80398 5'
10957	23877		1.76	3.0E-10	AA769294.1	EST_HUMAN	n236903.s1 NCI CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1288908 3'
12865	25488	31728	1.95	3.0E-10	BE79517.1	EST_HUMAN	IL3-HT0618-110500-136-E07 HT0618 Homo sapiens cDNA
37	13157	26088	1.55	2.0E-10	P48988	SWISSPROT	MAJOR CENTROMERE AUTOANTIGEN B (CENTROMERE PROTEIN B) (CENP-B)
37	13157	26059	1.55	2.0E-10	P48988	SWISSPROT	MAJOR CENTROMERE AUTOANTIGEN B (CENTROMERE PROTEIN B) (CENP-B)
1913	14937		1.88	2.0E-10	U80017.1	NT	Homo sapiens basic transcription factor 2 p44 (btf2p44) gene, partial cds, neuronal apoptosis inhibitory protein (nail) and survival motor neuron protein (smn) genes, complete cds
2999	19057		0.88	2.0E-10	BF675047.1	EST_HUMAN	602136640.F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4273377 5'
5901	18988		3.12	2.0E-10	Q28640	SWISSPROT	(HPRG)
6579	19447	32688	1.55	2.0E-10	AF280107.1	NT	Homo sapiens cytochrome P450 polypeptide 43 (CYP3A43) gene, partial cds; cytochrome P450 polypeptide 4 (CYP3A4) and cytochrome P450 polypeptide 7 (CYP3A7) genes, complete cds; and cytochrome P450 polypeptide 5 (CYP3A5) gene, partial cds
7605	20566	33926	6.24	2.0E-10	BE791082.1	EST_HUMAN	601586208.F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3940824 5'
8347	21316	34730	0.54	2.0E-10	P28809	SWISSPROT	POL POLYPROTEIN [CONTAINS: PROTEASE; REVERSE TRANSCRIPTASE; RIBONUCLEASE H]
8347	21316	34731	0.54	2.0E-10	P28809	SWISSPROT	POL POLYPROTEIN [CONTAINS: PROTEASE; REVERSE TRANSCRIPTASE; RIBONUCLEASE H]
9857	22600		0.85	2.0E-10	BF434565.1	EST_HUMAN	7678d08.x1 NCI CGAP_Kid11 Homo sapiens cDNA clone IMAGE:3642303 3' similar to contains L1.13 L1 repetitive element;
1509	14542		2.94	1.0E-10	AW867767.1	EST_HUMAN	MR0-SN0038-280300-001-f01 SN0038 Homo sapiens cDNA
1611	14643	27619	3.27	1.0E-10	AV652123.1	EST_HUMAN	AV652123 GLC Homo sapiens cDNA clone GLCCXA11 3'
2586	15587		1.92	1.0E-10	AW852001.1	EST_HUMAN	QV0-CT0225-191199-058-c08 CT0225 Homo sapiens cDNA
3511	16557	29481	0.64	1.0E-10	AW832912.1	EST_HUMAN	QV2-TT0003-161199-013-g10 TT0003 Homo sapiens cDNA
3550	16596		0.81	1.0E-10	AL041685.1	EST_HUMAN	DKFZp434N1317_r1 434 (synonym: htes3) Homo sapiens cDNA clone DKFZp434N1317 5'
3858	16596		0.94	1.0E-10	AL041685.1	EST_HUMAN	DKFZp434N1317_r1 434 (synonym: htes3) Homo sapiens cDNA clone DKFZp434N1317 5'
4043	17081		6.46	1.0E-10	AF213884.1	NT	Homo sapiens nuclear factor of kappa light polypeptide gene enhancer in B-cells 1 (NFKB1) gene, complete cds
4154	17185	30072	5.55	1.0E-10	U52111.2	NT	Homo sapiens X28 region near ALD locus containing dual specificity phosphatase 9 (DUSP9), ribosomal protein L18a (RPL18a), Ca2+/Calmodulin-dependent protein kinase I (CAMKI), creatine transporter (CRTR), CDM protein (CDM), adrenoleukodystrophy protein >
4154	17185	30073	5.55	1.0E-10	U52111.2	NT	Homo sapiens X28 region near ALD locus containing dual specificity phosphatase 9 (DUSP9), ribosomal protein L18a (RPL18a), Ca2+/Calmodulin-dependent protein kinase I (CAMKI), creatine transporter (CRTR), CDM protein (CDM), adrenoleukodystrophy protein >
4160	17191	30080	2.48	1.0E-10	AB031069.1	NT	Homo sapiens PCCX1 mRNA for protein containing CXXC domain 1, complete cds

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Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4199	17230		2.63	1.0E-10	M30629.1	NT	Human pregnancy-specific glycoprotein beta-1 (SP1) mRNA, last exon
5212	18221		0.92	1.0E-10	AI797745.1	EST_HUMAN	we8204.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2347616 3' similar to contains
6875	19928	33225	0.81	1.0E-10	AA631233.1	EST_HUMAN	MER31.11 MER31 repetitive element; nq81a05.s1 NCL_CGAP_C09 Homo sapiens cDNA clone IMAGE:1158704 3'
6891	20214	33543	0.49	1.0E-10	AF003528.1	NT	Homo sapiens X-linked anhidrotic ectodermal dysplasia protein gene (EDA), exon 2 and flanking repeat regions
7716	20673		0.56	1.0E-10	P08548	SWISSPROT	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG
7947	20898	34279	0.63	1.0E-10	AU128584.1	EST_HUMAN	AU128584 NT2RP2 Homo sapiens cDNA clone NT2RP2003751 5'
8582	21550	34968	1.11	1.0E-10	AW408990.1	EST_HUMAN	fb_6A4 Fetal brain library Homo sapiens cDNA
9002	21968		1.1	1.0E-10	AI288340.1	EST_HUMAN	gm04e10.x1 NCL_CGAP_Lu5 Homo sapiens cDNA clone IMAGE:1880874 3' similar to contains L1.11 L1 repetitive element;
10562	23484		3.95	1.0E-10	AA081868.1	EST_HUMAN	zn23g06.11 Stratagene neuroepithelium NT2RAMI 937234 Homo sapiens cDNA clone IMAGE:548314 5'
11259	24211	37734	3.25	1.0E-10	AJ038280.1	EST_HUMAN	oy65h03.x1 Soares_fetal_liver_spleen_INFLS_S1 Homo sapiens cDNA clone IMAGE:1672661 3'
12166	18354		2.46	1.0E-10	X87344.1	NT	H. sapiens DMA, DMB, HLA-Z1, IPP2, LMP2, TAP1, LMP7, TAP2, DOB, DOB2 and RING8, 9, 13 and 14 genes
261	13357	28282	0.98	9.0E-11	BE146600.1	EST_HUMAN	IL2-HT0203-291099-016-c08 HT0203 Homo sapiens cDNA
2114	15131	28151	6.21	9.0E-11	AL134395.1	EST_HUMAN	DKFZp547D225_r1 547 (synonym: hfb1) Homo sapiens cDNA clone DKFZp547D225 5'
2114	15131	28152	6.21	9.0E-11	AL134395.1	EST_HUMAN	DKFZp547D225_r1 547 (synonym: hfb1) Homo sapiens cDNA clone DKFZp547D225 5'
3394	16443	28370	2.6	9.0E-11	AL134395.1	EST_HUMAN	DKFZp547D225_r1 547 (synonym: hfb1) Homo sapiens cDNA clone DKFZp547D225 5'
3394	16443	28371	2.6	9.0E-11	AL134395.1	EST_HUMAN	DKFZp547D225_r1 547 (synonym: hfb1) Homo sapiens cDNA clone DKFZp547D225 5'
4528	17552	30440	0.72	9.0E-11	AA75985.1	EST_HUMAN	ae7801.s1 Stratagene schizo brain S11 Homo sapiens cDNA clone IMAGE:970297 3'
5654	18750		3.89	9.0E-11	BE079780.1	EST_HUMAN	RC6-BT0627-140200-011-E06 BT0627 Homo sapiens cDNA
10514	23436	36934	1.22	9.0E-11	AA324960.1	EST_HUMAN	EST27872 Cerebellum II Homo sapiens cDNA 5' end
10514	23436	36935	1.22	9.0E-11	AA324960.1	EST_HUMAN	EST27872 Cerebellum II Homo sapiens cDNA 5' end
12546	25269	31809	4.59	9.0E-11	C16635.1	EST_HUMAN	C16635 Clontech human aorta polyA+ mRNA (#6572) Homo sapiens cDNA clone GEN-506808 5'
3133	16190		8.85	8.0E-11	H19971.1	EST_HUMAN	vn53f11.s1 Soares adult brain N2b5HB55Y Homo sapiens cDNA clone IMAGE:172173 3' similar to contains L1 repetitive element;
4073	17109	30003	4.35	8.0E-11	N23712.1	EST_HUMAN	W46e06.s1 Weizmann Olfactory Epithelium Homo sapiens cDNA clone IMAGE:255298 3'
5890	18978	32170	0.65	8.0E-11	AW674316.1	EST_HUMAN	bae0g04.x1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:2900982 3'
6829	19883		0.65	8.0E-11	AW169158.1	EST_HUMAN	xf45h11.x1 NCL_CGAP_Brn50 Homo sapiens cDNA clone IMAGE:2621061 3' similar to contains MER10.11 MER10 repetitive element;
1442	14475	27452	1.87	7.0E-11	AA330842.1	EST_HUMAN	EST34392 Embryo, 6 week I Homo sapiens cDNA 5' end

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Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3885	16925	29834	1.11	7.0E-11	AJ277546.2	NT	Homo sapiens WEE1 gene for protein kinase and partial ZNF143 gene for zinc finger transcription factor
8843	21810	35229	2.79	7.0E-11	AF163864.1	NT	Homo sapiens SNCA isoform (SNCA) gene, complete cds, alternatively spliced
10590	23512		1.19	7.0E-11	P11369	SWISSPROT	RETROVIRUS-RELATED POLYPROTEIN [CONTAINS: REVERSE TRANSCRIPTASE; ENDONUCLEASE]
412	13485	26421	6.97	6.0E-11	M55270.1	NT	Human matrix Gla protein (MGP) gene, complete cds
412	13485	26422	6.97	6.0E-11	M55270.1	NT	Human matrix Gla protein (MGP) gene, complete cds
6884	19936	33232	0.88	6.0E-11	L44140.1	NT	Homo sapiens chromosome X region from filamin (FLN) gene to glucose-6-phosphate dehydrogenase (G6PD) gene, complete cds's
7957	20898	34291	3.22	6.0E-11	P08547	SWISSPROT	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG
8707	21675	35100	7.37	6.0E-11	AV727859.1	EST_HUMAN	AV727859 HTC Homo sapiens cDNA clone HTcASC06 5'
9688	22821	38072	0.42	6.0E-11	BE063509.1	EST_HUMAN	CMO-BT0281-031199-087-403 BT0281 Homo sapiens cDNA
12	13132	26030	0.75	5.0E-11	AL163283.2	NT	Homo sapiens chromosome 21 segment HS21C083
3377	13132	26030	1.31	5.0E-11	AL163283.2	NT	Homo sapiens chromosome 21 segment HS21C083
4256	17285	30167	1.51	5.0E-11	P48034	SWISSPROT	ALDEHYDE OXIDASE
6665	19722	32997	1.91	5.0E-11	AL163213.2	NT	Homo sapiens chromosome 21 segment HS21C013
7774	20727	34099	11.91	5.0E-11	11416799	NT	Homo sapiens protocadherin beta 3 (PCDH3), mRNA
1401	14434		1.88	4.0E-11	AA436042.1	EST_HUMAN	zu01b12.r1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:730559 5'
2802	15794	28812	7.63	4.0E-11	BE885900.1	EST_HUMAN	601507531F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3909295 5'
2981	16039	28662	0.92	4.0E-11	AL163247.2	NT	Homo sapiens chromosome 21 segment HS21C047
4649	17670	30557	1.24	4.0E-11	ID44666.1	EST_HUMAN	HUMSUPY069 Human brain cDNA Homo sapiens cDNA clone 069
6621	19679	32957	3.27	4.0E-11	P20095	SWISSPROT	PRE-MRNA SPLICING FACTOR RNA HELICASE PRP2
7197	20221	33552	0.54	4.0E-11	AA442630.1	EST_HUMAN	z659f10.r1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:757963 5' similar to TR:G1055250
7600	20561		3.97	4.0E-11	AF224669.1	NT	G1055250 PHEROMONE RECEPTOR VN4. ;
9750	22891		1.68	4.0E-11	BE149425.1	EST_HUMAN	Homo sapiens mammoside, beta A, lysosomal (MANBA) gene, and ubiquitin-conjugating enzyme E2D 3 (UBE2D3) genes, complete cds
10020	22847	36415	0.86	4.0E-11	AI609753.1	EST_HUMAN	R01-H10256-210100-013-108 HT0256 Homo sapiens cDNA
12736	25388	31752	1.56	4.0E-11	11545732	NT	#82g12.x1 NCI_CGAP_Bim23 Homo sapiens cDNA clone IMAGE:2105830 3' similar to WP:ZK353.1
1488	14521	27494	2.55	3.0E-11	6679077	NT	CE00385. ;
4305	17334		1.37	3.0E-11	AA309248.1	EST_HUMAN	Homo sapiens SH3-domain binding protein 1 (SH3BP1), mRNA
							Mus musculus expressed in non-mesodermic cells 2, protein (NIV23B) (Nme2), mRNA
							EST180120 Liver, hepatocellular carcinoma Homo sapiens cDNA 5' end
							q36c04.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1752102 3' similar to contains MER10.13
961	14014	26967	1.48	2.0E-11	AI150502.1	EST_HUMAN	MER10 repetitive element;

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Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1189	14229	27186	4.46	2.0E-11	R24807.1	EST_HUMAN	y943e12.1 Soares Infant brain 1N1B Homo sapiens cDNA clone IMAGE:35144 5'
1189	14229	27187	4.46	2.0E-11	R24807.1	EST_HUMAN	y943e12.1 Soares Infant brain 1N1B Homo sapiens cDNA clone IMAGE:35144 5'
1617	14649	27624	5.86	2.0E-11	L17432.1	NT	Gallus gallus rho-globin, beta-H globin, beta-A globin, epsilon-globin, and epsilon-like protein COR3 beta (COR3 beta) genes, complete cds
1617	14649	27625	5.86	2.0E-11	L17432.1	NT	Gallus gallus rho-globin, beta-H globin, beta-A globin, epsilon-globin, and epsilon-like protein COR3 beta (COR3 beta) genes, complete cds
1620	14653	27629	1.25	2.0E-11	A1126371.1	EST_HUMAN	qc51c10.x1 Soares_pregnant_uterus_NbHPU Homo sapiens cDNA clone IMAGE:1713138 3' similar to gb:U02932 PEROXISOME PROLIFERATOR ACTIVATED RECEPTOR ALPHA (HUMAN); contains L1, L1 L1 repetitive element;
2775	15787	28787	1.04	2.0E-11	AF087913.1	NT	Human endogenous retrovirus HERV-P-T47D
3211	16286	29189	8.7	2.0E-11	P10263	SWISSPROT	RETROVIRUS-RELATED GAG POLYPROTEIN (VERSION 1)
3337	16388	29309	1	2.0E-11	A1478617.1	EST_HUMAN	tm54c09.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2161938 3'
3375	16425	29350	0.71	2.0E-11	Q10473	SWISSPROT	POLYPEPTIDE N-ACETYL GALACTOSAMINYL TRANSFERASE (PROTEIN-JDP ACETYL GALACTOSAMINYL TRANSFERASE) (UDP-GALNAc:POLYPEPTIDE, N- ACETYL GALACTOSAMINYL TRANSFERASE) (GALNAc-T1)
3508	16554		1.09	2.0E-11	AF020503.1	NT	Homo sapiens FRA3B common fragile region, diadenosine triphosphate hydrolase (FHT) gene, exon 5
4472	17498		1.24	2.0E-11	BE065537.1	EST_HUMAN	RC3-BT0316-170200-014-e05 BT0316 Homo sapiens cDNA
4636	17657		0.96	2.0E-11	AL163227.2	NT	Homo sapiens chromosome 21 segment HS21C027
4973	17988		2.36	2.0E-11	BE062558.1	EST_HUMAN	QV2-BT0258-261059-014-a01 BT0258 Homo sapiens cDNA
6268	19331	32562	1	2.0E-11	AW87806.1	EST_HUMAN	QV2-PT0073-280300-109-h08 PT0073 Homo sapiens cDNA
6443	19508	32758	1.71	2.0E-11	AA581028.1	EST_HUMAN	nc83h05.1 NCI_CGAP_GC1 Homo sapiens cDNA clone IMAGE:797433 5' similar to SW:PR16_YEAST
7401	20369	33722	0.82	2.0E-11	BF592945.1	EST_HUMAN	P15938 PRE-MRNA SPLICING FACTOR RNA HELICASE PRP16 ;
8214	21183		0.51	2.0E-11	P37072	SWISSPROT	OLFACTORY RECEPTOR-LIKE PROTEIN COR6
9578	22540		1.31	2.0E-11	AF029308.1	NT	Homo sapiens chromosome 9 duplication of the T cell receptor beta locus and tyrosinogen gene families
10647	23569	37065	4.42	2.0E-11	Q13606	SWISSPROT	OLFACTORY RECEPTOR 51 (OLFACTORY RECEPTOR-LIKE PROTEIN OLF1)
10882	23802	37305	0.85	2.0E-11	AW885874.1	EST_HUMAN	RC4-OT0072-170400-013-c11 OT0072 Homo sapiens cDNA
10882	23802	37306	0.85	2.0E-11	AW885874.1	EST_HUMAN	RC4-OT0072-170400-013-c11 OT0072 Homo sapiens cDNA
11448	24391	37935	1.54	2.0E-11	AA035399.1	EST_HUMAN	zk27g02.s1 Soares_pregnant_uterus_NbHPU Homo sapiens cDNA clone IMAGE:471794 3'
11448	24391	37936	1.54	2.0E-11	AA035399.1	EST_HUMAN	zk27g02.s1 Soares_pregnant_uterus_NbHPU Homo sapiens cDNA clone IMAGE:471794 3'
11477	24420	37969	2.14	2.0E-11	AA281956.1	EST_HUMAN	zs18p04.1 NCI_CGAP_GC8 Homo sapiens cDNA clone IMAGE:685519 5'
12326	25128		4.12	2.0E-11	AW842143.1	EST_HUMAN	RC0-CN0027-210100-011-c01 CN0027 Homo sapiens cDNA

Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
12354	25148	31854	2.14	2.0E-11	BF377859.1	EST_HUMAN	CM2-TN0140-070900-372-g01 TN0140 Homo sapiens cDNA
12617	25313		1.49	2.0E-11	D25217.2	NT	Homo sapiens mRNA for KIAA0027 protein, partial cds
12754	25399		1.68	2.0E-11	P08547	SWISSPROT	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG
13070	25804		3.68	2.0E-11	11417968	NT	Homo sapiens SEC14 (S. cerevisiae)-like 2 (SEC14L2), mRNA
677	13740	26667	0.83	1.0E-11	AJ131016.1	NT	Homo sapiens SCL gene locus
784	13844	26789	1.89	1.0E-11	AL163209.2	NT	Homo sapiens chromosome 21 segment HS21C009
1221	14259	27216	4.66	1.0E-11	AL163279.2	NT	Homo sapiens chromosome 21 segment HS21C079
1498	14531		2.95	1.0E-11	AF118914.1	NT	Homo sapiens PRO3078 mRNA, complete cds
2053	15072	28091	1.41	1.0E-11	P16258	SWISSPROT	OXYSTEROL-BINDING PROTEIN
2136	15153	28168	3.18	1.0E-11	AF000573.1	NT	Homo sapiens homogenisate 1,2-dioxygenase gene, complete cds
2170	15186	28207	1.15	1.0E-11	AA309318.1	EST_HUMAN	EST180186 Liver, hepatocellular carcinoma Homo sapiens cDNA 5' end similar to EST containing Alu repeat
3510	16556	29480	0.8	1.0E-11	BE004315.1	EST_HUMAN	CM0-BN0105-170300-292-d12 BN0105 Homo sapiens cDNA
4960	17975	30866	1.01	1.0E-11	AH168625.1	EST_HUMAN	α65H06.s1 Soares_NHMPu_ST Homo sapiens cDNA clone IMAGE:1661243 3'
5405	18508	31385	14.43	1.0E-11	AL163247.2	NT	Homo sapiens chromosome 21 segment HS21C047
5931	19017	32212	0.77	1.0E-11	BF222846.1	EST_HUMAN	7p57d01.x1 NCI CGAP_P128 Homo sapiens cDNA clone IMAGE:3649945 3' similar to contains MER10.b3
8112	21049		0.51	1.0E-11	AB042297.1	NT	MER10 repetitive element;
8543	21511	34928	3.36	1.0E-11	4885546	NT	Homo sapiens PTS gene for 6-pyruoyltetrahydropterin synthase, complete cds
8928	21894	35322	4.18	1.0E-11	R13174.1	EST_HUMAN	Homo sapiens PHD finger protein 2 (PHF2) mRNA
9403	22368	35801	1.18	1.0E-11	BF365119.1	EST_HUMAN	QV4-NN1149-250900-423-a03 NN1149 Homo sapiens cDNA
9403	22368	35802	1.18	1.0E-11	BF365119.1	EST_HUMAN	QV4-NN1149-250900-423-a03 NN1149 Homo sapiens cDNA
11619	24557	38120	1.48	1.0E-11	BF680078.1	EST_HUMAN	602154807F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4295977 5'
2963	16021	28946	0.82	9.0E-12	P20742	SWISSPROT	PREGNANCY ZONE PROTEIN PRECURSOR
10157	23082	36558	1.02	9.0E-12	AL163300.2	NT	Homo sapiens chromosome 21 segment HS21C100
10157	23082	36559	1.02	9.0E-12	AL163300.2	NT	Homo sapiens chromosome 21 segment HS21C100
12075	24947	38542	2.85	9.0E-12	AL046939.1	EST_HUMAN	DKFZp886I0417.1 1566 (synonym: hute1) Homo sapiens cDNA clone DKFZp886I0417 5'
9693	22646		0.92	8.0E-12	BE074720.1	EST_HUMAN	IL5-BT0578-130300-036-G12 BT0578 Homo sapiens cDNA
12407	25180		3.22	8.0E-12	AJ121736.1	NT	Homo sapiens Xq pseudautosomal region; segment 2/2
4690	17711	30605	1.46	7.0E-12	Q05904	SWISSPROT	34 KD SPICULE MATRIX PROTEIN PRECURSOR (LSM34)
11677	24843	38220	7.41	7.0E-12	AA704735.1	EST_HUMAN	z23g01.s1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:451152 3'
3558	16804		0.95	6.0E-12	AV730554.1	EST_HUMAN	AV730554 HTF Homo sapiens cDNA clone HTFAFW06 5'
4375	17403	30283	9.29	6.0E-12	AA732516.1	EST_HUMAN	n28811.s1 NCL_CGAP_GC81 Homo sapiens cDNA clone IMAGE:1302573 3' similar to contains Alu repetitive element;

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Table 4

Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6528	19591	32851	0.65	6.0E-12	AF020503.1	NT	Homo sapiens FRA3B common fragile region, diadenosine triphosphate hydrolase (FHIT) gene, exon 5
9347	22312	35736	0.98	6.0E-12	AF003249.1	NT	Macaca saxatilis myosin heavy chain FM3A (FM3A) mRNA, complete cds
9829	22678		1.66	6.0E-12	AA847898.1	EST_HUMAN	cd10g11.s1 NCL_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1367588 similar to contains MER28.12
1044	14090	27043	3.57	6.0E-12	T06573.1	EST_HUMAN	MER29 repetitive element ;
3401	19450	29376	1.17	5.0E-12	BE047779.1	EST_HUMAN	EST04482 Fetal brain, Stratagene (cat#836206) Homo sapiens cDNA clone HFBDV33
3740	18782	29694	6.8	5.0E-12	AJ271736.1	NT	142805.y1 NCL_CGAP_Brn52 Homo sapiens cDNA clone IMAGE:2291217 5'
6137	19214	32441	4.99	5.0E-12	AL163278.2	NT	Homo sapiens Xq pseudautosomal region; segment 2/2
6137	19214	32442	4.99	5.0E-12	AL163278.2	NT	Homo sapiens chromosome 21 segment HS21C078
6639	19697	32973	9.52	5.0E-12	AW974760.1	EST_HUMAN	EST386850 IMAGE resequences, MAGN Homo sapiens cDNA
7232	19977	33274	1	5.0E-12	AL040739.1	EST_HUMAN	DKFZp434B1615.s1 434 (synonym: htes3) Homo sapiens cDNA clone DKFZp434B1615 3'
7242	19977	33274	1.03	5.0E-12	AL040739.1	EST_HUMAN	DKFZp434B1615.s1 434 (synonym: htes3) Homo sapiens cDNA clone DKFZp434B1615 3'
8571	21539	34960	1.14	5.0E-12	AA033745.1	EST_HUMAN	201g12.s1 Soares_fetal_heart_NbhH19W Homo sapiens cDNA clone IMAGE:375718 3' similar to contains L1.13 L1 repetitive element;
9015	21981		0.7	5.0E-12	AW887037.1	EST_HUMAN	RC1-OT0086-220300-011-b07 OT0086 Homo sapiens cDNA
9346	22311		0.54	5.0E-12	AL079581.1	EST_HUMAN	DKFZp434J0426_r1 434 (synonym: htes3) Homo sapiens cDNA clone DKFZp434J0426 5'
9464	22428	35667	2.76	5.0E-12	AJ271735.1	NT	Homo sapiens Xq pseudautosomal region; segment 1/2
9778	22719	36173	1.38	5.0E-12	P34982	SWISSPROT	OLFACTORY RECEPTOR 1D2 (OLFACTORY RECEPTOR-LIKE PROTEIN HGMP07E) (OLFACTORY RECEPTOR 17-4) (OR17-4)
10638	23560		4.14	5.0E-12	AL163303.2	NT	Homo sapiens chromosome 21 segment HS21C103
10729	23651	37144	0.81	5.0E-12	AL163302.2	NT	Homo sapiens chromosome 21 segment HS21C102
244	13342	26267	4.17	4.0E-12	AA700326.1	EST_HUMAN	274g11.s1 Soares_fetal_liver_spleen_INFLS_S1 Homo sapiens cDNA clone IMAGE:460676 3'
245	13342	26287	5.51	4.0E-12	AA700326.1	EST_HUMAN	274g11.s1 Soares_fetal_liver_spleen_INFLS_S1 Homo sapiens cDNA clone IMAGE:460676 3'
4650	17671	30558	0.74	4.0E-12	AI689984.1	EST_HUMAN	626h05.x1 NCL_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:2270745 3' similar to TRQ13539 Q13539 MARINER TRANSPOSASE ;
7881	20825		0.72	4.0E-12	BF445140.1	EST_HUMAN	had21b03.x1 NCL_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3366077 3' similar to contains MER7.b2 MER7 repetitive element ;
8585	21553		2.92	4.0E-12	AF109907.1	NT	Homo sapiens S164 gene, partial cds; PS1 and hypothetical protein genes, complete cds; and S171 gene, partial cds
9035	22001	35422	0.75	4.0E-12	AB042815.1	NT	Bos taurus Mth2 mRNA for mitochondrial carrier homolog 2, complete cds
11419	24363	37898	3.26	4.0E-12	AJ229043.1	NT	Homo sapiens 959 kb contig between AML1 and CBR1 on chromosome 21q22, segment 3/3
12658	25338		2.82	4.0E-12	U78027.1	NT	Homo sapiens Bruton's tyrosine kinase (BTK), alpha-D-galactosidase A (GLA), L44-like ribosomal protein (L44L) and FTP3 (FTP3) genes, complete cds

Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
618	13683	26600	3.06	3.0E-12	AW341883.1	EST_HUMAN	hd134d01.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2909377 3' similar to TR:O14517 O14517 SMRP.:
618	13683	26601	3.06	3.0E-12	AW341883.1	EST_HUMAN	hd134d01.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2909377 3' similar to TR:O14517 O14517 SMRP.:
5211	18220	31096	0.73	3.0E-12	AL163288.2	NT	Homo sapiens chromosome 21 segment HS21C068
5527	18626	31582	0.96	3.0E-12	AF111168.2	NT	Homo sapiens serine palmitoyl transferase, subunit II gene, complete cds; and unknown genes
7659	20619		0.54	3.0E-12	AB042297.1	NT	Homo sapiens PTS gene for 6-pyruvoyltetrahydropterin synthase, complete cds
8030	20987		0.55	3.0E-12	AW854328.1	EST_HUMAN	RC3-CT0255-031099-011-h02 CT0255 Homo sapiens cDNA
8718	21686	35114	0.48	3.0E-12	O35453	SWISSPROT	SERINE PROTEASE HEPSEN
9462	22426	35864	0.54	3.0E-12	O35453	SWISSPROT	SERINE PROTEASE HEPSEN
11016	23981	37507	2.71	3.0E-12	U37672.1	NT	Human prostate specific antigen gene, 5' flanking region
11016	23981	37508	2.71	3.0E-12	U37672.1	NT	Human prostate specific antigen gene, 5' flanking region
1661	14693	27668	2.41	2.0E-12	AW802131.1	EST_HUMAN	IL5-UM0071-120400-065-a05 UM0071 Homo sapiens cDNA
3480	16526	29451	0.85	2.0E-12	6754495	NT	Mus musculus keratin-associated protein 6.2 (Krtap6-2), mRNA
4141	17172	30060	1.09	2.0E-12	J01884.1	NT	Rat U3A small nuclear RNA
4141	17172	30061	1.09	2.0E-12	J01884.1	NT	Rat U3A small nuclear RNA
4451	17477		1.97	2.0E-12	BE063509.1	EST_HUMAN	CMO-BT0281-031199-087-a03 BT0281 Homo sapiens cDNA
5321	18427	31177	0.71	2.0E-12	P11369	SWISSPROT	RETROVIRUS-RELATED POLYPROTEIN [CONTAINS: REVERSE TRANSCRIPTASE ; ENDONUCLEASE]
6622	19680		1.83	2.0E-12	AW971857.1	EST_HUMAN	EST383946 MAGE resequences, MAGL Homo sapiens cDNA
7381	20351	33702	3.22	2.0E-12	T08163.1	EST_HUMAN	EST08060 Infant Brain, Bonto Soares Homo sapiens cDNA clone HIBBA13 5' end
7567	20530	33889	1.18	2.0E-12	BE173035.1	EST_HUMAN	MRQ-HT0559-200400-015-e08 HT0559 Homo sapiens cDNA
7778	20731		0.57	2.0E-12	AW842708.1	EST_HUMAN	MR2-CN0037-210200-101-b02 CN0037 Homo sapiens cDNA
7922	20865	34253	2.1	2.0E-12	11422229	NT	Homo sapiens Ac-like transposable element (ALTE), mRNA
9077	22043	35466	0.43	2.0E-12	Q10473	SWISSPROT	POLYPEPTIDE N-ACETYLGLACTOSAMINYLTRANSFERASE (PROTEIN-UDP ACETYLGLACTOSAMINYLTRANSFERASE) (UDP-GALNAC:POLYPEPTIDE, N- ACETYLGLACTOSAMINYLTRANSFERASE) (GALNAC-T1)
9663	22820		1.65	2.0E-12	AF196864.1	NT	Homo sapiens putative BPES syndrome breakpoint region protein gene, complete cds
10346	23269		14.41	2.0E-12	BE165980.1	EST_HUMAN	MR3-HT0487-150200-113-g01 HT0487 Homo sapiens cDNA
10881	23801	37304	0.8	2.0E-12	AI334130.1	EST_HUMAN	qq07f02.x1 Soares_NHMPJ_S1 Homo sapiens cDNA clone IMAGE:1931835 3' similar to TR:Q13538 Q13538 ORF2: FUNCTION UNKNOWN.:
12308	25116		3.11	2.0E-12	AL163283.2	NT	Homo sapiens chromosome 21 segment HS21C068
12511	25245		1.69	2.0E-12	11418248	NT	Homo sapiens sulfotransferase-related protein (SULTX3), mRNA

Table 4
Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
123	13231	28159	2.83	1.0E-12	AW627874.1	EST_HUMAN	hh90a09.x1 NCL_CGAP_GU1 Homo sapiens cDNA clone IMAGE:2970040 3' similar to contains MER18.11 MER18 repetitive element;
2004	15025		1.46	1.0E-12	AI871726.1	EST_HUMAN	wn51107.x1 NCL_CGAP_U12 Homo sapiens cDNA clone IMAGE:2438493 3' similar to contains L1.B3 L1 repetitive element;
3085	16142	28053	0.78	1.0E-12	AF000991.1	NT	Homo sapiens testis-specific Testis Transcript Y 2 (TTY2) mRNA, partial cds
3085	16142	28054	0.78	1.0E-12	AF000991.1	NT	Homo sapiens testis-specific Testis Transcript Y 2 (TTY2) mRNA, partial cds
3888	16928	29836	31.6	1.0E-12	AU132248.1	EST_HUMAN	AU132248 NT2RP3 Homo sapiens cDNA clone NT2RP3004070 5'
3888	16928	29837	31.6	1.0E-12	AU132248.1	EST_HUMAN	AU132248 NT2RP3 Homo sapiens cDNA clone NT2RP3004070 5'
6078	19168		2.05	1.0E-12	U82828.1	NT	Homo sapiens ataxia telangiectasia (ATM) gene, complete cds
6159	19234		1.65	1.0E-12	Q8Y2G7	SWISSPROT	HYPOTHETICAL ZINC FINGER PROTEIN KIAA0961
6277	19349	32582	0.57	1.0E-12	BF42800.1	EST_HUMAN	EST00008 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1847869 5'
6277	19349	32583	0.57	1.0E-12	BF42800.1	EST_HUMAN	EST00008 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1847869 5'
6882	19739	33014	0.78	1.0E-12	AF229843.1	NT	Mus musculus WNT-2 gene, partial cds; putative enkerin-related protein and cystic fibrosis transmembrane conductance regulator (CFTR) genes, section 1 of 2 of the complete cds; and unknown gene
7323	20294	33637	1.9	1.0E-12	AF106884.1	NT	Homo sapiens putative BPES syndrome breakpoint region protein gene, complete cds
7357	20327	33676	11.35	1.0E-12	AI248533.1	EST_HUMAN	qh68a04.x1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:1849814 3' similar to gbM19503 LINE-1 REVERSE TRANSCRIPTASE HOMOLOG (HUMAN); contains MER10.11 MER10 repetitive element;
7357	20327	33676	11.35	1.0E-12	AI248533.1	EST_HUMAN	qh68a04.x1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:1849814 3' similar to gbM19503 LINE-1 REVERSE TRANSCRIPTASE HOMOLOG (HUMAN); contains MER10.11 MER10 repetitive element;
8834	21801	35220	0.48	1.0E-12	U66039.1	NT	Human germline T-cell receptor beta chain Dopamine-beta-hydroxylase-like, TRY1, TRY2, TRY3, TCRBV27S1P, TCRBV22S1A2N1T, TCRBV6S1A1T, TCRBV7S1A1N2T, TCRBV6S1A1T, TCRBV13S3, TCRBV6S7P, TCRBV7S3A2T, TCRBV13S2A1T, TCRBV6S2A2PT, TCRBV7S2A1N4T, TCRBV13S9/13S>
9053	22019	35444	1.16	1.0E-12	AA782323.1	EST_HUMAN	ac26405.s1 Striatogene ovary (#637217) Homo sapiens cDNA clone IMAGE:357577 3'
12213	25052	38626	2.92	1.0E-12	AW962164.1	EST_HUMAN	EST374237 MAGF resequences, MAGG Homo sapiens cDNA
12434	25200		2.54	1.0E-12	AI738592.1	EST_HUMAN	w33h08.x1 NCL_CGAP_Col16 Homo sapiens cDNA clone IMAGE:2382095 3'
12582	25881		2.51	1.0E-12	AL163288.2	NT	Homo sapiens chromosome 21 segment HS21C068
1054	14100	27050	0.7	9.0E-13	AW082714.1	EST_HUMAN	x6107.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2550305 3' similar to contains MER28.13 MER28 repetitive element;
3643	16686		1.01	9.0E-13	AJ271735.1	NT	Homo sapiens Xq pseudautosomal region; segment 1/2
3967	17007	29923	0.96	9.0E-13	AB028900.1	NT	Homo sapiens CST gene for cerebroside sulfotransferase, exon 1, 2, 3, 4, 5

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Table 4
Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9660	22887		2.59	9.0E-13	N69663.1	EST_HUMAN	za26b06.s1 Soares fetal liver spleen 1N1LS Homo sapiens cDNA clone IMAGE:293661 3'
718	13780	26714	6.78	8.0E-13	U29185.1	NT	Homo sapiens prion protein (PrP) gene, complete cds
718	13780	26715	6.78	8.0E-13	U29185.1	NT	Homo sapiens prion protein (PrP) gene, complete cds
1855	14881	27877	3.1	8.0E-13	U80017.1	NT	Homo sapiens basic transcription factor 2 p44 (btf2p44) gene, partial cds, neuronal apoptosis inhibitory protein (nailp) and survival motor neuron protein (smn) genes, complete cds
8449	21418	34831	0.75	8.0E-13	A1884398.1	EST_HUMAN	wm31h09.x1 NCI_CGAP_U4 Homo sapiens cDNA clone IMAGE:2437601 3'
8449	21418	34832	0.75	8.0E-13	A1884398.1	EST_HUMAN	wm31h09.x1 NCI_CGAP_U4 Homo sapiens cDNA clone IMAGE:2437601 3'
10505	23427		4	8.0E-13	U78027.1	NT	Homo sapiens Bruton's tyrosine kinase (BTK), alpha-D-galactosidase A (GLA), L44-like ribosomal protein (L44L) and FTP3 (FTP3) genes, complete cds
8127	21064	34462	0.58	7.0E-13	A1884398.1	EST_HUMAN	wm31h09.x1 NCI_CGAP_U4 Homo sapiens cDNA clone IMAGE:2437601 3'
8127	21064	34463	0.58	7.0E-13	A1884398.1	EST_HUMAN	wm31h09.x1 NCI_CGAP_U4 Homo sapiens cDNA clone IMAGE:2437601 3'
8578	21644		0.49	7.0E-13	Q96155	SWISSPROT	OLFACTORY RECEPTOR-LIKE PROTEIN OLF2
12682	26360		5.56	7.0E-13	BE778223.1	EST_HUMAN	807463285F1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:3856613 5'
2111	16128	28148	3.56	8.0E-13	AL163207.2	NT	Homo sapiens chromosome 21 segment HS21C007
3333	18384		0.74	5.0E-13	R78338.1	EST_HUMAN	y8204.r1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:145759 5'
3408	16457		1.35	5.0E-13	AA435773.1	EST_HUMAN	z177a12.s1 Soares testis, NHT Homo sapiens cDNA clone IMAGE:728350 3' similar to contains Alu repetitive element/contains element MER22 repetitive element ;
7060	20082	33390	0.7	5.0E-13	P08983	SWISSPROT	GAP JUNCTION BETA-1 PROTEIN (CONNEXIN 30) (CX30)
11209	24163	37693	2.07	5.0E-13	P07313	SWISSPROT	MYOSIN LIGHT CHAIN KINASE, SKELETAL MUSCLE (MLCK)
1883	14908		6.02	4.0E-13	AW378614.1	EST_HUMAN	PM2-HT0224-221098-001-e11 HT0224 Homo sapiens cDNA
2467	15471		2.44	4.0E-13	AF003529.1	NT	Homo sapiens glycylalanine 3 (GPC3) gene, partial cds and flanking repeat regions
4778	17798		0.99	4.0E-13	AA454054.1	EST_HUMAN	z48d07.r1 Soares testis, NHT Homo sapiens cDNA clone IMAGE:795469 5'
5667	18782	31931	4.36	4.0E-13	BE169131.1	EST_HUMAN	PM3-HT0520-230200-002-c08 HT0520 Homo sapiens cDNA
7413	20380	33731	1.05	4.0E-13	AB037750.1	NT	Homo sapiens mRNA for KIAA1329 protein, partial cds
7870	20814	34192	0.98	4.0E-13	AA491529.1	EST_HUMAN	zw76g12.r1 Soares testis, NHT Homo sapiens cDNA clone IMAGE:782182 5' similar to TR:G452763
7989	20928		1.47	4.0E-13	N44291.1	EST_HUMAN	G452763 COR1 MRNA. ;
9193	22159	35587	1.2	4.0E-13	AL043810.1	EST_HUMAN	y63g05.r1 Soares melanocyte 2NbrHM Homo sapiens cDNA clone IMAGE:273080 5' similar to PIR:A32895
9860	22796	36249	0.59	4.0E-13	AA076907.1	EST_HUMAN	A32995 t complex sterility protein - mouse ;
10380	23303	36779	5.26	4.0E-13	AL289831.1	EST_HUMAN	DKFZp434A0128 r1 434 (synonym: htes3) Homo sapiens cDNA clone DKFZp434A0128 5'
11502	24444	37995	1.9	4.0E-13	AA435819.1	EST_HUMAN	7804H11 Chromosome 7 Fetal Brain cDNA Library/Homo sapiens cDNA clone 7804H11
11502	24444	37996	1.9	4.0E-13	AA435819.1	EST_HUMAN	qk32a05.x1 NCI_CGAP_Kids Homo sapiens cDNA clone IMAGE:1899945 3' similar to contains Alu repetitive element;
						EST_HUMAN	repetitive element;
						EST_HUMAN	z178g10.s1 Soares testis, NHT Homo sapiens cDNA clone IMAGE:728514 3'
						EST_HUMAN	z178g10.s1 Soares testis, NHT Homo sapiens cDNA clone IMAGE:728514 3'

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
181	13281		5.91	3.0E-13	AF003528.1	NT	Homo sapiens X-linked anhidrotic ectodermal dysplasia protein gene (EDA), exon 2 and flanking repeat regions
868	13922		3.35	3.0E-13	AA430310.1	EST_HUMAN	zvf68g08.r1 Scores_tests_NHT Homo sapiens cDNA clone IMAGE:781408 5'
2378	15386	28410	1.65	3.0E-13	AJ271738.1	NT	Homo sapiens Xq pseudautosomal region, segment 2/2
2487	15491		2.11	3.0E-13	AL163210.2	NT	Homo sapiens chromosome 21 segment HS21C010
2673	15670	28688	2.5	3.0E-13	BF372962.1	EST_HUMAN	CM3-FT0100-140700-242-R08 FT0100 Homo sapiens cDNA
3201	16256		2.19	3.0E-13	AA745944.1	EST_HUMAN	cb18d02.s1 NCL_CGAP_Kid5 Homo sapiens cDNA clone IMAGE:1324035 3'
3514	16560	29484	0.9	3.0E-13	P18616	SWISSPROT	DNA-DIRECTED RNA POLYMERASE II LARGEST SUBUNIT (VERSION 1)
3514	16560	29485	0.9	3.0E-13	P18616	SWISSPROT	DNA-DIRECTED RNA POLYMERASE II LARGEST SUBUNIT (VERSION 1)
5618	18714	31872	0.64	3.0E-13	AA134017.1	EST_HUMAN	zn88h10.r1 Stratagene lung carcinoma 937218 Homo sapiens cDNA clone IMAGE:565315 5' similar to contains THR.12 THR repetitive element ;
5618	18714	31873	0.64	3.0E-13	AA134017.1	EST_HUMAN	zn88h10.r1 Stratagene lung carcinoma 937218 Homo sapiens cDNA clone IMAGE:565315 5' similar to contains THR.12 THR repetitive element ;
6106	19185	32404	0.71	3.0E-13	AW005639.1	EST_HUMAN	wz88c02.x1 NCL_CGAP_Bn25 Homo sapiens cDNA clone IMAGE:2565890 3' similar to TR.O75139 O75139 KIAA0944 PROTEIN ;
8215	21184	34594	8.24	3.0E-13	U52111.2	NT	Homo sapiens X28 region near ALD locus containing dual specificity phosphatase 9 (DUSP9), ribosomal protein L18a (RPL18a), Ca2+/Calmodulin-dependent protein kinase I (CAMKI), creatine transporter (CRTR), CDM protein (CDM), adrenoleukodystrophy protein >
8412	21381	34787	0.51	3.0E-13	AA352487.1	EST_HUMAN	EST60487 Activated T-cells XX Homo sapiens cDNA 5' end similar to similar to serine protease P100, Ra-reactive factor
8412	21381	34788	0.51	3.0E-13	AA352487.1	EST_HUMAN	EST60487 Activated T-cells XX Homo sapiens cDNA 5' end similar to similar to serine protease P100, Ra-reactive factor
10558	23480	36975	0.46	3.0E-13	AW935487.1	EST_HUMAN	RC2-DT0007-110100-014-g10 DT0007 Homo sapiens cDNA
11036	24000		2.68	3.0E-13	AJ084768.1	EST_HUMAN	HA0536 Human fetal liver cDNA library Homo sapiens cDNA
11385	24332	37861	3.32	3.0E-13	BE063509.1	EST_HUMAN	CM0-BT0281-031199-087-a03 BT0281 Homo sapiens cDNA
11924	24805	38398	1.54	3.0E-13	AL163248.2	NT	Homo sapiens chromosome 21 segment HS21C048
151	13254	26183	3.93	2.0E-13	U52111.2	NT	Homo sapiens X28 region near ALD locus containing dual specificity phosphatase 9 (DUSP9), ribosomal protein L18a (RPL18a), Ca2+/Calmodulin-dependent protein kinase I (CAMKI), creatine transporter (CRTR), CDM protein (CDM), adrenoleukodystrophy protein >
1275	14310	27271	7.14	2.0E-13	AF239710.1	NT	Homo sapiens DNA polymerase delta small subunit (POLD2) gene, exons 1 through 11 and complete cds
3294	16347	29267	1.08	2.0E-13	BF431899.1	EST_HUMAN	nab7805.x1 Scores_NSIF_F8_gw_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE: 3'
3518	16564	29489	1.25	2.0E-13	AF109907.1	NT	Homo sapiens S164 gene, partial cds; PS1 and hypothetical protein genes, complete cds; and S171 gene, partial cds

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4135	17167		1.61	2.0E-13	AL163278.2	NT	Homo sapiens chromosome 21 segment HS21C078
6245	19318	32548	4.71	2.0E-13	Q06852	SWISSPROT	CELL SURFACE GLYCOPROTEIN 1 PRECURSOR (OUTER LAYER PROTEIN B) (S-LAYER PROTEIN 1)
6987	20210	33538	6.49	2.0E-13	X16912.1	NT	Human PFKL gene for liver-type 6-phosphofructokinase (EC 2.7.1.11) exon 2
7255	19990	33287	0.59	2.0E-13	10835072	NT	Homo sapiens N-myristoyltransferase 1 (NMT1), mRNA
7255	19990	33288	0.59	2.0E-13	10835072	NT	Homo sapiens N-myristoyltransferase 1 (NMT1), mRNA
10824	23745	37246	4.53	2.0E-13	5031898	NT	Homo sapiens mab-21 [C. elegans]-like 1 (MAB21L1) mRNA
12387	25185		5.43	2.0E-13	AW892155.1	EST_HUMAN	CMD-NN0001-100300-274-e11 NN0001 Homo sapiens cDNA
291	13385	26312	1.49	1.0E-13	S74129.1	NT	FGF-1-fibroblast growth factor 1 [human, kidney, Genomic, 342 nt, segment 2 of 2]
889	13944	26902	4.85	1.0E-13	AJ007073.1	NT	Homo sapiens LGMD2B gene
1339	14373	27343	1.39	1.0E-13	X87344.1	NT	H. sapiens DNA, DMBS, HLA-Z1, IPP2, LMP2, TAP1, LMP7, TAP2, DOB, DOB2 and RING8, 9, 13 and 14 genes
2037	15056	28074	2.43	1.0E-13	AA720574.1	EST_HUMAN	nm21g02.s1 NCL_CGAP_GCB0 Homo sapiens cDNA clone IMAGE:1241138 3' similar to contains THR.13 THR repetitive element;
4623	17644	30532	2.2	1.0E-13	BF340987.1	EST_HUMAN	602038009F1 NCL_CGAP_Bm64 Homo sapiens cDNA clone IMAGE:4189968 5'
6586	19646	32915	0.61	1.0E-13	AA090732.1	EST_HUMAN	y1535.seq.F Human fetal heart, Lambda ZAP Express Homo sapiens cDNA 5'
8242	21211	34616	0.78	1.0E-13	AA577812.1	EST_HUMAN	nm24d01.s1 NCL_CGAP_Gas1 Homo sapiens cDNA clone IMAGE:1084801 3' similar to contains Alu repetitive element; contains element MER24 repetitive element;
8242	21211	34617	0.78	1.0E-13	AA577812.1	EST_HUMAN	nm24d01.s1 NCL_CGAP_Gas1 Homo sapiens cDNA clone IMAGE:1084801 3' similar to contains Alu repetitive element; contains element MER24 repetitive element;
10450	23372		0.82	1.0E-13	O16481	SWISSPROT	MELANOMA-ASSOCIATED ANTIGEN B4 (MAGE-B4 ANTIGEN)
10664	23586	37084	0.49	1.0E-13	AF300701.1	NT	Mus musculus osteofesticular protein tyrosine phosphatase mRNA, complete cds
11707	24672	38249	10.13	1.0E-13	BF108755.1	EST_HUMAN	7145e10.x1 Soares_NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:3524443 3' similar to contains MER29.b2 MER29 repetitive element;
12206	25048		2.34	1.0E-13	AV715377.1	EST_HUMAN	AV715377 DOB Homo sapiens cDNA clone DOBAIE03 5'
12844	25454		3.21	1.0E-13	AJ271735.1	NT	Homo sapiens Xq pseudautosomal region, segment 1/2
333	13422	26345	3.14	9.0E-14	AA781159.1	EST_HUMAN	aj24c01.s1 Soares_testis_NHT Homo sapiens cDNA clone 1391232 3' similar to contains MER19.11 MER19 repetitive element;
334	13423	26346	2.37	9.0E-14	AA781159.1	EST_HUMAN	aj24c01.s1 Soares_testis_NHT Homo sapiens cDNA clone 1391232 3' similar to contains MER19.11 MER19 repetitive element;
2508	15511		4.8	9.0E-14	AW861577.1	EST_HUMAN	RC4-CT0322-080100-013-c09 CT0322 Homo sapiens cDNA
2597	15598	28617	1.03	9.0E-14	AJ133127.1	NT	Homo sapiens mRNA for sodium-glucose cotransporter (SGLT2 gene)
2597	15598	28618	1.03	9.0E-14	AJ133127.1	NT	Homo sapiens mRNA for sodium-glucose cotransporter (SGLT2 gene)
2764	15756	28777	6.94	9.0E-14	AB038182.1	NT	Homo sapiens TFF gene cluster for trefoil factor, complete cds

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3128	16185	26094	5.43	9.0E-14	AW513296.1	EST_HUMAN	xc54h06.x1 NCI_CGAP_U1t Homo sapiens cDNA clone IMAGE:2707833 3'
3252	13422	26345	0.67	9.0E-14	AA781159.1	EST_HUMAN	aj24c01.s1 Soares_testis_NHT Homo sapiens cDNA clone 1397232 3' similar to contains MER19.11 MER19
3811	16861	29759	7.16	9.0E-14	D14547.1	NT	repetitive element ;
4789	17807	30699	1.68	9.0E-14	AJ002153.1	NT	Human DNA, SINE repetitive element
3509	16555		1.44	8.0E-14	BE469263.1	EST_HUMAN	Sagittarius oedipus gene for seminal vesicle secreted protein semenogelin I
3978	17018		3.46	8.0E-14	R76289.1	EST_HUMAN	hz71c09.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3213424 3'
9803	21126	34530	21.45	8.0E-14	X89211.1	NT	y72e03.r1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:144796 3'
9918	22738	36192	3.1	8.0E-14	AA210316.1	EST_HUMAN	zq17c10.s1 Stratagene fetal retina 937202 Homo sapiens cDNA clone IMAGE:629970 3'
11762	24690		1.52	8.0E-14	BE062598.1	EST_HUMAN	QV2.BT0258-281099-074-a01 BT0258 Homo sapiens cDNA
12590	25294	31783	2.99	8.0E-14	A1688118.1	EST_HUMAN	we92108.x1 NCI_CGAP_Co3 Homo sapiens cDNA clone IMAGE:2328143 3'
1633	15873		3.99	7.0E-14	AW151673.1	EST_HUMAN	x67e10.x1 NCI_CGAP_Gas4 Homo sapiens cDNA clone IMAGE:2623146 3' similar to contains MER10.12
9272	22238		0.51	7.0E-14	AL163285.2	NT	repetitive element ;
						NT	Homo sapiens chromosome 21 segment HS21C085
367	13453	26381	16.94	6.0E-14	AF020503.1	NT	Homo sapiens FRA3B common fragile region, diadenosine triphosphate hydrolase (FHIT) gene, exon 5
10181	23106	36587	2.54	6.0E-14	AF020503.1	NT	Homo sapiens FRA3B common fragile region, diadenosine triphosphate hydrolase (FHIT) gene, exon 5
10181	23106	36588	2.54	6.0E-14	AF020503.1	NT	Homo sapiens FRA3B common fragile region, diadenosine triphosphate hydrolase (FHIT) gene, exon 5
620	13685	26603	5.23	5.0E-14	Q63120	SWISSPROT	CANALICULAR MULTISPECIFIC ORGANIC ANION TRANSPORTER 1 (MULTIDRUG RESISTANCE-ASSOCIATED PROTEIN 2) (CANALICULAR MULTIDRUG RESISTANCE PROTEIN)
3683	16728		0.95	5.0E-14	AL163247.2	NT	Homo sapiens chromosome 21 segment HS21C047
5093	18103	30979	1.39	5.0E-14	AW073791.1	EST_HUMAN	x003b05.x1 NCI_CGAP_GU1 Homo sapiens cDNA clone IMAGE:2576185 3' similar to contains L1.12 L1
5611	18707	31864	4.84	5.0E-14	P08547	SWISSPROT	repetitive element ;
1125	16859		1.95	4.0E-14	P04928	SWISSPROT	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG
1895	14920	27916	7	4.0E-14	AJ007973.1	NT	S-ANTIGEN PROTEIN PRECURSOR
3765	16807		1	4.0E-14	AA046502.1	EST_HUMAN	Homo sapiens LGMD2B gene
4320	17349	30233	0.96	4.0E-14	N46328.1	EST_HUMAN	z667a06.r1 Soares_pregnant_uterus_NbHPU Homo sapiens cDNA clone IMAGE:467858 5'
8291	21260		0.6	4.0E-14	X87344.1	NT	y773c12.s1 Soares_multiple_sclerosis_2NbHWP Homo sapiens cDNA clone IMAGE:279190 3' similar to contains L1.13 L1 repetitive element ;
						NT	H. sapiens DMA, DMB, HLA-Z1, IPP2, LMP2, TAP1, LMP7, TAP2, DOB, DOB2 and RING8, 9, 13 and 14 genes

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12905	25988		6.38	4.0E-14	AI886224.1	EST_HUMAN	wm08d03.x1 NCL CGAP_U14 Homo sapiens cDNA clone IMAGE:2435332 3' similar to contains Alu repetitive element;
950	14003	26955	4.69	3.0E-14	X95466.1	NT	R.norvegicus mRNA for CPG2 protein
4963	17978	30868	1.16	3.0E-14	7656864	NT	Homo sapiens a disintegrin and metalloproteinase domain 28 (ADAM28), mRNA
6898	19950	33246	0.96	3.0E-14	AI420786.1	EST_HUMAN	fa91c12.x1 NCL CGAP_P128 Homo sapiens cDNA clone IMAGE:2094070 3' similar to TR:O00519 O00519 FATTY ACID AMIDE HYDROLASE. ;
6898	19950	33247	0.96	3.0E-14	AI420786.1	EST_HUMAN	fa91c12.x1 NCL CGAP_P128 Homo sapiens cDNA clone IMAGE:2094070 3' similar to TR:O00519 O00519 FATTY ACID AMIDE HYDROLASE. ;
7021	25675		0.51	3.0E-14	AL163248.2	NT	Homo sapiens chromosome 21 segment HS21C048
7229	20251	33585	0.57	3.0E-14	AA386311.1	EST_HUMAN	EST185054 Brain IV Homo sapiens cDNA
9139	22105	35531	0.83	3.0E-14	NA2165.1	EST_HUMAN	y07b10.11 Soares melanocyte 2N6HM Homo sapiens cDNA clone IMAGE:270523 5'
11337	24287	37811	2.83	3.0E-14	BE886016.1	EST_HUMAN	601511530F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3913087 5'
11568	18347	31293	6.06	3.0E-14	AW265354.1	EST_HUMAN	xp45f12.x1 NCL CGAP_HN11 Homo sapiens cDNA clone IMAGE:2743343 3' similar to contains Alu repetitive element; contains element MER9 repetitive element ;
12824	25854		1.68	3.0E-14	AL163285.2	NT	Homo sapiens chromosome 21 segment HS21C085
390	13465	26395	2.76	2.0E-14	AJ271736.1	NT	Homo sapiens Xq pseudautosomal region, segment 2/2
390	13465	26396	2.76	2.0E-14	AJ271736.1	NT	Homo sapiens Xq pseudautosomal region, segment 2/2
691	15847	26682	9.98	2.0E-14	AL163303.2	NT	Homo sapiens chromosome 21 segment HS21C103
2397	15404		1.89	2.0E-14	AW372868.1	EST_HUMAN	RC5-BT0377-091289-031-D12 BT0377 Homo sapiens cDNA
2472	15476		1.4	2.0E-14	7657529	NT	Homo sapiens rhabdoid tumor deletion region protein 1 (RTDR1), mRNA
2531	15534	28554	2.2	2.0E-14	AL163209.2	NT	Homo sapiens chromosome 21 segment HS21C009
2547	15548		1.03	2.0E-14	BE222432.1	EST_HUMAN	h960g10.x1 NCL CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3180738 3' similar to contains Alu repetitive element; contains OFR.t1 OFR repetitive element ;
2683	16679		1.48	2.0E-14	P06548	SWISSPROT	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG
5602	18698	31669	0.91	2.0E-14	BF380661.1	EST_HUMAN	IL2-UT0072-240800-142-D07 UT0072 Homo sapiens cDNA
5702	18797	31972	0.81	2.0E-14	AI312351.1	EST_HUMAN	ta78n01.x2 NCL CGAP_HSC2 Homo sapiens cDNA clone IMAGE:2050225 3' similar to contains L1.13 L1 repetitive element ;
5809	18899	32082	3.16	2.0E-14	U01317.1	NT	Human beta globin region on chromosome 11
7067	20089		0.92	2.0E-14	BE000550.1	EST_HUMAN	RC3-BN0072-240200-011-a08 BN0072 Homo sapiens cDNA
7290	20262	33596	0.57	2.0E-14	4585709	NT	Homo sapiens a disintegrin and metalloproteinase domain 11 (ADAM11), mRNA
7502	20487	33528	0.87	2.0E-14	P56163	SWISSPROT	ZINC-FINGER PROTEIN NEURO-D4
7751	20704	34072	21.51	2.0E-14	BE158761.1	EST_HUMAN	IL2-HT0397-071289-024-D04 HT0397 Homo sapiens cDNA
7751	20704	34073	21.51	2.0E-14	BE158761.1	EST_HUMAN	IL2-HT0397-071289-024-D04 HT0397 Homo sapiens cDNA

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10277	23202	36687	0.52	2.0E-14	AI978795.1	EST_HUMAN	vr59g10.x1 NCI_CGAP_U11 Homo sapiens cDNA clone IMAGE:2492034 3' similar to contains Alu repetitive element
10783	23704	37203	0.53	2.0E-14	AV741648.1	EST_HUMAN	AV741648 CB Homo sapiens cDNA clone CBFBBF04 5'
11133	24093	37622	3.94	2.0E-14	AW139800.1	EST_HUMAN	UIH-B11-adv-a-10-0-UI.s1 NCI_CGAP_Sub3 Homo sapiens cDNA clone IMAGE:2718234 3'
12822	25857		1.71	2.0E-14	AF008191.1	NT	Homo sapiens putative G6 protein (GR6) gene, complete cds
1068	14113	27063	2.09	1.0E-14	AL163246.2	NT	Homo sapiens chromosome 21 segment HS21C046
1405	14438	27406	8.16	1.0E-14	AL163268.2	NT	Homo sapiens chromosome 21 segment HS21C068
1405	14438	27407	8.16	1.0E-14	AL163268.2	NT	Homo sapiens chromosome 21 segment HS21C068
2017	15038	28049	15.42	1.0E-14	L44140.1	NT	Homo sapiens chromosome X region from filamin (FLN) gene to glucose-6-phosphate dehydrogenase (G6PD) gene, complete cds's
2195	15210	28228	5.77	1.0E-14	AL163303.2	NT	Homo sapiens chromosome 21 segment HS21C103
2419	15426	28449	5.29	1.0E-14	AF001689.1	NT	Homo sapiens ribosomal protein L23A (RPL23A) gene, complete cds
2955	16013	28940	1.05	1.0E-14	P05227	SWISSPROT	HISTIDINE-RICH PROTEIN PRECURSOR (CLONE PFHRP-II)
3182	16237	29154	6.2	1.0E-14	BF33527.1	EST_HUMAN	RC2-CT0432-310700-013-a09_1 CT0432 Homo sapiens cDNA
3182	16237	29155	6.2	1.0E-14	BF33527.1	EST_HUMAN	RC2-CT0432-310700-013-a09_1 CT0432 Homo sapiens cDNA
3901	16941	29852	1.75	1.0E-14	AA682994.1	EST_HUMAN	ae89c12.s1 Stralagene schizo brain S11 Homo sapiens cDNA clone IMAGE:971350 3'
4500	17525	30410	2.07	1.0E-14	AW275852.1	EST_HUMAN	xq39h10.x1 NCI_CGAP_Luz28 Homo sapiens cDNA clone IMAGE:2753059 3'
5907	18993	32184	2.1	1.0E-14	AF128145.1	NT	Bos taurus xenobiotic/medium-chain fatty acid:CoA ligase form XL-III mRNA, nuclear mRNA encoding mitochondrial protein, complete cds
6831	25669	33178	11.02	1.0E-14	11437150	NT	Homo sapiens prominin (mouse)-like 1 (PROML1), mRNA
6831	25669	33177	11.02	1.0E-14	11437150	NT	Homo sapiens prominin (mouse)-like 1 (PROML1), mRNA
1579	14612	27584	1.78	9.0E-15	7427522	NT	Homo sapiens protein tyrosine phosphatase, receptor type, T (PTPRT), mRNA
2183	15198		1.37	9.0E-15	AF106779.1	NT	JM10 protein, A4 differentiation-dependent protein, triple LIM domain protein 6, and synaptophysin genes, complete cds; and L-type calcium channel a2
7738	20693	34056	4.28	9.0E-15	P21416	SWISSPROT	GAG POLYPROTEIN [CONTAINS: CORE PROTEINS P15, P12, P30, P10]
8350	21319	34733	1.17	9.0E-15	BE903559.1	EST_HUMAN	601677750F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3960156 5'
2822	13553		1.42	8.0E-15	BE261482.1	EST_HUMAN	601148632F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:3164023 5'
7387	20356	33708	1.55	7.0E-15	BF035327.1	EST_HUMAN	601458531F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3862066 5'
10801	23722		2.45	7.0E-15	AW241958.1	EST_HUMAN	xn7f402.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2700483 3' similar to contains THR12 THR repetitive element;
966	14047	27001	6.55	6.0E-15	AJ271738.1	NT	Homo sapiens Xq pseudocytosomal region, segment 2/2
6027	19110	32311	1.11	6.0E-15	X73462.1	NT	O.aries mRNA for hair keratin cysteine-rich protein
6027	19110	32312	1.11	6.0E-15	X73462.1	NT	O.aries mRNA for hair keratin cysteine-rich protein

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
410	13483	26418	5.24	3.0E-15	AL163208.2	NT	Homo sapiens chromosome 21 segment HS21C008
2771	15763	26784	2.05	5.0E-15	U91328.1	NT	Human hereditary haemochromatosis region, histone 2A-like protein gene, hereditary haemochromatosis (HLA-H) gene, RoRet gene, and sodium phosphate transporter (NP13) gene, complete cds
3482	16528		1.08	6.0E-15	AW296817.1	EST_HUMAN	U1-HBW0-ajp-g-10-U1.s1 NCI_CGAP_Sub6 Homo sapiens cDNA clone IMAGE:2731219 3'
11035	23989		2.27	5.0E-15	AV730056.1	EST_HUMAN	AV730056 HTF Homo sapiens cDNA clone HTFAVE06 5'
427	13122	26020	3.54	4.0E-15	AL163303.2	NT	Homo sapiens chromosome 21 segment HS21C103
6822	19876	33165	0.98	4.0E-15	AB007970.1	NT	Homo sapiens mRNA, chromosome 1 specific transcript KIAA0501
11401	21088	34487	1.79	4.0E-15	AJ130894.1	NT	Homo sapiens mRNA for transcription factor
11401	21088	34488	1.79	4.0E-15	AJ130894.1	NT	Homo sapiens mRNA for transcription factor
4245	17274		6.54	3.0E-15	N89452.1	EST_HUMAN	LY1142F Human fetal heart, Lambda ZAP Express Homo sapiens cDNA clone LY1142 5' similar to ANF(CARDIODILATIN)
5057	18077	30958	0.67	3.0E-15	AA078097.1	EST_HUMAN	7P01F03 Chromosome 7 Placental cDNA Library Homo sapiens cDNA clone 7P01F03
5057	18077	30959	0.67	3.0E-15	AA078097.1	EST_HUMAN	7P01F03 Chromosome 7 Placental cDNA Library Homo sapiens cDNA clone 7P01F03
6986	20208		1.27	3.0E-15	Q64625	SWISSPROT	GLUTATHIONE PEROXIDASE RY2D1 PRECURSOR (ODORANT-METABOLIZING PROTEIN RY2D1)
7495	20460	33819	3.66	3.0E-15	M27685.1	NT	Mus musculus ultra high sulfur keratin gene, complete cds
7495	20460	33820	3.66	3.0E-15	M27685.1	NT	Mus musculus ultra high sulfur keratin gene, complete cds
10285	23210		2.66	3.0E-15	AA807128.1	EST_HUMAN	oc36a07.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1351784 3' similar to contains MER19.11
11146	24106	37633	3.42	3.0E-15	AB026898.1	NT	MER19 repetitive element;
250	13347	26273	4.45	2.0E-15	AF223391.1	NT	Homo sapiens DNA, DLEC1 to ORCTL4 gene region, section 1/2 (DLEC1, ORCTL3, ORCTL4 genes, complete cds)
368	13454	26382	4.01	2.0E-15	AF223391.1	NT	Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced
368	13454	26383	4.01	2.0E-15	AF223391.1	NT	Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced
2381	15389	28413	1.02	2.0E-15	BE350127.1	EST_HUMAN	Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced
2381	15389	28414	1.02	2.0E-15	BE350127.1	EST_HUMAN	Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced
4095	17129	30023	1.21	2.0E-15	AW238499.1	EST_HUMAN	Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4853	17874		2.73	2.0E-15	AI080335.1	EST_HUMAN	wf0706.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2349923 3' similar to TR:Q61043 Q61043 NINEIN.;
6306	19377	32616	1.02	2.0E-15	BE662352.1	EST_HUMAN	601344233F1 NIH_MGC_8 Homo sapiens cDNA clone IMAGE:3677268 5'
6308	19377	32617	1.02	2.0E-15	BE662352.1	EST_HUMAN	601344233F1 NIH_MGC_8 Homo sapiens cDNA clone IMAGE:3677268 5'
7321	20292		1.42	2.0E-15	AJ400877.1	NT	Homo sapiens ASOL3 gene, CEGP1 gene, C1orf15 gene, C1orf16 gene and C1orf17 gene
7486	20451	33810	2.64	2.0E-15	AA704195.1	EST_HUMAN	z177ec3.s1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:460924 3'
7825	20585	33948	4.75	2.0E-15	W05084.1	EST_HUMAN	za78d10.r1 Soares_fetal_liver_NbHL19W Homo sapiens cDNA clone IMAGE:298675 5' similar to WP:F44F4.8 CE02227 TRANSPOSASE;
8117	21054	34451	0.67	2.0E-15	AL163247.2	NT	Homo sapiens chromosome 21 segment HS21C047
9257	22223	35653	2.73	2.0E-15	D14547.1	NT	Human DNA, SINE repetitive element
9427	22391	35829	0.74	2.0E-15	AA397768.1	EST_HUMAN	z177g03.r1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:728414 5'
9427	22391	35830	0.74	2.0E-15	AA397768.1	EST_HUMAN	z177g03.r1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:728414 5'
9759	22700	36157	1.19	2.0E-15	AW379465.1	EST_HUMAN	GM0-HT0244-201099-078-at12 HT0244 Homo sapiens cDNA
9759	22700	36158	1.19	2.0E-15	AW379465.1	EST_HUMAN	GM0-HT0244-201099-078-at12 HT0244 Homo sapiens cDNA
11187	24143		4.15	2.0E-15	AJ271735.1	NT	Homo sapiens Xq pseudautosomal region; segment 1/2
12934	18339	31288	3.19	2.0E-15	AF223391.1	NT	Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced
12934	18339	31289	3.19	2.0E-15	AF223391.1	NT	Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced
2785	15777		2.95	1.0E-15	AI689984.1	EST_HUMAN	b26h05.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:2270745 3' similar to TR:Q13539 Q13539 MARINER TRANSPOSASE.;
3025	16082	29005	1.53	1.0E-15	BE043584.1	EST_HUMAN	hk40602.y1 NCI_CGAP_Ov34 Homo sapiens cDNA clone IMAGE:2999162 5'
3168	16214	29129	1.2	1.0E-15	P08547	SWISSPROT	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG
5189	18198	31071	1.11	1.0E-15	AI984928.1	EST_HUMAN	wr86a04.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2494590 3'
6508	19572	32825	1.63	1.0E-15	T96763.1	EST_HUMAN	ye40e10.s1 Soares_fetal_liver_spleen_1NFLS Homo sapiens cDNA clone IMAGE:120234 3' similar to contains MER6 repetitive element;
7205	20229		1.93	1.0E-15	BE074217.1	EST_HUMAN	QV3-BT0569-270100-074-g05 BT0569 Homo sapiens cDNA
7239	16974	33272	0.78	1.0E-15	P39057	SWISSPROT	DYNEIN BETA CHAIN, CILIARY
8574	21542	34962	1.04	1.0E-15	AL163280.2	NT	Homo sapiens chromosome 21 segment HS21C080
8763	21730	35152	4.51	1.0E-15	AJ200976.1	EST_HUMAN	qf68h06.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1755227 3'
8763	21730	35153	4.51	1.0E-15	AJ200976.1	EST_HUMAN	qf68h06.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1755227 3'
9394	22359	35789	0.49	1.0E-15	AL163207.2	NT	Homo sapiens chromosome 21 segment HS21C007
9397	22362	35793	1.5	1.0E-15	4507208	NT	Homo sapiens spermidine synthase (SRM) mRNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9602	22806	36055	0.79	1.0E-15	Q39575	SWISSPROT	DYNEIN GAMMA CHAIN, FLAGELLAR OUTER ARM
9990	22917	36383	0.95	1.0E-15	AA864653.1	EST_HUMAN	oh37c03.s1 NCL_CGAP_Kid6 Homo sapiens cDNA clone IMAGE:145972 3' similar to contains L1.3 L1
11169	24127	37657	4.18	1.0E-15	AF044083.1	NT	repetitive element:
13008	25720	31612	9.25	1.0E-15	AI783944.1	EST_HUMAN	Homo sapiens major histocompatibility locus class III region
4532	17555	30443	1.15	9.0E-16	4503168	NT	element;
11338	24288	37812	1.94	9.0E-16	F08688.1	EST_HUMAN	Homo sapiens cut (Drosophila)-like 1 (CCAAT displacement protein) (CUTL1) mRNA
5796	18878	32060	0.79	7.0E-16	485120	NT	HSC23F051 normalized infant brain cDNA Homo sapiens cDNA clone c-23f05
7564	20527	33885	1.45	7.0E-16	O88807	SWISSPROT	Homo sapiens chemokine (C-C motif) receptor 8 (CCR8) mRNA
7564	20527	33886	1.45	7.0E-16	O88807	SWISSPROT	PROTEIN-ARGININE DEIMINASE TYPE IV (PEPTIDYLARGININE DEIMINASE IV) (PAD-R4)
12957	25809		1.88	7.0E-16	T94149.1	EST_HUMAN	PROTEIN-ARGININE DEIMINASE TYPE IV (PEPTIDYLARGININE DEIMINASE IV) (PAD-R4)
2151	15157		7.77	6.0E-16	AW972811.1	EST_HUMAN	PROTEIN-ARGININE DEIMINASE TYPE IV (PEPTIDYLARGININE DEIMINASE IV) (PAD-R4)
1489	14522	27495	1.28	5.0E-16	AJ251154.1	NT	ye28c12.1 StrataGene lung (#937210) Homo sapiens cDNA clone IMAGE:119062 5'
2689	15685	28702	2.52	5.0E-16	AA992176.1	EST_HUMAN	EST384702 IMAGE resequences, MAGL Homo sapiens cDNA
10414	23336	36821	0.48	5.0E-16	AL163246.2	NT	Mus musculus olfactory receptor cluster, OR37A, OR37B, OR37C, OR37E genes and OR37D pseudogene
11849	24732	38319	2.54	5.0E-16	BF217388.1	EST_HUMAN	ol80c04.s1 Scores, total, fetus, Nb2HF8_gw Homo sapiens cDNA clone IMAGE:1623078 3' similar to
13044	25585		10.88	5.0E-16	11418127	NT	contains element L1 repetitive element:
2249	15263		1.64	4.0E-16	AB001523.1	NT	Homo sapiens chromosome 21 segment HS21C046
2388	15396	28421	2.21	4.0E-16	AW797168.1	EST_HUMAN	607885734F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4104129 5'
2388	15396	28422	2.21	4.0E-16	AW797168.1	EST_HUMAN	Homo sapiens GTP binding protein 1 (GTPBP1), mRNA
3471	16517	29438	3.94	4.0E-16	Q18863	SWISSPROT	Homo sapiens gene for TMEM1 and PWP2, complete and partial cds
4166	17197	30083	4.74	4.0E-16	BE083875.1	EST_HUMAN	QV1-UM0036-200300-115-g02 UN0036 Homo sapiens cDNA
4166	17197	30084	4.74	4.0E-16	BE083875.1	EST_HUMAN	QV1-UM0036-200300-115-g02 UN0036 Homo sapiens cDNA
7980	20919	34310	37.37	4.0E-16	AL163384.2	NT	MYELIN-OLIGODENDROCYTE GLYCOPROTEIN PRECURSOR
9650	22594	36042	0.97	4.0E-16	11423191	NT	PM4-BT0650-010400-002-g09 BT0650 Homo sapiens cDNA
12290	25106		2.41	4.0E-16	P08548	SWISSPROT	PM4-BT0650-010400-002-g09 BT0650 Homo sapiens cDNA
12392	25169	31816	2.11	4.0E-16		NT	Homo sapiens chromosome 21 segment HS21C084
12656	25336		1.36	4.0E-16	R18591.1	EST_HUMAN	Homo sapiens hypothetical protein FLJ10024 (FLJ10024), mRNA
133	13238	28169	1.24	3.0E-16	AW022862.1	EST_HUMAN	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG
						SWISSPROT	Homo sapiens Gb2-associated binder 2 (KIAA0571), mRNA
						NT	y96b11.1 Scores infant brain 1N1B Homo sapiens cDNA clone IMAGE:30489 5'
						EST_HUMAN	d145c01.y1 Morton Fetal Cochlea Homo sapiens cDNA clone IMAGE:2486376 5'

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
133	13238	26170	1.24	3.0E-16	AW022862.1	EST_HUMAN	df45c01.y1 Morton Fetal Cochlea Homo sapiens cDNA clone IMAGE:2486376 5'
466	13539		1.91	3.0E-16	AL046445.1	EST_HUMAN	DKFZp434P037.1 434 (synonym: htes3) Homo sapiens cDNA clone DKFZp434P037 5'
476	13548		3.08	3.0E-16	AF135446.1	NT	Homo sapiens TSX (TSX) pseudogene, exon 5
1446	14479	27455	1.53	3.0E-16	Q28983	SWISSPROT	ZONADHESIN PRECURSOR
2988	16046	28966	3.94	3.0E-16	P03200	SWISSPROT	ENVELOPE GLYCOPROTEIN GP340 (MEMBRANE ANTIGEN) (MA) [CONTAINS: GLYCOPROTEIN GP220]
3953	16993	28909	0.96	3.0E-16	T08189.1	EST_HUMAN	EST06060 Infant Brain, Berto Soares Homo sapiens cDNA clone HIBBA13 5' end
3980	17020		0.77	3.0E-16	AF020503.1	NT	Homo sapiens FRA3B common fragile region, diadenosine triphosphate hydrolase (FHT) gene, exon 5
3981	17021		1.06	3.0E-16	U03887.1	NT	Human BXP20 gene
5350	18455		1.11	3.0E-16	AA077225.1	EST_HUMAN	7B10F02 Chromosome 7 Fetal Brain cDNA Library Homo sapiens cDNA clone 7B10F02
5698	18793	31966	1.2	3.0E-16	AF003529.1	NT	Homo sapiens glypican 3 (GPC3) gene, partial cds and flanking repeat regions
9005	21971	35392	4.92	3.0E-16	AI002836.1	EST_HUMAN	am98h05.s1 Stragene schizo brain S11 Homo sapiens cDNA clone IMAGE:1684185 3' similar to contains THR.b2 THR repetitive element:
10250	23175		0.9	3.0E-16	BF690617.1	EST_HUMAN	602246538F1 NIH_MGC 62 Homo sapiens cDNA clone IMAGE:4332032 5'
10478	23400	36897	5.77	3.0E-16	L78810.1	NT	Homo sapiens ADP/ATP carrier protein (ANT-2) gene, complete cds
13079	25981	31317	1.4	3.0E-16	AL043288.2	EST_HUMAN	DKFZp434L1623.1 434 (synonym: htes3) Homo sapiens cDNA clone DKFZp434L1623 5'
973	14025		1.04	2.0E-16	AL163279.2	NT	Homo sapiens chromosome 21 segment HS21C079
2395	15402		1.32	2.0E-16	AA621781.1	EST_HUMAN	af06c04.s1 Soares testis_NHT Homo sapiens cDNA clone IMAGE:1030855 3'
2699	15695		1.26	2.0E-16	J03061.1	NT	Human SSAN-related endogenous retroviral L TR-like element
4207	17236	30123	1.74	2.0E-16	X89211.1	NT	H. sapiens DNA for endogenous retroviral like element
6905	19957	33254	0.83	2.0E-16	Q31125	SWISSPROT	HISTIDINE-RICH PROTEIN KE4
7884	20923	34316	1.4	2.0E-16	AI470723.1	EST_HUMAN	tf16e11.x1 NCL_CGAP_Gas4 Homo sapiens cDNA clone IMAGE:2141708 3' similar to contains element MER33 repetitive element:
8300	21269	34881	1.86	2.0E-16	AI732837.1	EST_HUMAN	n24706.x5 NCL_CGAP_P12 Homo sapiens cDNA clone IMAGE:1290947 similar to TR:O54849 O54849 HYPOTHETICAL 42.9 KD PROTEIN. [2] TR:O08905 contains MER7.1 MER7 repetitive element;
8498	21466	34882	0.73	2.0E-16	BE858026.1	EST_HUMAN	782h09.x1 NCL_CGAP_P28 Homo sapiens cDNA clone IMAGE:3303521 3'
8498	21468	34883	0.73	2.0E-16	BE858026.1	EST_HUMAN	782h09.x1 NCL_CGAP_P28 Homo sapiens cDNA clone IMAGE:3303521 3'
8872	21839	35261	0.75	2.0E-16	AW877214.1	EST_HUMAN	GM4-PT0034-180200-506-a01 PT0034 Homo sapiens cDNA
8872	21839	35262	0.75	2.0E-16	AW877214.1	EST_HUMAN	GM4-PT0034-180200-506-a01 PT0034 Homo sapiens cDNA
11274	24226	37752	1.58	2.0E-16	5902145	NT	Homo sapiens ubiquitin carrier protein E2-C (UBCH10), mRNA
186	13286	26210	2.57	1.0E-16	AF200719.1	NT	Homo sapiens pituitary tumor transforming gene protein (PTTG) gene, complete cds

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
382	13495		37.96	1.0E-16	AA628592.1	EST_HUMAN	af39g11.s1 Soares_total_fetus_Nb2HF8_9w Homo sapiens cDNA clone IMAGE:1034084 3' similar to contains OFR.12 OFR repetitive element;
1988	15009	28014	2.22	1.0E-16	BF327942.1	EST_HUMAN	QV0-BN0148-070700-283-at10 BN0148 Homo sapiens cDNA
5810	18900	32083	0.68	1.0E-16	AF163894.1	NT	Homo sapiens SNCA isoform (SNCA) gene, complete cds, alternatively spliced
6574	19634		25.8	1.0E-16	U45983.1	NT	Homo sapiens CCR8 chemokine receptor (CMKBR8) gene, complete cds
6726	19782	33061	3.06	1.0E-16	Q02779	SWISSPROT	MITOGEN-ACTIVATED PROTEIN KINASE KINASE 10 (MIXED LINEAGE KINASE 2) (PROTEIN KINASE MST)
7802	19634		6.75	1.0E-16	U45983.1	NT	Homo sapiens CCR8 chemokine receptor (CMKBR8) gene, complete cds
9638	22592	36031	1.06	1.0E-16	AW875661.1	EST_HUMAN	QV2-P10012-040400-124-e05 P10012 Homo sapiens cDNA
3751	16793	29704	2.77	9.0E-17	AW900048.1	EST_HUMAN	GM1-NN1003-200300-153-e01 NN1003 Homo sapiens cDNA
6886	19938		2.35	9.0E-17	AI322964.1	EST_HUMAN	tg22e11.x1 NCL_CGAP_CLL1 Homo sapiens cDNA clone IMAGE:2109524 3' similar to contains MER28.12 MER28 repetitive element;
8445	21414		5.47	9.0E-17	AW150257.1	EST_HUMAN	xg49g12.x1 NCL_CGAP_Ut1 Homo sapiens cDNA clone IMAGE:2630350 3' similar to contains OFR.12 OFR repetitive element;
10584	23506		2.3	9.0E-17	AF200719.1	NT	Homo sapiens pituitary tumor transforming gene protein (PTTG) gene, complete cds
1020	14066		2.01	8.0E-17	AW880701.1	EST_HUMAN	QV0-OT0032-080300-155-d01 OT0032 Homo sapiens cDNA
3907	16947		0.88	8.0E-17	AL163280.2	NT	Homo sapiens chromosome 21 segment HS21C080
5663	25642	31927	3.24	8.0E-17	BE172081.1	EST_HUMAN	MR0-HT0559-060300-003-e04 HT0559 Homo sapiens cDNA
7490	20455		1.82	8.0E-17	AV730759.1	EST_HUMAN	AV730759 HTF Homo sapiens cDNA clone HTFAQB07 5'
8019	20956	34349	0.54	8.0E-17	6753651	NT	Mus musculus dynein, exon, heavy chain 11 (Dnahc11), mRNA
1452	14485		2.63	7.0E-17	6753097	NT	Mus musculus apolipoprotein B editing complex 2 (ApoBec2), mRNA
5396	18499		3.14	7.0E-17	AF216650.1	NT	Homo sapiens putative MTAP (MTAP) mRNA, partial cds, alternatively spliced
8845	19898	33193	7.34	7.0E-17	AF229843.1	NT	Mus musculus WNT-2 gene, partial cds; putative ankyrin-related protein and cystic fibrosis transmembrane conductance regulator (CFTR) genes, section 1 of 2 of the complete cds, and unknown gene
204	13305	26234	6.62	6.0E-17	AW983880.1	EST_HUMAN	RC1-HN0003-220300-021-e04 HN0003 Homo sapiens cDNA
6446	19511	32761	1.8	6.0E-17	AW662772.1	EST_HUMAN	h181d04.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2878695 3' similar to contains L1.12 L1 repetitive element;
10655	23577	37074	0.54	6.0E-17	P20138	SWISSPROT	MYELOID CELL SURFACE ANTIGEN CD33 PRECURSOR (GP67)
10926	23946		0.46	6.0E-17	W92331.1	EST_HUMAN	ze15h03.s1 Soares_fetal_heart_NbHH19W Homo sapiens cDNA clone IMAGE:359093 3'
421	13116	28014	3.22	5.0E-17	T64110.1	EST_HUMAN	ycc5h08.r1 StrataGene lung (#837210) Homo sapiens cDNA clone IMAGE:79839 5'
7840	20787	34162	1.76	5.0E-17	T81043.1	EST_HUMAN	y028b04.r1 Soares_fetal_liver_spleen_1NFLS Homo sapiens cDNA clone IMAGE:109327 5'
9717	22745	36198	1.24	4.0E-17	AW129165.1	EST_HUMAN	xz20e04.x1 NCL_CGAP_Kid8 Homo sapiens cDNA clone IMAGE:2618622 3' similar to contains Alu repetitive element; contains MER19.b1 MER19 repetitive element;

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Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
11821	24704	38286	1.96	4.0E-17	AL163247.2	NT	Homo sapiens chromosome 21 segment HS21C047
12303	25114		2.02	4.0E-17	AI073546.1	EST_HUMAN	ov45a04.x1 Scarses_testis_NHT Homo sapiens cDNA clone IMAGE:1640286 3' similar to TR:Q16530
1480	14523		1.72	3.0E-17	D14547.1	NT	Q16530 PMS3 MRNA, contains MER10.12 MER10 repetitive element;
2108	15125	28144	1.22	3.0E-17	AW110123.1	EST_HUMAN	Human DNA, SINE repetitive element
3208	16263		1.66	3.0E-17	P35410	SWISSPROT	xd89c09.x1 Scarses_NFL_I_GBC_S1 Homo sapiens cDNA clone IMAGE:2604784 3'
3656	16699	29614	1.33	3.0E-17	BE326522.1	EST_HUMAN	MAS-RELATED G PROTEIN-COUPLED RECEPTOR MRG
3656	16699	29615	1.33	3.0E-17	BE326522.1	EST_HUMAN	hw05b04.x1 NCL_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3181999 3'
5068	18078		1.17	3.0E-17	BF511266.1	EST_HUMAN	hw05b04.x1 NCL_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3181999 3'
							UI-H-B14-aq-c-06-0-UJ.s1 NCL_CGAP_Sub8 Homo sapiens cDNA clone IMAGE:3085043 3'
							zat14b02.s1 Scarses fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:292491 3' similar to contains
8611	21579	34995	1.16	3.0E-17	N68451.1	EST_HUMAN	PTR5.13 PTR5 repetitive element;
							Homo sapiens DNA, DLEC1 to ORCTL4 gene region, section 1/2 (DLEC1, ORCTL3, ORCTL4 genes, complete cds)
10060	22987	36455	4.84	3.0E-17	AB028898.1	NT	
10746	23698	37164	0.73	3.0E-17	BF327012.1	EST_HUMAN	QV3-BN0047-270700-283-at12 BN0047 Homo sapiens cDNA
10746	23698	37165	0.73	3.0E-17	BF327012.1	EST_HUMAN	QV3-BN0047-270700-283-at12 BN0047 Homo sapiens cDNA
12266	25089		3.31	3.0E-17	11417966	NT	Homo sapiens SEC14 (S. cerevisiae)-like 2 (SEC14L2), mRNA
353	13442	26367	3.4	2.0E-17	AI270080.1	EST_HUMAN	q163a08.x1 NCL_CGAP_Eso2 Homo sapiens cDNA clone IMAGE:1859922 3' similar to contains Alu repetitive element;
354	13442	26367	3.97	2.0E-17	AI270080.1	EST_HUMAN	q163a08.x1 NCL_CGAP_Eso2 Homo sapiens cDNA clone IMAGE:1859922 3' similar to contains Alu repetitive element;
990	14042		2.04	2.0E-17	AA722892.1	EST_HUMAN	zg81a04.s1 Scarses_fetal_heart_NBH18W Homo sapiens cDNA clone IMAGE:389751 3'
2453	15458	28479	2.3	2.0E-17	Q28983	SWISSPROT	ZONADHESIN PRECURSOR
2453	15458	28480	2.3	2.0E-17	Q28983	SWISSPROT	ZONADHESIN PRECURSOR
2941	15999	28922	6.23	2.0E-17	P12036	SWISSPROT	NEUROFILAMENT TRIPLET H PROTEIN (200 KDA NEUROFILAMENT PROTEIN) (NEUROFILAMENT HEAVY POLYPEPTIDE) (NF-H)
5440	18542	31452	1.8	2.0E-17	M27695.1	NT	Mus musculus ultra high sulfur keratin gene, complete cds
5440	18542	31453	1.8	2.0E-17	M27695.1	NT	Mus musculus ultra high sulfur keratin gene, complete cds
6395	19463		1.99	2.0E-17	AF055086.1	NT	Homo sapiens MHC class 1 region
6638	19696		1.66	2.0E-17	AL134891.1	EST_HUMAN	DKFZp762J0610_r1.762 (synonym: hmel2) Homo sapiens cDNA clone DKFZp762J0610 5'
8193	21070	34468	0.85	2.0E-17	AB037839.1	NT	Homo sapiens mRNA for KIAA1418 protein, partial cds
8420	21399	34799	1.47	2.0E-17	Q95166	SWISSPROT	OLFACTORY RECEPTOR-LIKE PROTEIN OLF3
8800	21767	35191	1.29	2.0E-17	AA300640.1	EST_HUMAN	EST13504 Testis tumor Homo sapiens cDNA 5' end similar to similar to glycogenin
10228	23133	36643	2.35	2.0E-17	BE298888.1	EST_HUMAN	600944690F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:2960615 5'
10264	23189	36673	2.83	2.0E-17	AL163247.2	NT	Homo sapiens chromosome 21 segment HS21C047

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10264	23189	36674	2.83	2.0E-17	AL163247.2	NT	Homo sapiens chromosome 21 segment HS21C047
10622	23544	37044	5.23	2.0E-17	D13391.1	NT	Human CYP19 gene for aromatase cytochrome P-450, promoter region (containing two cis-acting transcriptional regulatory elements)
10745	23667	37162	0.66	2.0E-17	P98063	SWISSPROT	BONE MORPHOGENETIC PROTEIN 1 PRECURSOR (BMP-1)
10745	23667	37163	0.66	2.0E-17	P98063	SWISSPROT	BONE MORPHOGENETIC PROTEIN 1 PRECURSOR (BMP-1)
10772	23693	37190	0.57	2.0E-17	AI798902.1	EST_HUMAN	w694504.x1 Scores_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2348719 3'
10772	23693	37191	0.57	2.0E-17	AI798902.1	EST_HUMAN	w694504.x1 Scores_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2348719 3'
12366	25153		1.31	2.0E-17	AF213884.1	NT	Homo sapiens nuclear factor of kappa light polypeptide gene enhancer in B-cells 1 (NFKB1) gene, complete cds
751	13512	26755	3.24	1.0E-17	P08183	SWISSPROT	MULTIDRUG RESISTANCE PROTEIN 1 (P-GLYCOPROTEIN 1)
1721	14751		1.35	1.0E-17	AJ271736.1	NT	Homo sapiens Xq pseudautosomal region, segment 2/2
1782	14811	27797	4.54	1.0E-17	AL163207.2	NT	Homo sapiens chromosome 21 segment HS21C007
2124	15141	28158	1.95	1.0E-17	P02461	SWISSPROT	COLLAGEN ALPHA 1(III) CHAIN PRECURSOR
2343	15353	28374	2.43	1.0E-17	U79410.1	NT	Homo sapiens thrombospondin 2 (THBS2) gene, promoter region and exons 1A and 1B
3581	16626		1.05	1.0E-17	AF224569.1	NT	Homo sapiens mannosidase, beta A, lysosomal (MANBA) gene, and ubiquitin-conjugating enzyme E2D 3 (UBE2D3) genes, complete cds
4162	17183		8.5	1.0E-17	R09942.1	EST_HUMAN	y93067.r1 Scores_fetal liver spleen tNfLS Homo sapiens cDNA clone IMAGE:128388 5'
5600	19650		0.68	1.0E-17	AW468468.1	EST_HUMAN	h638605.x1 NCL_CGAP_CVL1 Homo sapiens cDNA clone IMAGE:2921312 3' similar to contains Alu repetitive element/contains LTR8.1 LTR8 repetitive element;
6809	19863	33151	1.73	1.0E-17	AI185642.1	EST_HUMAN	q665505.x1 Scores_fetal_lung_NbHL19W Homo sapiens cDNA clone IMAGE:1743825 3'
6809	19863	33152	1.73	1.0E-17	AI185642.1	EST_HUMAN	q665505.x1 Scores_fetal_lung_NbHL19W Homo sapiens cDNA clone IMAGE:1743825 3'
7296	20268	33603	0.96	1.0E-17	Q16831	SWISSPROT	URIDINE PHOSPHORYLASE (UDRPASE)
8939	21905	35329	1.7	1.0E-17	BE082744.1	EST_HUMAN	QV0-BT0263-101299-072-d07 BT0263 Homo sapiens cDNA
10366	23289	36766	0.87	1.0E-17	AW996538.1	EST_HUMAN	QV3-BN0046-220300-129-c10 BN0046 Homo sapiens cDNA
11747	24632	38212	1.64	1.0E-17	Q28824	SWISSPROT	MYOSIN LIGHT CHAIN KINASE, SMOOTH MUSCLE (MLCK) [CONTAINS: TELOKIN]
13104	25825		1.63	1.0E-17	BE221470.1	EST_HUMAN	hu25e05.x1 NCL_CGAP_Mel15 Homo sapiens cDNA clone IMAGE:3171104 3' similar to contains MER13.b1
9856	22792		2.96	9.0E-18	AI472167.1	EST_HUMAN	MER13 repetitive element;
3800	16840	29747	1.87	8.0E-18	4758977	NT	q66403.x1 Scores_NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:2148389 3'
							Homo sapiens protein tyrosine phosphatase, non-receptor type substrate 1 (PTPNS1) mRNA
3899	16939	29850	3.75	8.0E-18	Q07537	SWISSPROT	POLYPEPTIDE N-ACETYL GALACTOSAMINYLTRANSFERASE (PROTEIN-UDP ACETYL GALACTOSAMINYLTRANSFERASE) (UDP-GALNAC:POLYPEPTIDE, N-ACETYL GALACTOSAMINYLTRANSFERASE) (GALNAC-T1)
349	13438	26361	23.15	7.0E-18	AW316976.1	EST_HUMAN	xx10b04.x1 NCL_CGAP_Pan1 Homo sapiens cDNA clone IMAGE:2837071 3' similar to gbl:20868 60S RIBOSOMAL PROTEIN L4 (HUMAN);

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
349	13438	26362	23.15	7.0E-18	AW316976.1	EST_HUMAN	xx10b04.x1 NCL CGAP_Pan1 Homo sapiens cDNA clone IMAGE:2837071 3' similar to gb:L20868 60S
7677	20635	33997	0.95	7.0E-18	AW887642.1	EST_HUMAN	RIBOSOMAL PROTEIN L4 (HUMAN); RC3-OT0091-170300-011-d03 OT0091 Homo sapiens cDNA
12769	13438	26361	2.67	7.0E-18	AW316976.1	EST_HUMAN	xx10b04.x1 NCL CGAP_Pan1 Homo sapiens cDNA clone IMAGE:2837071 3' similar to gb:L20868 60S
12769	13438	26362	2.67	7.0E-18	AW316976.1	EST_HUMAN	RIBOSOMAL PROTEIN L4 (HUMAN); xx10b04.x1 NCL CGAP_Pan1 Homo sapiens cDNA clone IMAGE:2837071 3' similar to gb:L20868 60S
3306	16359	29278	1.29	6.0E-18	X71791.2	NT	RIBOSOMAL PROTEIN L4 (HUMAN); Rattus norvegicus partial Gdn/Pn-1 gene for gila-derived nexin/protease nexin I, enhancer region
4777	17797		4.3	6.0E-18	P52181	SWISSPROT	PROTEIN-GLUTAMINE GAMMA-GLUTAMYLTRANSFERASE (TISSUE TRANSGLUTAMINASE) (TGASE C) (TGC)
8593	21561		2.64	6.0E-18	11428155	NT	Homo sapiens similar to high-mobility group (nonhistone chromosomal) protein 4 (H. sapiens) (LOC63446), mRNA
8691	21659	35082	0.57	6.0E-18	AL163210.2	NT	Homo sapiens chromosome 21 segment HS21C010
11469	24412	37961	1.54	6.0E-18	AL163246.2	NT	Homo sapiens chromosome 21 segment HS21C046
11657	24593	38166	2.06	6.0E-18	X87344.1	NT	H. sapiens DNA, DMB, HLA-Z1, IPP2, LMP2, TAP1, LMP7, DOB, DOB2 and RING8, 9, 13 and 14 genes
12527	25266	31805	2.95	6.0E-18	U87926.1	NT	Human acitlate hydratase (ACO2) gene, exon 4 similar to contains Alu repetitive element;
1150	14192	27144	17.6	5.0E-18	AI280214.1	EST_HUMAN	Human endogenous retrovirus HERV-P-T47D
5345	18450	31321	0.99	5.0E-18	AF087913.1	NT	MFR0-HT0161-221099-002-c06 HT0161 Homo sapiens cDNA
9070	22036	35459	5.53	5.0E-18	BE143312.1	EST_HUMAN	Homo sapiens lymphocyte activation-associated protein (LOC51088), mRNA
11323	24273	37800	3.26	5.0E-18	10242378	NT	Homo sapiens lymphocyte activation-associated protein (LOC51088), mRNA
11323	24273	37801	3.26	5.0E-18	10242378	NT	Homo sapiens lymphocyte activation-associated protein (LOC51088), mRNA
12649	25332		6.29	5.0E-18	AW867182.1	EST_HUMAN	MR1-SN0035-060400-001-g11 SN0035 Homo sapiens cDNA
12680	25544		3.2	5.0E-18	AV650547.1	EST_HUMAN	AV650547 GLC Homo sapiens cDNA clone GLCOGA02 3'
125	13232	26160	1.04	4.0E-18	BE044076.1	EST_HUMAN	h036h04.x1 NCL CGAP_UH1 Homo sapiens cDNA clone IMAGE:3039511 3' similar to contains MER29 b3
125	13232	26161	1.04	4.0E-18	BE044076.1	EST_HUMAN	MER29 repetitive element; h036h04.x1 NCL CGAP_UH1 Homo sapiens cDNA clone IMAGE:3039511 3' similar to contains MER29 b3
1729	14769	27744	1.61	4.0E-18	AA621814.1	EST_HUMAN	h024f11.s1 NCL CGAP_Cot10 Homo sapiens cDNA clone IMAGE:1144845 3' similar to gb:M26326
1908	14930		0.95	4.0E-18	AI736592.1	EST_HUMAN	KERATIN, TYPE I CYTOSKELETAL 18 (HUMAN); w033h08.x1 NCL CGAP_Cot16 Homo sapiens cDNA clone IMAGE:2392095 3'
2211	15226	28247	1.1	4.0E-18	Q06430	SWISSPROT	N-ACETYLGLUCOSAMINIDE BETA-1,6-N-ACETYLGLUCOSAMINYLTRANSFERASE (N-ACETYLGLUCOSAMINYLTRANSFERASE) (L-BRANCHING ENZYME) (GNT)

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2211	15226	28248	1.1	4.0E-18	Q06430	SWISSPROT	N-ACETYLGLUCOSAMINIDE BETA-1,6-N-ACETYLGLUCOSAMINYLTRANSFERASE (N-ACETYLGLUCOSAMINYLTRANSFERASE) (L-BRANCHING ENZYME) (IGNT)
3806	16846	29763	0.76	4.0E-18	AI581586.1	EST_HUMAN	ar63b06.x1 Barstead colon HPLRB7 Homo sapiens cDNA clone IMAGE:2173139 3' similar to contains Alu repetitive element
5437	18539	31447	2.29	4.0E-18	AI017565.1	EST_HUMAN	cu23e06.x1 Scores_NFL_I_GBC_S1 Homo sapiens cDNA clone IMAGE:1627138 3'
5437	18539	31448	2.29	4.0E-18	AI017565.1	EST_HUMAN	cu23e06.x1 Scores_NFL_I_GBC_S1 Homo sapiens cDNA clone IMAGE:1627138 3'
8178	21148		0.67	4.0E-18	AA746811.1	EST_HUMAN	nx64a08.s1 NCL_CGAP_Alv1 Homo sapiens cDNA clone IMAGE:1266998 similar to contains L1.12 L1 repetitive element
11348	24298	37826	4.22	4.0E-18	AA371807.1	EST_HUMAN	EST83633 Pituitary gland, subtracted (prolactin/growth hormone) II Homo sapiens cDNA 5' end similar to EST containing O family repeat
850	13906	26865	24.96	3.0E-18	AA814196.1	EST_HUMAN	ob23h11.s1 NCL_CGAP_Kid5 Homo sapiens cDNA clone IMAGE:1324581 3' similar to SW/RS5_HUMAN
930	13983	26936	3.54	3.0E-18	BE068634.1	EST_HUMAN	P46782 40S RIBOSOMAL PROTEIN S5.
3972	17012	29926	1.31	3.0E-18	AL163247.2	NT	CUJO-BT0690-210300-298-g07 BT0690 Homo sapiens cDNA
7003	20129	33444	6.43	3.0E-18	BE001671.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C047
11271	24223	37748	1.76	3.0E-18	BF218650.1	EST_HUMAN	PVJO-BN0081-100300-001-b08 BN0081 Homo sapiens cDNA
12774	25412		5.15	3.0E-18	AW022015.1	EST_HUMAN	601884856F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4103652 5'
251	13348	28274	5.97	2.0E-18	AW836820.1	EST_HUMAN	di31h12.y1 Morten Fetal Cochlea Homo sapiens cDNA clone IMAGE:2485126 5'
1155	14197		67.85	2.0E-18	BE256097.1	EST_HUMAN	QV1-LT0036-150200-070-e07 LT0036 Homo sapiens cDNA
3140	16197	29107	1.27	2.0E-18	Q39675	SWISSPROT	601114352F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3355044 5'
5485	18585		3.85	2.0E-18	AA888610.1	EST_HUMAN	DYNEIN GAMMA CHAIN, FLAGELLAR OUTER ARM
5584	18680	31644	3.38	2.0E-18	D14547.1	NT	ak53a07.s1 Scores_tests_NHT Homo sapiens cDNA clone IMAGE:1409652 3' similar to TR.O14577
5584	18680	31645	3.38	2.0E-18	D14547.1	NT	O14577 BAC CLONE RG114A06 FROM 7Q31, COMPLETE SEQUENCE. ;
5978	19063		1.67	2.0E-18	BF347229.1	EST_HUMAN	Human DNA, SINE repetitive element
6289	19361	32598	1	2.0E-18	X60459.1	NT	Human IFNAR gene for interferon alpha/beta receptor
6289	19361	32599	1	2.0E-18	X60459.1	NT	Human IFNAR gene for Interferon alpha/beta receptor
6409	19477	32724	0.75	2.0E-18	BF352940.1	EST_HUMAN	IL3-HT0619-220700-222-C12 HT0619 Homo sapiens cDNA
6451	19516	32767	4.42	2.0E-18	AW665853.1	EST_HUMAN	h04g01.s1 Scores_NFL_I_GBC_S1 Homo sapiens cDNA clone IMAGE:2879984 3' similar to contains MER19.12 MER19 repetitive element
7670	20629	33993	0.72	2.0E-18	AA457619.1	EST_HUMAN	aa89d11.l1 Stratagene fetal retina 937202 Homo sapiens cDNA clone IMAGE:838485 5' similar to TR:G61634 G61634 POLYPEPTIDE PR77 ;
8487	21455	34872	0.52	2.0E-18	BE439524.1	EST_HUMAN	HTM1-160F1 HTM1 Homo sapiens cDNA

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Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10407	23329	36813	1.31	2.0E-18	AW151673.1	EST_HUMAN	x67e10.x1 NCI_CGAP_Gas4 Homo sapiens cDNA clone IMAGE:2623146 3' similar to contains MER10.12 MER10 repetitive element;
10407	23329	36814	1.31	2.0E-18	AW151673.1	EST_HUMAN	x67e10.x1 NCI_CGAP_Gas4 Homo sapiens cDNA clone IMAGE:2623146 3' similar to contains MER10.12 MER10 repetitive element;
11319	24269	37797	3.07	2.0E-18	AW470791.1	EST_HUMAN	ha33d06.x1 NCI_CGAP_Kid12 Homo sapiens cDNA clone IMAGE:2875499 3' similar to contains THR.b3 THR repetitive element;
12039	24914	38508	2.88	2.0E-18	AW151299.1	EST_HUMAN	xg47e09.x1 NCI_CGAP_U11 Homo sapiens cDNA clone IMAGE:2630728 3' similar to contains MER8.b2 MER8 repetitive element;
12461	14197		3.97	2.0E-18	BE266097.1	EST_HUMAN	601114352F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3355044 5' ye49g05.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:120536 5' similar to contains L1 repetitive element;
4445	17471		0.93	1.0E-18	T95406.1	EST_HUMAN	
5429	18532	31412	2.71	1.0E-18	AV653405.1	EST_HUMAN	AV653405 GLC Homo sapiens cDNA clone GLCKE11 3'
5650	18746	31914	1.87	1.0E-18	D00099.1	NT	Homo sapiens mRNA for Na,K-ATPase alpha-subunit, complete cds
5650	18746	31915	1.87	1.0E-18	D00099.1	NT	Homo sapiens mRNA for Na,K-ATPase alpha-subunit, complete cds
6597	19657	32929	1.33	1.0E-18	AL163280.2	NT	Homo sapiens chromosome 21 segment HS21C080
8785	21752	35174	1.13	1.0E-18	AI148288.1	EST_HUMAN	oz69d09.x1 Soares, senescent, fibroblasts_NbHSF Homo sapiens cDNA clone IMAGE:1680593 3' similar to contains L1.11 L1 repetitive element;
10259	23184	36659	4.28	1.0E-18	U91328.1	NT	Human hereditary haemochromatosis region, histone 2A-like protein gene, hereditary haemochromatosis (HLA-H) gene, RoRet gene, and sodium phosphate transporter (NP T3) gene, complete cds
12412	25184	31821	6.49	1.0E-18	AF003529.1	NT	Homo sapiens glypican 3 (GPC3) gene, partial cds and flanking repeat regions
547	13618	26540	5.55	9.0E-19	AA281961.1	EST_HUMAN	z111d06.r1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:712811 5' similar to contains MER19.12 MER19 repetitive element;
548	13618	26540	4.1	9.0E-19	AA281961.1	EST_HUMAN	z111d06.r1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:712811 5' similar to contains MER19.12 MER19 repetitive element;
8181	21151		5.71	9.0E-19	F08688.1	EST_HUMAN	HSC23F051 normalized infant brain cDNA Homo sapiens cDNA clone c-23f05
9036	22002	35423	2.64	9.0E-19	AL163203.2	NT	Homo sapiens chromosome 21 segment HS21C003
9036	22002	35424	2.64	9.0E-19	AL163203.2	NT	Homo sapiens chromosome 21 segment HS21C003
11462	24405	37653	3.37	9.0E-19	AB032669.1	NT	Homo sapiens mRNA for KIAA1143 protein, partial cds
12172	13618	26540	1.84	9.0E-19	AA281961.1	EST_HUMAN	z111d06.r1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:712811 5' similar to contains MER19.12 MER19 repetitive element;
1050	14098		1.31	8.0E-19	AW974902.1	EST_HUMAN	EST387007 MAGE resequences, MAGN Homo sapiens cDNA
4433	17460		0.96	8.0E-19	P08548	SWISSPROT	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG
8488	21456	34873	1.04	8.0E-19	BE186936.1	EST_HUMAN	MRO-HT0404-210200-001-g06 HT0404 Homo sapiens cDNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2257	15271	28296	1.43	7.0E-19	4758139	NT	Homo sapiens DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 6 (RNA helicase, 54kd) (DDX6) mRNA
6598	19658	32930	1.95	7.0E-19	AF092090.1	NT	Rattus norvegicus cp151 mRNA, partial cds
7519	20484	33845	1.02	7.0E-19	P26444	SWISSPROT	BETA CRYSTALLIN A2
10372	23295	36771	0.43	7.0E-19	A1344951.1	EST_HUMAN	fb07c08.x1 NCI_CGAP_Lu28 Homo sapiens cDNA clone IMAGE:2052302 3'
12313	25969		3.28	7.0E-19	AA705684.1	EST_HUMAN	z180b01.s1 Soares fetal_liver_spleen_1NLS_S1 Homo sapiens cDNA clone IMAGE:435145 3'
3792	16833		1.6	6.0E-19	AW852830.1	EST_HUMAN	PM0-CT0248-131099-001-g01 CT0248 Homo sapiens cDNA
4490	17515	30403	1.44	6.0E-19	P34986	SWISSPROT	OLFACTORY RECEPTOR 6 (M50)
4490	17515	30404	1.44	6.0E-19	P34986	SWISSPROT	OLFACTORY RECEPTOR 6 (M50)
4837	17854		1.47	6.0E-19	AJ271735.1	NT	Homo sapiens Xq pseudautosomal region; segment 1/2
5064	18074	30954	1.29	6.0E-19	AL120817.1	EST_HUMAN	DKFZp762f192.1 762 (synonym: hma2) Homo sapiens cDNA clone DKFZp762f192 5'
5958	19043	32242	4.88	5.0E-19	Q00193	SWISSPROT	ZONA PELLUCIDA SPERM-BINDING PROTEIN B PRECURSOR (ZONA PELLUCIDA GLYCOPROTEIN ZP-X) (RC55)
6342	19411	32652	0.89	5.0E-19	AW693302.1	EST_HUMAN	hh77b06.y1 NCI_CGAP_GU1 Homo sapiens cDNA clone IMAGE:2868787 5'
10790	23711	37213	0.78	5.0E-19	AJ297699.1	NT	Homo sapiens partial IL-12RB1 gene for IL-12 receptor beta1 chain, exon 14
11865	24747	36329	4.78	5.0E-19	AW183725.1	EST_HUMAN	x187b02.x1 Soares NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2864171 3' similar to contains element MSR1 repetitive element ;
556	13626	26544	0.89	4.0E-19	AB007970.1	NT	Homo sapiens mRNA, chromosome 1 specific transcript KIAA0501
2891	15687	28704	1.69	4.0E-19	BF697362.1	EST_HUMAN	602130910F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4287674 5'
5470	18571	31481	1.05	4.0E-19	AF224669.1	NT	Homo sapiens mannosidase, beta A, lysosomal (MANBA) gene, and ubiquitin-conjugating enzyme E2D 3 (UBE2D3) genes, complete cds
3866	16905	29812	1.4	3.0E-19	Q28997	SWISSPROT	BETA-2 ADRENERGIC RECEPTOR
3866	16905	29813	1.4	3.0E-19	Q28997	SWISSPROT	BETA-2 ADRENERGIC RECEPTOR
4315	17344	30227	0.69	3.0E-19	O43900	SWISSPROT	LIM-ONLY PROTEIN 6 (TRIPLE LIM DOMAIN PROTEIN 6)
4315	17344	30228	0.69	3.0E-19	O43900	SWISSPROT	LIM-ONLY PROTEIN 6 (TRIPLE LIM DOMAIN PROTEIN 6)
4475	17501	30385	1.79	3.0E-19	AV708136.1	EST_HUMAN	AV708136 ADC Homo sapiens cDNA clone ADCAMA11 5'
5352	18457		0.63	3.0E-19	AF223467.1	NT	Homo sapiens NPD008 protein (NPD008) mRNA, complete cds
7612	20572		1.81	3.0E-19	11432214	NT	Homo sapiens similar to aldo-keto reductase family 1, member B11 (aldose reductase-like) (H. sapiens) (LOC83222), mRNA
9814	21137	34539	1.11	3.0E-19	X89685.1	NT	Musculus mRNA for TPCR33 protein
12552	25275		16.28	3.0E-19	AF165520.1	NT	Homo sapiens phorbol 1 protein (PB1) mRNA, complete cds
2557	15568	26588	27.04	2.0E-19	AL163201.2	NT	Homo sapiens chromosome 21 segment HS21G001
4474	17500		1.23	2.0E-19	A1311783.1	EST_HUMAN	qs91e02.x1 NCI_CGAP_Kid5 Homo sapiens cDNA clone IMAGE:1915898 3' similar to TR:Q69386 Q69386 POLIENV GENE ;

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6172	19247	32480	0.61	2.0E-19	AV731382.1	EST_HUMAN	AV731382 HTF Homo sapiens cDNA clone HTFAZC06 5'
7561	20524	33982	0.72	2.0E-19	7657286	NT	Mus musculus keratin-associated protein 9-1 (Krtap9-1), mRNA
8673	21641	35068	0.35	2.0E-19	AA012854.1	EST_HUMAN	z634c09.r1 Soares retina N2b4HR Homo sapiens cDNA clone IMAGE:360880 5'
10269	23194	36982	0.66	2.0E-19	Q95155	SWISSPROT	OLFACTORY RECEPTOR-LIKE PROTEIN OL12
482	13555		2.11	1.0E-19	BE408611.1	EST_HUMAN	607304125F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3638310 5'
							y078p07.r1 Soares adult brain N2b4HB5Y Homo sapiens cDNA clone IMAGE:184188 5' similar to contains MER10 repetitive element;
2174	15190	28211	1.68	1.0E-19	H30795.1	EST_HUMAN	Human gene for Ah-receptor, exon 7-9
2729	15723		2.48	1.0E-19	D38044.1	NT	Homo sapiens protein tyrosine phosphatase, non-receptor type substrate 1 (PTPNS1) mRNA
2860	15920		4.26	1.0E-19	4758977	NT	el49b12.s1 Soares testis_NHT Homo sapiens cDNA clone IMAGE:1393631 3' similar to contains MER37.12
3412	16460	29381	1.18	1.0E-19	AA834967.1	EST_HUMAN	MER37 repetitive element;
5186	18195		0.8	1.0E-19	AW117377.1	EST_HUMAN	xd88h10.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2604739 3' similar to contains L1.b2 L1 repetitive element;
6193	19267	32502	2.73	1.0E-19	U12188.1	NT	Oryctolagus cuniculus sodium/dicarboxylate cotransporter mRNA, partial cds
6333	25895		0.63	1.0E-19	AA585527.1	EST_HUMAN	nh22403.s1 NCI_CGAP_P1 Homo sapiens cDNA clone IMAGE:953093 similar to contains L1.11 L1 repetitive element;
7890	20834	34213	0.99	1.0E-19	U08813.1	NT	Oryctolagus cuniculus Na ⁺ /glucose cotransporter-related protein mRNA, complete cds
7890	20834	34214	0.99	1.0E-19	U08813.1	NT	Oryctolagus cuniculus Na ⁺ /glucose cotransporter-related protein mRNA, complete cds
8085	25894		0.71	1.0E-19	AF200719.1	NT	Homo sapiens pituitary tumor transforming gene protein (PTTG) gene, complete cds
8793	21760	35182	1.72	1.0E-19	IM64657.1	NT	Rabbit phosphorylase kinase beta subunit mRNA, complete cds
9093	22059		2.74	1.0E-19	T99920.1	EST_HUMAN	y972b02.r1 Soares fetal liver spleen 1N1FS Homo sapiens cDNA clone IMAGE:123243 5' similar to contains OFR repetitive element;
10106	23032		0.97	1.0E-19	U50822.1	NT	Human dystrophin (DMD) gene, exons 7, 8 and 9, and partial cds
10547	23489	36964	27.33	1.0E-19	AW812259.1	EST_HUMAN	RC0-ST0174-191099-031-b05 ST0174 Homo sapiens cDNA
10557	23479	36974	2.1	1.0E-19	NA4831.1	EST_HUMAN	W31e09.r1 Soares melanocyte 2N5HM Homo sapiens cDNA clone IMAGE:272872 5'
11809	24894		3.69	1.0E-19	AW023137.1	EST_HUMAN	df49h01.y1 Morton Fetal Cochlea Homo sapiens cDNA clone IMAGE:2487000 5'
6803	19857	33143	2.45	8.0E-20		NT	Mus musculus keratin-associated protein 9-1 (Krtap9-1), mRNA
6803	19857	33144	2.45	8.0E-20		NT	Mus musculus keratin-associated protein 9-1 (Krtap9-1), mRNA
7761	20714	34084	1.31	8.0E-20	A1221371.1	EST_HUMAN	qg86f09.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1842089 3'
7761	20714	34085	1.31	8.0E-20	A1221371.1	EST_HUMAN	qg86f09.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1842089 3'
3289	16342	29263	0.72	7.0E-20	BF328455.1	EST_HUMAN	PM4-AN0098-050900-003-a04 AN0098 Homo sapiens cDNA
7188	18419	31220	5.56	7.0E-20	AL138120.1	EST_HUMAN	DKFZp547D092.J1 547 (synonym: hfbt1) Homo sapiens cDNA clone DKFZp547D092 5'
8841	21808	35227	9.11	7.0E-20	AA557657.1	EST_HUMAN	nl48c04.s1 NCI_CGAP_P14 Homo sapiens cDNA clone IMAGE:1043718 similar to contains MER29.b2

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8841	21808	35228	9.11	7.0E-20	AA557657.1	EST_HUMAN	nl46c04.s1 NCI_CGAP_P14 Homo sapiens cDNA clone IMAGE:1043718 similar to contains MER29 b2
12023	24899		6.31	7.0E-20	6912633	NT	MER29 repetitive element;
3568	16613	26535	3.93	6.0E-20	P39188	SW/ISSPROT	Homo sapiens ribosomal protein L13a (RPL13A), mRNA
4301	17330	30210	2.98	6.0E-20	BE622434.1	EST_HUMAN	ALU SUBFAMILY J SEQUENCE CONTAMINATION WARNING ENTRY
4628	17647		1.05	5.0E-20	AV725123.1	EST_HUMAN	601441231F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3916231 5'
7322	20293	33636	1.19	5.0E-20	AF075301.1	EST_HUMAN	AV725123 HTC Homo sapiens cDNA clone H7C8TA01 5'
8277	21246	34657	5	5.0E-20	W90525.1	EST_HUMAN	AF075301 Human fetal liver cDNA library Homo sapiens cDNA clone HA0250
8277	21246	34658	5	5.0E-20	W90525.1	EST_HUMAN	zh78d08.s1 Soares_fetal_liver_spleen_1INFLS_S1 Homo sapiens cDNA clone IMAGE:418191 3' similar to contains MER30.11 MER30 repetitive element;
8440	21409	34822	0.79	5.0E-20	BE165980.1	EST_HUMAN	zh78d08.s1 Soares_fetal_liver_spleen_1INFLS_S1 Homo sapiens cDNA clone IMAGE:418191 3' similar to contains MER30.11 MER30 repetitive element;
9187	22153	35582	1.24	5.0E-20	AB028174.1	NT	MR3-HT0487-150200-113-g01 HT0487 Homo sapiens cDNA
9187	22153	35583	1.24	5.0E-20	AB028174.1	NT	Mus musculus MMAN-g mRNA, complete cds
9800	21123		0.93	5.0E-20	O60809	SW/ISSPROT	Mus musculus MMAN-g mRNA, complete cds
1624	14657	27635	1.79	4.0E-20	AL163247.2	NT	HYPOTHETICAL PROTEIN DJ845O24.1
5732	18826		0.89	4.0E-20	Q99880	SW/ISSPROT	Homo sapiens chromosome 21 segment HS21C047
8258	21227		5.27	4.0E-20	AI874352.1	EST_HUMAN	HISTONE H2B C (H2B/C)
10865	23785	37286	1.9	4.0E-20	AW937469.1	EST_HUMAN	tz4q03.x1 NCI_CGAP_Ov35 Homo sapiens cDNA clone IMAGE:2293396 3'
2149	15165	28181	0.91	3.0E-20	U03888.1	NT	QV3-DT0043-090200-080-c04 DT0043 Homo sapiens cDNA
4237	17266	30153	1.63	3.0E-20	P23273	SW/ISSPROT	Human BXP21 gene
4655	17676	30562	1.43	3.0E-20	AA037616.1	EST_HUMAN	OLFACTORY RECEPTOR-LIKE PROTEIN 114
9287	22253		3.32	3.0E-20	D14547.1	NT	z46b12.s1 Soares_pregant_uterus_NihPU Homo sapiens cDNA clone IMAGE:484895 3' similar to contains L1.13 L1 repetitive element;
10684	23606	37099	0.68	3.0E-20	BF165264.1	EST_HUMAN	Human DNA, SINE repetitive element
11024	23989		1.59	3.0E-20	P11369	SW/ISSPROT	601843561F1 NIH_MGC_54 Homo sapiens cDNA clone IMAGE:4064343 5'
11840	24723	38308	8.22	3.0E-20	A1284244.1	EST_HUMAN	RETROVIRUS-RELATED POLYPROTEIN [CONTAINS: REVERSE TRANSCRIPTASE ; ENDONUCLEASE]
11840	24723	38309	8.22	3.0E-20	A1284244.1	EST_HUMAN	q70d02.x1 NCI_CGAP_Kid3 Homo sapiens cDNA clone IMAGE:1864803 3' similar to contains Alu repetitive element;
12328	25130	31849	4.15	3.0E-20	BE88422.1	EST_HUMAN	q70d02.x1 NCI_CGAP_Kid3 Homo sapiens cDNA clone IMAGE:1864803 3' similar to contains Alu repetitive element;
831	13888		33.91	2.0E-20	AW303888.1	EST_HUMAN	601514180F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3915522 5'

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1113	14157	27107	3.88	2.0E-20	AA516335.1	EST_HUMAN	ng59h09.s1 NCL CGAP_Lip2 Homo sapiens cDNA clone IMAGE:940097 similar to TR:G1224066 G1224066 ORF2: FUNCTION UNKNOWN.;
1113	14157	27108	3.88	2.0E-20	AA516335.1	EST_HUMAN	ng59h09.s1 NCL CGAP_Lip2 Homo sapiens cDNA clone IMAGE:940097 similar to TR:G1224066 G1224066 ORF2: FUNCTION UNKNOWN.;
2828	13888		15.67	2.0E-20	AW303868.1	EST_HUMAN	xt24e10.x1 NCL CGAP_U14 Homo sapiens cDNA clone IMAGE:2761098 3' similar to SW:RS5_MOUSE p97461 40S RIBOSOMAL PROTEIN S6.;
4983	17998	30886	4.76	2.0E-20	Q28983	SWISSPROT	ZONADHESIN PRECURSOR
4983	17998	30887	4.76	2.0E-20	Q28983	SWISSPROT	ZONADHESIN PRECURSOR
8455	21424	34840	0.9	2.0E-20	AA309457.1	EST_HUMAN	EST180328 Liver III Homo sapiens cDNA 5' end
9545	22508	35957	7.56	2.0E-20	D10083.1	NT	Homo sapiens RGH1 gene, retrovirus-like element
9545	22508	35958	7.56	2.0E-20	D10083.1	NT	Homo sapiens RGH1 gene, retrovirus-like element
12703	25714	31611	3.98	2.0E-20	H55371.1	EST_HUMAN	CHR220310 Chromosome 22 exon Homo sapiens cDNA clone C22_391 5'
2029	15822	28063	4.32	1.0E-20	AA281961.1	EST_HUMAN	z11d06.r1 NCL CGAP_GCB1 Homo sapiens cDNA clone IMAGE:712811 5' similar to contains MER19.12 MER19 repetitive element;
4467	17493	30380	1.04	1.0E-20	BF115158.1	EST_HUMAN	tr84b06.x1 NCL CGAP_Kid11 Homo sapiens cDNA clone IMAGE:3135155 3' similar to contains L1.12 L1 repetitive element;
7079	20100	33411	1.04	1.0E-20	AF049587.1	EST_HUMAN	AF049587 Human activated dendritic cell mRNA Homo sapiens cDNA clone GA05
9518	22481	35926	2.24	1.0E-20	11418491	NT	Homo sapiens Autosomal Highly Conserved Protein (AHCP), mRNA
11879	24761	38346	2.11	1.0E-20	AF223391.1	NT	Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced
12458	25215		3.09	1.0E-20	AA420453.1	EST_HUMAN	trc60g08.r1 NCL CGAP_P11 Homo sapiens cDNA clone IMAGE:745694 similar to contains L1.13 L1 repetitive element;
2923	15981		1	9.0E-21	AJ003514.1	EST_HUMAN	AJ003514 Selected chromosome 21 cDNA library Homo sapiens cDNA clone MPI12-B/21
12175	25023		3.77	9.0E-21	AW898189.1	EST_HUMAN	RC3-NN0068-090500-021-b03 NN0068 Homo sapiens cDNA
9163	22129		1.13	8.0E-21	AW674891.1	EST_HUMAN	b630a02.y1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:2984714 5' similar to SW:NIAM_HUMAN O95169 NADHUBIQUINONE OXIDOREDUCTASE ASH1 SUBUNIT PRECURSOR;
11866	24748	38330	4.38	8.0E-21	AA809411.1	EST_HUMAN	ob71f06.s1 NCL CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1336835 3'
12342	25140		2.94	8.0E-21	O21330	SWISSPROT	ATP SYNTHASE A CHAIN (PROTEIN 6)
2082	15099	28115	1.59	7.0E-21	P15800	SWISSPROT	LAMININ BETA-2 CHAIN PRECURSOR (S-LAMININ) (LAMININ CHAIN B3)
2082	15099	28116	1.59	7.0E-21	P15800	SWISSPROT	LAMININ BETA-2 CHAIN PRECURSOR (S-LAMININ) (LAMININ CHAIN B3)
3716	16759	29671	0.63	7.0E-21	AL163300.2	NT	Homo sapiens chromosome 21 segment HS21C100
4283	17312		5.22	7.0E-21	AA046502.1	EST_HUMAN	z167a06.r1 Soares pregnant uterus NBHPU Homo sapiens cDNA clone IMAGE:487858 5'
6573	19633	32900	0.81	7.0E-21	AL163218.2	NT	Homo sapiens chromosome 21 segment HS21C018

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Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8731	21699	35124	1.42	7.0E-21	AJ277557.1	NT	Homo sapiens dNT-2 gene for mitochondrial 5'(3')-deoxyribonucleotidase (dNT-2 gene), exons 1-5
9024	21990	35411	11.21	7.0E-21	D14718.1	NT	Human chromosomal protein HMG1 related gene
10472	23394	36891	0.82	7.0E-21	AW856922.1	EST_HUMAN	RCO-CT0301-271198-031-F03 CT0301 Homo sapiens cDNA
							zq73d03.s1 Soares_fetal_NbHH19W Homo sapiens cDNA clone IMAGE:368981 3' similar to
							gbM14338 VITAMIN K-DEPENDENT PROTEIN S PRECURSOR (HUMAN);contains THR.3 OFR
							repetitive element;
11054	24017	37540	1.69	7.0E-21	AA72340.1	EST_HUMAN	Homo sapiens PT0013 protein (PT0013), mRNA
11599	24537	38094	1.67	7.0E-21	7706668	NT	601304125F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3638310 5'
4130	17163	30052	1.68	6.0E-21	BE408611.1	EST_HUMAN	PM1-HT0454-080100-002-H09 HT0454 Homo sapiens cDNA
9491	22455		0.59	6.0E-21	BE162737.1	EST_HUMAN	601649671F1 NIH_MGC_74 Homo sapiens cDNA clone IMAGE:3933880 5'
4390	17418	30302	3.16	5.0E-21	BE968839.1	EST_HUMAN	Homo sapiens melanoma antigen, family C, 1 (MAGEC1), mRNA
4839	17856	30753	6.18	5.0E-21	4885474	NT	he05e10.x1 NCI_CGAP_GML1 Homo sapiens cDNA clone IMAGE:2918154 3'
6927	20151		0.92	5.0E-21	AW440864.1	EST_HUMAN	7833d11.x1 NCI_CGAP_Pr28 Homo sapiens cDNA clone IMAGE:3303573 3' similar to contains OFR.11
							OFR repetitive element;
7213	20236	33570	0.96	5.0E-21	BE866505.1	EST_HUMAN	ZINC FINGER PROTEIN GLI1 (GLI-1)
10939	23859	37374	0.43	5.0E-21	Q91690	SWISSPROT	ZINC FINGER PROTEIN GLI1 (GLI-1)
10939	23859	37375	0.43	5.0E-21	Q91690	SWISSPROT	ZINC FINGER PROTEIN GLI1 (GLI-1)
12255	25081		5.38	5.0E-21	AA393574.1	EST_HUMAN	cc88e08.s1 NCI_CGAP_Kid5 Homo sapiens cDNA clone IMAGE:727878 5'
							PMS3 MRNA ;contains OFR.11 OFR repetitive element;
1748	14777	27762	1.95	4.0E-21	AA970713.1	EST_HUMAN	Rattus norvegicus mRNA for rTIM, complete cds
7055	20077	33386	3.35	4.0E-21	AB019576.1	NT	
							Human hereditary haemochromatosis region, histone 2A-like protein gene, hereditary haemochromatosis (HLA-H) gene, RoRet gene, and sodium phosphate transporter (NPT3) gene, complete cds
10139	23065	36541	0.59	4.0E-21	U91328.1	NT	zq15d06.s1 Stralagene fetal retina 937202 Homo sapiens cDNA clone IMAGE:629771 3'
1854	14880	27876	1.05	3.0E-21	AA218891.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C001
2282	15295	28319	1.48	3.0E-21	AL163201.2	NT	Homo sapiens LGMD2B gene
3096	16153	29066	4.17	3.0E-21	AJ007973.1	NT	
							Homo sapiens dNT-2 gene for mitochondrial 5'(3')-deoxyribonucleotidase (dNT-2 gene), exons 1-5
5577	18673	31636	0.93	3.0E-21	AJ277557.1	NT	
							Homo sapiens dNT-2 gene for mitochondrial 5'(3')-deoxyribonucleotidase (dNT-2 gene), exons 1-5
5577	18673	31637	0.93	3.0E-21	AJ277557.1	NT	AV681044 GLC Homo sapiens cDNA clone GLCGO10 3'
5828	18918		0.74	3.0E-21	AV681044.1	EST_HUMAN	601844465F1 NIH_MGC_54 Homo sapiens cDNA clone IMAGE:4064945 5'
6303	19374		1.89	3.0E-21	BF184739.1	EST_HUMAN	
7271	20006	33306	7.18	3.0E-21	BF361093.1	EST_HUMAN	RC1-OT0083-100800-019-g08 OT0083 Homo sapiens cDNA

Table 4

Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10051	22878	36445	0.77	3.0E-21	AW867780.1	EST_HUMAN	QM1-NN0063-280-400-203-108 NN0063 Homo sapiens cDNA
147	13250		28.45	2.0E-21	BE163247.1	EST_HUMAN	QV3-HT0458-170200-080-g12 HT0458 Homo sapiens cDNA
1219	14257		3.29	2.0E-21	BE064410.1	EST_HUMAN	RC4-BT0311-141198-011-108 BT0311 Homo sapiens cDNA
2648	15643	28667	2.26	2.0E-21	Q28983	SWISSPROT	ZONADHESIN PRECURSOR
2846	15643	28668	2.26	2.0E-21	Q28983	SWISSPROT	ZONADHESIN PRECURSOR
5561	18658	31604	1.54	2.0E-21	AI624592.1	EST_HUMAN	is3003.x1 NCL_CGAP_Pan1 Homo sapiens cDNA clone IMAGE:2230109 3' similar to TR:Q99854 Q99854 HYPOTHETICAL 51.1 KD PROTEIN ;
5658	18752	31918	0.81	2.0E-21	AA027211.1	EST_HUMAN	z697a12.r1 Soares_fetal_heart_NbHH19W Homo sapiens cDNA clone IMAGE:366910 5'
5658	18752	31919	0.81	2.0E-21	AA027211.1	EST_HUMAN	z697a12.r1 Soares_fetal_heart_NbHH19W Homo sapiens cDNA clone IMAGE:366910 5'
6149	19224	32454	0.61	2.0E-21	W44493.1	EST_HUMAN	z228h02.r1 Soares_senescent_fibroblasts_NbHSF Homo sapiens cDNA clone IMAGE:323667 5'
8615	21583	34998	0.48	2.0E-21	AJ010701	NT	Homo sapiens hypoxanthine gene, exons 1-50
8708	21674	35099	6.84	2.0E-21	BE141785.1	EST_HUMAN	QV0-HT0103-091199-050-g11 HT0103 Homo sapiens cDNA
9175	22141	35567	3.96	2.0E-21	AJ136778.1	EST_HUMAN	AU136779 PLACE1 Homo sapiens cDNA clone PLACE1005052 5'
11847	24584	38152	1.72	2.0E-21	BE973829.1	EST_HUMAN	601680636F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:3951008 5'
11647	24584	38153	1.72	2.0E-21	BE973829.1	EST_HUMAN	601680636F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:3951008 5'
12660	25279		17.61	2.0E-21	AF176615.1	NT	Homo sapiens putative 8-hydroxyguanine DNA glycosylase gene, complete cds
1260	14295	27259	2.06	1.0E-21	AA557657.1	EST_HUMAN	n146c04.s1 NCL_CGAP_P14 Homo sapiens cDNA clone IMAGE:1043718 similar to contains MER29.b2 MER29 repetitive element ;
1402	14435		7.17	1.0E-21	AI601264.1	EST_HUMAN	a88d12.x1 Barstead colon HPLRB7 Homo sapiens cDNA clone IMAGE:2152343 3'
6634	19692		2.6	1.0E-21	AL079752.1	EST_HUMAN	DKFZp434i0830_r1 434 (synonym: h1es3) Homo sapiens cDNA clone DKFZp434i0830 5'
7398	20396	33719	4.83	1.0E-21	AI223104.1	EST_HUMAN	qg47e05.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1838336 3' similar to gb:IM64241 QM PROTEIN (HUMAN);
10603	23525	37021	0.46	1.0E-21	AL163203.2	NT	Homo sapiens chromosome 21 segment HS21C003
10603	23525	37022	0.46	1.0E-21	AL163203.2	NT	Homo sapiens chromosome 21 segment HS21C003
10949	23869		1.67	1.0E-21	5730038	NT	Homo sapiens SET domain and mariner transposase fusion gene (SETMAR) mRNA
12632	25514		1.32	1.0E-21	AF046133.1	NT	Homo sapiens chromosome Xp22 410-8
4439	17465	30355	2.03	9.0E-22	AI702438.1	EST_HUMAN	t224a03.x1 NCL_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2266204 3' similar to TR:Q15408 Q15408 NEUTRAL PROTEASE LARGE SUBUNIT ;
8951	21917	35341	1.29	9.0E-22	AL163201.2	NT	Homo sapiens chromosome 21 segment HS21C001
8951	21917	35342	1.29	9.0E-22	AL163201.2	NT	Homo sapiens chromosome 21 segment HS21C001
11144	24104	37631	3.13	9.0E-22	AV761874.1	EST_HUMAN	AV761874 MDS Homo sapiens cDNA clone MDSGCC06 5'
949	14002		7.03	8.0E-22	BE144748.1	EST_HUMAN	CM0-HT0179-281099-076-h08 HT0179 Homo sapiens cDNA
8228	21197		3.82	8.0E-22	AA046502.1	EST_HUMAN	z167a06.r1 Soares_pregnant_uterus_NbHPU Homo sapiens cDNA clone IMAGE:487858 5'
686	13731	26556	6.78	7.0E-22	AL163246.2	NT	Homo sapiens chromosome 21 segment HS21C048

Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4312	17341	30221	2.36	7.0E-22	Q61838	SWISSPROT	ALPHA-2-MACROGLOBULIN PRECURSOR (ALPHA2M)
5076	18086	30968	0.97	7.0E-22	AB008681.1	NT	Homo sapiens gene for activin receptor type IIB, complete cds
9038	22004		2.46	7.0E-22	AF151054.1	NT	Homo sapiens HSPC220 mRNA, complete cds
9184	22150	35578	3.96	7.0E-22	M78580.1	EST_HUMAN	EST00738 Fetal brain, Striatum (cat#836206) Homo sapiens cDNA clone HFBCF07
9961	22888	36349	1.92	7.0E-22	AF009660.1	NT	Homo sapiens T cell receptor beta locus, TCRBV7S3A2 to TCRBV12S2 region
8584	21552		1.88	6.0E-22	AF009660.1	EST_HUMAN	w005g07.x1 NCI CGAP Gas4 Homo sapiens cDNA clone IMAGE:2542812 3'
5285	18291		0.72	5.0E-22	D14547.1	NT	Human DNA, SINE repetitive element
6666	19723	32998	3.05	5.0E-22	AL163303.2	NT	Homo sapiens chromosome 21 segment HS21C103
10682	23604	37098	7.82	5.0E-22	U60822.1	NT	Human dystrophin (DMD) gene, exons 7, 8 and 9, and partial cds
12776	25413		2.76	5.0E-22	BF476511.1	EST_HUMAN	naa27b06.x1 NCI CGAP_P128 Homo sapiens cDNA clone IMAGE:3256888 3' similar to contains Alu repetitive element
3650	16693		0.83	4.0E-22	AJ271736.1	NT	Homo sapiens Xq pseudautosomal region; segment 1/2
8442	21411	34824	0.42	4.0E-22	AV703223.1	EST_HUMAN	AV703223 ADB Homo sapiens cDNA clone ADBAU12 5'
8756	28006		3.36	4.0E-22	AL163202.2	NT	Homo sapiens chromosome 21 segment HS21C002
11077	24039	37563	2.15	4.0E-22	BF218030.1	EST_HUMAN	601882813F1 NIH MGC 57 Homo sapiens cDNA clone IMAGE:4095434 5'
12938	25518		2.74	4.0E-22	AL163209.2	NT	Homo sapiens chromosome 21 segment HS21C009
960	14013		1.06	3.0E-22	AI469679.1	EST_HUMAN	(m14h10.x1 NCI CGAP Co14 Homo sapiens cDNA clone IMAGE:2156611 3' similar to gbl:19593 HIGH AFFINITY INTERLEUKIN-8 RECEPTOR B (HUMAN); contains L1.L1 repetitive element
2576	15577	28596	2.15	3.0E-22	AI859038.1	EST_HUMAN	w166504.x1 NCI CGAP Brn25 Homo sapiens cDNA clone IMAGE:2429839 3' similar to SW:RL21_HUMAN
3686	16729		1.35	3.0E-22	D14718.1	NT	Human chromosomal protein HMG1 related gene
4838	17855	30752	2.88	3.0E-22	AJ080125.1	EST_HUMAN	qb28c07.x1 Soares_pregnant_uterus_NbHPU Homo sapiens cDNA clone IMAGE:1697580 3' similar to contains MER12.12 MER12 repetitive element
8572	21540		1.21	3.0E-22	BE156613.1	EST_HUMAN	QV0-HT0368-090200-099-12 HT0368 Homo sapiens cDNA
8577	21545	34964	3.4	3.0E-22	BE089841.1	EST_HUMAN	RC8-BT0707-150300-021-H10 BT0707 Homo sapiens cDNA
8703	21871	35093	0.77	3.0E-22	X60660.1	NT	R. rattus RY2G5 mRNA for a potential ligand-binding protein
8703	21871	35094	0.77	3.0E-22	X60660.1	NT	R. rattus RY2G5 mRNA for a potential ligand-binding protein
1970	14991		4.79	2.0E-22	N24942.1	EST_HUMAN	yx73d05.s1 Soares melanocyte 2NbHM Homo sapiens cDNA clone IMAGE:267369 3'
2528	15631	28552	1.82	2.0E-22	P24916	SWISSPROT	IMMEDIATE EARLY GENE 13 PROTEIN PRECURSOR
3431	16479	29398	4.76	2.0E-22	8394043	NT	Homo sapiens protein kinase, AMP-activated, gamma 3 non-catalytic subunit (PRKAG3), mRNA
4253	17282	30163	1.26	2.0E-22	AW817794.1	EST_HUMAN	PM1-ST0262-261199-001-d12 ST0262 Homo sapiens cDNA
5951	25848	32232	1.34	2.0E-22	W39456.1	EST_HUMAN	zs20f01.1 Soares_senescent_fibroblasts_NbHSF Homo sapiens cDNA clone IMAGE:322873 5' similar to gb:272308 MONOCYTE CHEMOTACTIC PROTEIN 3 PRECURSOR (HUMAN);
6301	18372	32611	3.57	2.0E-22	BF092116.1	EST_HUMAN	RC0-TN0079-150900-025-h12 TN0079 Homo sapiens cDNA

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Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10061	22988	36456	1.61	2.0E-22	AI276522.1	EST_HUMAN	q176h08.x1 Soares_NihMPu_S1 Homo sapiens cDNA clone IMAGE:1878289 3' similar to contains
10156	23081	36556	0.65	2.0E-22	AA715315.1	EST_HUMAN	MER29.13 MER29 repetitive element;
10166	23081	36557	0.65	2.0E-22	AA715315.1	EST_HUMAN	nv04h11.s1 NCI_CGAP_P122 Homo sapiens cDNA clone IMAGE:1219269 3'
10991	23911	37426	0.55	2.0E-22	R15209.1	EST_HUMAN	nv04h11.s1 NCI_CGAP_P122 Homo sapiens cDNA clone IMAGE:1219269 3'
12054	24927	38525	1.68	2.0E-22	AW418960.1	EST_HUMAN	yf88c09.f1 Soares Infant brain 1N1B Homo sapiens cDNA clone IMAGE:29740 5'
12139	25504	31705	1.92	2.0E-22	AL163280.2	NT	ha24f04.x1 NCI_CGAP_Kid12 Homo sapiens cDNA clone IMAGE:2874655 3'
1895	14921	27917	1.76	1.0E-22	AW865517.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C080
2588	15589	28606	1.82	1.0E-22	U50871.1	NT	PM4-SN0020-070400-009-H02 SN0020 Homo sapiens cDNA
3422	16470	29390	1.49	1.0E-22	D14547.1	NT	Human familial Alzheimer's disease (STM2) gene, complete cds
5295	18300		1.5	1.0E-22	AF003528.1	NT	Human DNA, SINE repetitive element
8015	20953	34347	0.95	1.0E-22	BE084687.1	EST_HUMAN	Homo sapiens X-linked anthrithritic ectodermal dysplasia protein gene (EDA), exon 2 and flanking repeat regions
10918	23838	37354	0.8	1.0E-22	AI365435.1	EST_HUMAN	MRO-BT0659-220200-002-h07 BT0659 Homo sapiens cDNA
10918	23838	37355	0.8	1.0E-22	AI365435.1	EST_HUMAN	q208b07.x1 NCI_CGAP_OLL1 Homo sapiens cDNA clone IMAGE:2020981 3' similar to contains MER29.b2
12981	25561		9.05	9.0E-23	AW802801.1	EST_HUMAN	MER29 repetitive element;
3585	16630	28548	0.73	8.0E-23	AF198349.1	NT	MER29 repetitive element;
3322	16373		1.96	7.0E-23	AV647246.1	EST_HUMAN	IL2JM0076-070400-061-F11 UN0076 Homo sapiens cDNA
11376	24323	37852	4.11	7.0E-23	5031952	NT	Gallus gallus Dach2 protein (Dach2) mRNA, complete cds
3447	16494		1.68	6.0E-23	AF199333.1	NT	AV647246 GLC Homo sapiens cDNA clone GLCAW(C07 3'
4297	17326	30206	1.13	6.0E-23	AL163249.2	NT	Homo sapiens Nof66 (O. melanogaster)-like protein (NOT56L) mRNA
12281	25099	31834	4.64	6.0E-23	AF224669.1	NT	Rattus norvegicus RIM1B (Rim1B) mRNA, complete cds
12281	25099	31835	4.64	6.0E-23	AF224669.1	NT	Homo sapiens chromosome 21 segment HS21C049
12480	25228	31795	3.03	6.0E-23	AI209130.1	EST_HUMAN	Homo sapiens mannosidase, beta A, lysosomal (MANBA) gene, and ubiquitin-conjugating enzyme E2D 3
5519	18618	31552	4	5.0E-23	U82971.2	NT	Homo sapiens mannosidase, beta A, lysosomal (MANBA) gene, and ubiquitin-conjugating enzyme E2D 3
6397	25659	32679	3.55	5.0E-23	AF179818.1	NT	Homo sapiens mannosidase, beta A, lysosomal (MANBA) gene, and ubiquitin-conjugating enzyme E2D 3
7871	25659	32679	3.26	5.0E-23	AF179818.1	NT	q959c03.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1839480 3' similar to
							SW:MOV10_MOUSE_P23249 PROTEIN MOV-10 ;
							Homo sapiens chromosome Xq28 melanoma antigen family A2a (MAGEA2A), melanoma antigen family A12 (MAGEA12), melanoma antigen family A2b (MAGEA2B), melanoma antigen family A3 (MAGEA3), caltractin (CALT), NAD(P)H dehydrogenase-like protein (NSDHL), and L1>
							Pongo pygmaeus olfactory receptor (PPY116) gene, partial cds
							Pongo pygmaeus olfactory receptor (PPY116) gene, partial cds

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Table 4
Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6580	19640	32906	1.07	3.0E-23	AL163227.2	NT	Homo sapiens chromosome 21 segment HS21C027
6580	19640	32907	1.07	3.0E-23	AL163227.2	NT	Homo sapiens chromosome 21 segment HS21C027
8171	21141	34547	4.18	3.0E-23	AA130165.1	EST_HUMAN	z35g09.r1 Soares_pregnant_uterus_NbHPU Homo sapiens cDNA clone IMAGE:503968 5' similar to contains MER29.12 MER29 repetitive element;
9604	22608	36058	2.74	3.0E-23	Z70664.1	NT	Human endogenous retroviral element HC2
9604	22608	36059	2.74	3.0E-23	Z70664.1	NT	Human endogenous retroviral element HC2
10680	23602	26657	1.27	3.0E-23	AW887927.1	EST_HUMAN	RC3-NN0066-270400-011-h01 NN0066 Homo sapiens cDNA
667	13732	26657	3.75	2.0E-23	AJ289880.1	NT	Homo sapiens KIAA0851 gene (partial), X73 gene and LZTFL1 gene
1145	15817	28817	3.02	2.0E-23	M55270.1	NT	Human matrix Gla protein (MGP) gene, complete cds
2807	15799	28817	2.08	2.0E-23	P22105	SWISSPROT	TENASCIN-X PRECURSOR (TN-X) (HEXABRACHION-LIKE)
2807	15799	28818	2.08	2.0E-23	P22105	SWISSPROT	TENASCIN-X PRECURSOR (TN-X) (HEXABRACHION-LIKE)
3384	16433		1.5	2.0E-23	AI201458.1	EST_HUMAN	gs73f11.x1 NCL CGAP_P128 Homo sapiens cDNA clone IMAGE:1943757 3' similar to TR:Q13537 Q13537
3729	16771		2.97	2.0E-23	BE165980.1	EST_HUMAN	MER37 TRANSPOSABLE ELEMENT, COMPLETE CONSENSUS SEQUENCE.;
4001	17040	29947	2.59	2.0E-23	H59931.1	EST_HUMAN	MR3-HT0487-150200-113-g01 HT0487 Homo sapiens cDNA
4001	17040	29948	2.59	2.0E-23	H59931.1	EST_HUMAN	yt16a02.r1 Soares fetal liver spleen TNFLS Homo sapiens cDNA clone IMAGE:205418 5'
5062	18072	30952	8.49	2.0E-23	D14547.1	NT	yt16a02.r1 Soares fetal liver spleen TNFLS Homo sapiens cDNA clone IMAGE:205418 5'
						NT	Human DNA, SINE repetitive element
8205	21175		4.26	2.0E-23	AF280107.1	NT	Homo sapiens cytochrome P450 polypeptide 43 (CYP3A43) gene, partial cds; cytochrome P450 polypeptide 4 (CYP3A4) and cytochrome P450 polypeptide 7 (CYP3A7) genes, complete cds; and cytochrome P450 polypeptide 5 (CYP3A5) gene, partial cds
9195	22161	35589	1.12	2.0E-23	AL163303.2	NT	Homo sapiens chromosome 21 segment HS21C103
12262	25086		3.91	2.0E-23	M32658.1	NT	Human alcohol dehydrogenase gamma subunit (ADH3) gene, exon 1
12787	25419		2.55	2.0E-23	AF009660.1	NT	Homo sapiens T cell receptor beta locus, TCRBV7S3A2 to TCRBV72S2 region
4558	17581	30472	1.44	1.0E-23	AL163252.2	NT	Homo sapiens chromosome 21 segment HS21C052
4799	17816		4.76	1.0E-23	AL163210.2	NT	Homo sapiens chromosome 21 segment HS21C010
6882	19834		3.11	1.0E-23	BE378471.1	EST_HUMAN	601236456F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3608663 5'
8699	21667	35090	4.73	1.0E-23	AA448097.1	EST_HUMAN	zw82c06.r1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:782698 5' similar to contains PTR5.12 PTR5 repetitive element;
554	13624		3.05	9.0E-24	AA663213.1	EST_HUMAN	ab75a06.s1 Stratagene fetal retina 937202 Homo sapiens cDNA clone IMAGE:852768 3' similar to TRE19822 E19822 CA PROTEIN.;
4678	17699	30586	1.15	8.0E-24	P23269	SWISSPROT	OLFACTORY RECEPTOR-LIKE PROTEIN I3
4678	17699	30587	1.15	8.0E-24	P23269	SWISSPROT	OLFACTORY RECEPTOR-LIKE PROTEIN I3
6591	19651	32922	1.34	8.0E-24		NT	Homo sapiens capping protein (actin filament) muscle Z-line, alpha 2 (CAPZA2), mRNA
8155	21093	34492	0.77	8.0E-24	11422027	NT	Homo sapiens capping protein (actin filament) muscle Z-line, alpha 2 (CAPZA2), mRNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3886	16826		1.36	7.0E-24	AW937954.1	EST_HUMAN	QV0-DT0047-170200-122-06 DT0047 Homo sapiens cDNA
707	13769		2.31	8.0E-24	AB001421.1	NT	Macaca fasciata mRNA for Testis-Specific Protein Y (TSPY), complete cds
839	13896	26851	15.66	6.0E-24	AL163249.2	NT	Homo sapiens chromosome 21 segment HS21C049
3994	17034	26942	8.31	5.0E-24	AJ228043.1	NT	Homo sapiens 959 kb contig between AML1 and CBR1 on chromosome 21q22, segment 3/3
8034	20971	34365	1.34	5.0E-24	AF22391.1	NT	Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced
6039	19121	32328	3.63	4.0E-24	AA594178.1	EST_HUMAN	nm31h05.s1 NCL_CGAP_Gas1 Homo sapiens cDNA clone IMAGE:1085529 3' similar to SW-POL_MLVK
9029	21895	35415	1.29	4.0E-24	AW81371.1	EST_HUMAN	P31785 POL POLYPROTEIN;
11514	24455	38005	1.52	4.0E-24	BE544822.1	EST_HUMAN	RC3-ST0197-130100-014-06 ST0197 Homo sapiens cDNA
12844	25328	31790	5.56	4.0E-24	AB026016.1	NT	601078812F1 NIH_MGC 12 Homo sapiens cDNA clone IMAGE:3484498 5'
12807	25713	31610	9.62	4.0E-24	M20707.1	NT	Homo sapiens mRNA for KIAA1083 protein, partial cds
12876	25509	31708	1.88	4.0E-24	11418318	NT	Human kappa-immunoglobulin germline pseudogene (Chr22.4) variable region (subgroup V kappa II)
						NT	Homo sapiens G-2 and S-phase expressed 1 (GTSE1), mRNA
7285	20062	33368	0.6	3.0E-24	U66081.1	NT	Human germline T-cell receptor beta chain TCRBV17S1A1T, TCRBV2S1, TCRBV10S1P, TCRBV29S1P, TCRBV19S1P, TCRBV15S1, TCRBV11S1A1T, HVB relic, TCRBV28S1P, TCRBV34S1, TCRBV14S1, TCRBV3S1, TCRBV4S1A1T, TRY4, TRY6, TRY8, TRY7, TRY8, TCRBD1, TCRBJ1S1, TCRBJ1S2, >
7285	20062	33369	0.6	3.0E-24	U66081.1	NT	Human germline T-cell receptor beta chain TCRBV17S1A1T, TCRBV2S1, TCRBV10S1P, TCRBV29S1P, TCRBV19S1P, TCRBV15S1, TCRBV11S1A1T, HVB relic, TCRBV28S1P, TCRBV34S1, TCRBV14S1, TCRBV3S1, TCRBV4S1A1T, TRY4, TRY6, TRY8, TRY7, TRY8, TCRBD1, TCRBJ1S1, TCRBJ1S2, >
8768	21733		2.89	3.0E-24	AW614871.1	EST_HUMAN	h168c08.x1 NCL_CGAP_GU1 Homo sapiens cDNA clone IMAGE:2867950 3' similar to contains MER28.b2
8822	21789		1.25	3.0E-24	AW962078.1	EST_HUMAN	MER28 repetitive element;
9820	22669	36126	4.11	3.0E-24	AL163252.2	NT	EST374149 IMAGE resequences, MAGG Homo sapiens cDNA
12715	25369	31772	2.16	3.0E-24	BF127762.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C052
2354	15363	28365	2.8	2.0E-24	AA167539.1	EST_HUMAN	601810449F1 NIH_MGC 46 Homo sapiens cDNA clone IMAGE:4053396 5'
3812	16852		0.99	2.0E-24	AW898189.1	EST_HUMAN	zp1109.r1 Striatogene fetal retina 937202 Homo sapiens cDNA clone IMAGE:609161 5'
7583	26001		0.61	2.0E-24	AL163209.2	NT	RC3-NN0068-090500-021-b03 NN0068 Homo sapiens cDNA
7715	20672	34039	1.12	2.0E-24	AF096924.1	NT	Homo sapiens chromosome 21 segment HS21C009
7720	20677	34042	0.55	2.0E-24	AJ003536.1	EST_HUMAN	Mus musculus rho/rao-interacting citron kinase (Crik) mRNA, complete cds
9092	22058	35484	3.09	2.0E-24	AL119158.1	EST_HUMAN	AJ003536 Selected chromosome 21 cDNA library Homo sapiens cDNA clone MPIpl12-5H13
						EST_HUMAN	DKFZp761L1712_r1_761 (synonym: hary2) Homo sapiens cDNA clone DKFZp761L1712 5'

Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9130	22096		0.96	2.0E-24	H69214.1	EST_HUMAN	y92b09.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:212729 5' similar to contains
10213	23138	36828	0.98	2.0E-24	A1521759.1	EST_HUMAN	MER28 repetitive element ;
10213	23138	36627	0.98	2.0E-24	A1521759.1	EST_HUMAN	ti77a09.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2138008 3'
12568	25947		10.03	2.0E-24	M28877.1	NT	ti77a09.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2138008 3'
1705	14735	27717	2.63	1.0E-24	7706340	NT	Human O family dispersed repeat element
2681	15677		1.52	1.0E-24	AW820194.1	EST_HUMAN	Homo sapiens CGI-127 protein (LOC51646), mRNA
3033	16091	29009	0.78	1.0E-24	D86423.1	NT	QV0-S10294-100400-185-c10 ST0294 Homo sapiens cDNA
4299	17328		2	1.0E-24	AF143313.1	NT	Mus musculus mRNA for HGT keratin, partial cds
6541	19603	32865	0.68	1.0E-24	7106336	NT	Homo sapiens PTEN (PTEN) gene, exon 2
7796	20748	34123	3.96	1.0E-24	AL163303.2	NT	Mus musculus keratin complex-1, gene C29 (Krt1-c29), mRNA
8002	20941	34334	0.68	1.0E-24	BE144526.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21 C103
8276	21245	34656	1.81	1.0E-24	AW901164.1	EST_HUMAN	MRC-HT0166-271199-005-009 HT0166 Homo sapiens cDNA
8625	19683	32961	0.52	9.0E-25	11420402	NT	CM0-NN1010-130300-281-007 NN1010 Homo sapiens cDNA
12008	24885	38480	1.53	9.0E-25	7706707	NT	Homo sapiens helicase-like protein NHL (LOC51750), mRNA
							Homo sapiens putative secreted protein (SIG11), mRNA
5031	18045	30927	2.85	7.0E-25	AA483944.1	EST_HUMAN	ne92e10.s1 NCI_CGAP_Kid1 Homo sapiens cDNA clone IMAGE:911754 similar to contains MER1.b2
8561	21529	34949	6.63	7.0E-25	AA468546.1	EST_HUMAN	MER1 repetitive element ;
12012	24889	36486	3.24	7.0E-25	AA583540.1	EST_HUMAN	ne08a09.s1 NCI_CGAP_Co3 Homo sapiens cDNA clone IMAGE:880408 3' similar to contains THR.b2 THR
7184	18415		4.41	6.0E-25	W87623.1	EST_HUMAN	repetitive element ;
7982	20931	34326	10.28	6.0E-25	7305360	NT	rf25h06.s1 NCI_CGAP_Prl Homo sapiens cDNA clone IMAGE:914843 similar to SW:R14A_YEAST
1659	14991	27667	1.67	5.0E-25	AW850271.1	EST_HUMAN	P36105 PROBABLE 60S RIBOSOMAL PROTEIN L14EA. ;
							zh66h07.r1 Soares fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:416989 5'
							Mus musculus obogelin (Obog), mRNA
5183	18192		0.92	5.0E-25	AA994228.1	EST_HUMAN	IL3-CT0219-161199-031-D04 CT0219 Homo sapiens cDNA
11645	24982	38150	3.16	5.0E-25	AW979107.1	EST_HUMAN	cu49f01.s1 NCI_CGAP_Br2 Homo sapiens cDNA clone IMAGE:1631161 3' similar to contains Alu repetitive
1441	14474	27451	2.3	4.0E-25	T88107.1	EST_HUMAN	element ;
3413	16461		2.68	4.0E-25	AW687671.1	EST_HUMAN	EST*391217 MAGC resequences, MAGP Homo sapiens cDNA
3923	16963	29876	0.93	4.0E-25	AF000368.1	NT	y56h04.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:121783 5'
4345	17372		3.13	4.0E-25	BE170987.1	EST_HUMAN	PM3-OT0093-280200-001-g07 OT0093 Homo sapiens cDNA
3331	16382	29303	2.77	3.0E-25		NT	Rattus norvegicus voltage-gated sodium channel mRNA, complete cds
3331	16382	29304	2.77	3.0E-25	8923321	NT	QV3-HT0543-140400-149-e11 HT0543 Homo sapiens cDNA
5877	18966	32157	0.64	3.0E-25	U53212.1	NT	Homo sapiens hypothetical protein FLJ20344 (FLJ20344), mRNA
							Homo sapiens hypothetical protein FLJ20344 (FLJ20344), mRNA
							Human degenerate channel MDEG mRNA, partial cds

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Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8769	19824	33107	0.86	3.0E-25	AA603590.1	EST_HUMAN	np27b02.s1 NCI_CGAP_P722 Homo sapiens cDNA clone IMAGE:1117515 3' similar to gb:M61866 ZINC FINGER PROTEIN 85 (HUMAN);
8880	21648	35070	4.08	3.0E-25	AL163210.2	NT	Homo sapiens chromosome 21 segment HS21C010
1350	14385	27354	2.6	2.0E-25	5032158	NT	Homo sapiens transducin (beta)-like 1 (TBL1) mRNA
2317	15328	28351	7.52	2.0E-25	BE888016.1	EST_HUMAN	601511530F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3913087 5'
2842	15561	28572	3.35	2.0E-25	P17008	SWISSPROT	40S RIBOSOMAL PROTEIN S16
4218	17247	30131	1.96	2.0E-25	P17008	SWISSPROT	40S RIBOSOMAL PROTEIN S16
4218	17247	30132	1.96	2.0E-25	P17008	SWISSPROT	40S RIBOSOMAL PROTEIN S16
10123	23049	36528	2.03	2.0E-25	AL449573.1	EST_HUMAN	AL449573 Homo sapiens Testis (Stavrides GS) Homo sapiens cDNA
364	13450	26378	1.4	1.0E-25	AL040220.1	EST_HUMAN	DKFZp434H0313.1 434 (synonym: htes3) Homo sapiens cDNA clone DKFZp434H0313 5'
1253	14289		1.34	1.0E-25	9635487	NT	Human endogenous retrovirus, complete genome
2441	15448	28466	1.04	1.0E-25	Q08055	SWISSPROT	ATP SYNTHASE LIPID-BINDING PROTEIN P2 PRECURSOR (ATPASE PROTEIN 9) (SUBUNIT C)
4895	17912	30802	2.33	1.0E-25	BE162737.1	EST_HUMAN	PM1-HT0464-080100-002-h08 HT0454 Homo sapiens cDNA
6719	19775		0.83	1.0E-25	AA189080.1	EST_HUMAN	zq45506.s1 Stratagene NNT neuron (#837233) Homo sapiens cDNA clone IMAGE:632827 3' similar to contains Alu repetitive element;
6965	25676	33516	3.22	1.0E-25	AA582690.1	EST_HUMAN	nm54ht11.s1 NCI_CGAP_Kid6 Homo sapiens cDNA clone IMAGE:1087749 3'
8248	21215	34623	4.36	1.0E-25	AA709079.1	EST_HUMAN	z06g04.s1 Soares_fetal_heart_NbHH10W Homo sapiens cDNA clone IMAGE:384822 3' similar to contains PTR5.13 PTR5 repetitive element ;
9904	22856	36317	0.86	1.0E-25	X60660.1	NT	R. rattus RY2G5 mRNA for a potential ligand-binding protein
9904	22856	36318	0.89	1.0E-25	X60660.1	NT	R. rattus RY2G5 mRNA for a potential ligand-binding protein
11318	24266	37794	2.91	1.0E-25	U93163.1	NT	Homo sapiens MAGE-B2 (MAGE-B2), MAGE-B3 (MAGE-B3), MAGE-B4 (MAGE-B4), and MAGE-B1 (MAGE-B1) genes, complete cds
12278	25097	38180	1.47	1.0E-25	D14547.1	NT	Human DNA, SINE repetitive element
12278	25097	38181	1.47	1.0E-25	D14547.1	NT	Human DNA, SINE repetitive element
13053	25591		1.83	1.0E-25	X61755.1	NT	Human lambda-immunoglobulin constant region complex (germline)
2491	15494	28518	1.47	9.0E-26	AL163218.2	NT	Homo sapiens chromosome 21 segment HS21C018
5778	18870		1.58	8.0E-26	D14547.1	NT	Human DNA, SINE repetitive element
1580	14613	27585	2.88	7.0E-26	AF003528.1	NT	Homo sapiens X-linked anhidrotic ectodermal dysplasia protein gene (EDA), exon 2 and flanking repeat regions
4005	17044	29952	1.21	7.0E-26	X89211.1	NT	Hi sapiens DNA for endogenous retroviral like element
4186	17217	30103	1.69	7.0E-26	AW340753.1	EST_HUMAN	hd02e12.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2908386 3'
5721	18815	31994	0.72	7.0E-26	AL163202.2	NT	Homo sapiens chromosome 21 segment HS21C002
11978	24855		8.08	7.0E-26	AA115895.1	EST_HUMAN	zn30d08.r1 Stratagene neuroepithelium NT2RAM1 937234 Homo sapiens cDNA clone IMAGE:548943 5' similar to gb:M14338 VITAMIN K-DEPENDENT PROTEIN S PRECURSOR (HUMAN);

Table 4

Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2234	15248	28272	2.26	6.0E-26	AF028308.1	NT	Homo sapiens chromosome 9 duplication of the T cell receptor beta locus and trypsinogen gene families
3357	19407	29328	1.03	6.0E-26	AA208131.1	EST_HUMAN	zq52h04.r1 Stratagene neuroepithelium (#937231) Homo sapiens cDNA clone IMAGE:645271 5'
11990	24867	38462	1.91	6.0E-26	AL163210.2	NT	Homo sapiens chromosome 21 segment HS21C010
1181	14222	27178	1.86	5.0E-26	AI708235.1	EST_HUMAN	as38h08.x1 Barslead actin HPLRB6 Homo sapiens cDNA clone IMAGE:2319519 3' similar to WP:F49C12.11 CE03371 ;
1181	14222	27179	1.86	5.0E-26	AI708235.1	EST_HUMAN	as38h08.x1 Barslead actin HPLRB6 Homo sapiens cDNA clone IMAGE:2319519 3' similar to WP:F49C12.11 CE03371 ;
1546	14579		0.96	4.0E-26	AA329548.1	EST_HUMAN	EST33446 Embryo, 12 week II Homo sapiens cDNA 5' and
9767	22708		3.77	4.0E-26	7657670	NT	Homo sapiens upstream binding transcription factor, RNA polymerase I (UBTF), mRNA
11022	23987	37514	2.93	4.0E-26	BE266187.1	EST_HUMAN	601191345F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3535210 5'
1773	14802	27787	2.15	3.0E-26	D14547.1	NT	Human DNA, SINE repetitive element
2019	15040	28051	1.27	3.0E-26	AL045655.2	EST_HUMAN	DKFZp434i066_r1 434 (synonym: hies3) Homo sapiens cDNA clone DKFZp434i066 5'
2047	15066		3.59	3.0E-26	AA115895.1	EST_HUMAN	zr30d08.r1 Stratagene neuroepithelium NT2RAMI 937234 Homo sapiens cDNA clone IMAGE:548943 5' similar to gb:MI4338 VITAMIN K-DEPENDENT PROTEIN S PRECURSOR (HUMAN);
3791	16832	29738	1.12	3.0E-26	AA152464.1	EST_HUMAN	zo30f10.r1 Stratagene colon (#937204) Homo sapiens cDNA clone IMAGE:588427 5' similar to TR:G695374
3791	16832	29739	1.12	3.0E-26	AA152464.1	EST_HUMAN	G695374 THYROID RECEPTOR INTERACTOR ;
7096	20030	33334	6.22	3.0E-26	BF245458.1	EST_HUMAN	G695374 THYROID RECEPTOR INTERACTOR ;
11894	24775	38361	2.03	3.0E-26	AW875651.1	EST_HUMAN	601864963F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4083278 5'
11894	24775	38362	2.03	3.0E-26	AW875651.1	EST_HUMAN	QV2-PT0012-040400-124-605 PT0012 Homo sapiens cDNA
11928	24809	38404	4.91	3.0E-26	AA583173.1	EST_HUMAN	QV2-PT0012-040400-124-605 PT0012 Homo sapiens cDNA
13101	25624	31678	1.37	3.0E-26	AF165520.1	NT	nr37d05.s1 NCI_CGAP_GC5 Homo sapiens cDNA clone IMAGE:1086057 3' similar to contains OFR.11
682	13745	26672	10.08	2.0E-26	AL163282.2	NT	OFR repetitive element ;
1884	14909		3.56	2.0E-26	AL038099.2	EST_HUMAN	Homo sapiens phorbol 1 protein (PBI) mRNA, complete cds
3245	16300	29225	4.92	2.0E-26	X86694.1	NT	Homo sapiens chromosome 21 segment HS21C082
11105	24065		2.38	2.0E-26	D87675.1	NT	DKFZp566L171_s1 566 (synonym: hfrd2) Homo sapiens cDNA clone DKFZp566L171 3'
11553	24493	38049	2.55	2.0E-26	AI801412.1	EST_HUMAN	M.musculus mRNA for asfocytic phosphoprotein, PEA-15
11748	24633		1.78	2.0E-26	AF050566.1	NT	Homo sapiens DNA for amyloid precursor protein, complete cds
12097	24968	38565	1.94	2.0E-26	M32788.1	NT	to89a01.x1 NCI_CGAP_Gas4 Homo sapiens cDNA clone IMAGE:2185416 3' similar to contains Alu repetitive element; contains element MER20 MER20 repetitive element ;
12388	25168		1.7	2.0E-26	AB037859.1	NT	Homo sapiens MHC class 1 region
						NT	Human endogenous retroviral element S71
						NT	Homo sapiens mRNA for KIAA1438 protein, partial cds

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Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
137	13242	28172	37.48	1.0E-26	BE170371.1	EST_HUMAN	QV4-HT0538-020300-123-a02 HT0538 Homo sapiens cDNA
2063	15081	28100	1.33	1.0E-26	AL039383.2	EST_HUMAN	DKFZp434H1910_1 434 (synonym: htes3) Homo sapiens cDNA clone DKFZp434H1910 5'
2697	15683		11.4	1.0E-26	AF261085.1	NT	Homo sapiens glyceraldehyde-3-phosphate dehydrogenase (GADPH) mRNA, complete cds
7016	20142		2.79	1.0E-26	BE165980.1	EST_HUMAN	MR3-HT0487-150200-113-g01 HT0487 Homo sapiens cDNA
11239	24182		2.12	1.0E-26	AL038487.1	EST_HUMAN	DKFZp566C2146_1 566 (synonym: hfrd2) Homo sapiens cDNA clone DKFZp566C2146 5'
12630	25966		2.65	1.0E-26	H55093.1	EST_HUMAN	CHR220032 Chromosome 22 exon Homo sapiens cDNA clone C22_45 5'
7837	20784		1.24	9.0E-27	BF371227.1	EST_HUMAN	RC8-FN0138-110800-022-A02 FN0138 Homo sapiens cDNA
9658	22815		4.04	9.0E-27	U93163.1	NT	Homo sapiens MAGE-B2 (MAGE-B2), MAGE-B3 (MAGE-B3), MAGE-B4 (MAGE-B4), and MAGE-B1 (MAGE-B1) genes, complete cds
12142	25008		5.95	9.0E-27	BF445556.1	EST_HUMAN	nead3c07.x1 NCI_CGAP_P28 Homo sapiens cDNA clone IMAGE:3253644 3' similar to contains OFR.11
11	13131	28029	4.71	8.0E-27	AI831482.1	EST_HUMAN	wf49c04.x1 NCI_CGAP_Lu19 Homo sapiens cDNA clone IMAGE:2406160 3' similar to contains THR.b2
559	13629		4.61	8.0E-27	AL163227.2	NT	THR repetitive element ;
1414	14447	27419	30.06	8.0E-27	AW162737.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C027
1414	14447	27420	30.06	8.0E-27	AW162737.1	EST_HUMAN	eu87h08.x1 Schneider fetal brain 00004 Homo sapiens cDNA clone IMAGE:2783295 3' similar to gb:K00558
2177	15192	28214	1.1	8.0E-27	AW864776.1	EST_HUMAN	TUBULIN ALPHA-1 CHAIN (HUMAN);
3199	16254	29174	1.17	8.0E-27	P12236	SWISSPROT	TUBULIN ALPHA-1 CHAIN (HUMAN);
3364	16414	29339	0.84	8.0E-27	AF181897.1	NT	PM2-SN0018-220300-002-a07 SN0018 Homo sapiens cDNA
5779	18871	32053	0.97	8.0E-27	AV732214.1	EST_HUMAN	ADP-ATP CARRIER PROTEIN, LIVER ISOFORM T2 (ADP/ATP TRANSLOCASE 3) (ADENINE NUCLEOTIDE TRANSLOCATOR 3) (ANT 3)
7170	18401		2.12	8.0E-27	BE265690.1	EST_HUMAN	Homo sapiens WRN (WRN) gene, complete cds
7248	19983	33280	2.41	8.0E-27	N84970.1	EST_HUMAN	AV732214 HTF Homo sapiens cDNA clone HTFBCB06 5'
9564	22526	35975	1.41	8.0E-27	AW857579.1	EST_HUMAN	MR4-BT0398-250800-204-d06 BT0398 Homo sapiens cDNA
9564	22526	35978	1.41	8.0E-27	AW857579.1	EST_HUMAN	J1751F Human fetal heart, Lambda ZAP Express Homo sapiens cDNA clone J1751 5' similar to
884	13747		1.65	7.0E-27	Z70564.1	NT	REPETITIVE ELEMENT L1
5126	18135		2.05	7.0E-27	AW829172.1	EST_HUMAN	Human endogenous retroviral element HC2
9209	22175		0.98	7.0E-27	D86984.1	NT	h15h12.x1 Scores_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2975879 3' similar to TR:O76040
11101	24081		3.24	7.0E-27	AJ274735.1	NT	O76040 ORF2: FUNCTION UNKNOWN. ;
12759	25402		1.54	7.0E-27	AV723365.1	EST_HUMAN	Human mRNA for KIAA0231 gene, partial cds
						NT	Homo sapiens Xq pseudautosomal region; segment 1/2
						EST_HUMAN	AV723365 HTB Homo sapiens cDNA clone HTBAHE02 5'

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Table 4
Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
11080	24042	37565	10.71	6.0E-27	M28697.1	NT	Human nuclear protein (B23) mRNA, complete cds
8055	20992		0.79	5.0E-27	AL163303.2	NT	Homo sapiens chromosome 21 segment HS21C103
10597	23519	37010	3.37	5.0E-27	BF666814.1	EST_HUMAN	602121491 F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4278527 5'
10597	23519	37011	3.37	5.0E-27	BF666814.1	EST_HUMAN	602121491 F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4278527 5'
6808	19960	33256	1.72	4.0E-27	9810509	NT	Mus musculus sperm tail associated protein (Slap), mRNA
8271	21240		1.22	4.0E-27	AL163209.2	NT	Homo sapiens chromosome 21 segment HS21C009
8316	21285		1.25	4.0E-27	AF078779.1	NT	Rattus norvegicus putative four repeat ion channel mRNA, complete cds
10101	23027	38504	0.72	4.0E-27	AW880859.1	EST_HUMAN	QV0-OT0033-070300-152-b10 OT0033 Homo sapiens cDNA
11929	24810	38405	1.98	4.0E-27	X89211.1	NT	H. sapiens DNA for endogenous retroviral like element
2057	15076	28096	4.38	3.0E-27	X60658.1	NT	R. rattus RYA3 mRNA for a potential ligand-binding protein
4300	17329	30209	1.08	3.0E-27	BE071824.1	EST_HUMAN	PNC-BT0527-090100-001-d11 BT0527 Homo sapiens cDNA
5419	18522	31400	5.66	3.0E-27	AA077705.1	EST_HUMAN	7B44C08 Chromosome 7 Fetal Brain cDNA Library Homo sapiens cDNA clone 7B44C08
8089	21025	34424	0.57	3.0E-27	BE670351.1	EST_HUMAN	7c33f02.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3284283 3'
9660	22817	36271	4.46	3.0E-27	BF035327.1	EST_HUMAN	60145853 F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3862086 5'
43	13163	28066	9.25	2.0E-27	AF054187.1	NT	Homo sapiens alpha NAC mRNA, complete cds
1911	14935		24.32	2.0E-27	AA565345.1	EST_HUMAN	nk01b10.s1 NCI_CGAP_Prl1 Homo sapiens cDNA clone IMAGE:1000699 similar to gb:M17886 60S
3126	18183		10.81	2.0E-27	AW629172.1	EST_HUMAN	ACIDIC RIBOSOMAL PROTEIN P1 (HUMAN); h151h12.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2975879 3' similar to TR:O76040
3238	16293	29215	1.61	2.0E-27	AF111167.2	NT	Homo sapiens jun dimerization protein gene, partial cds; cfos gene, complete cds; and unknown gene
3238	16293	29216	1.61	2.0E-27	AF111167.2	NT	Homo sapiens jun dimerization protein gene, partial cds; cfos gene, complete cds; and unknown gene
6833	19886	33179	0.72	2.0E-27	H02855.1	EST_HUMAN	y36e01.r1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:150840 5' similar to
8427	21396	34807	1.44	2.0E-27	A1866347.1	EST_HUMAN	SP:HMGC_MOUSE_Q02591 HOMEBOX PROTEIN ; w129g07.x1 NCI_CGAP_U11 Homo sapiens cDNA clone IMAGE:2428268 3'
9624	22568		2.61	2.0E-27	AA551527.1	EST_HUMAN	nk08h05.s1 NCI_CGAP_Thy1 Homo sapiens cDNA clone IMAGE:943737 similar to contains L1.13 L1
10151	23076	36552	0.78	2.0E-27	X60658.1	NT	R. rattus RYA3 mRNA for a potential ligand-binding protein
10395	23317	36797	1.32	2.0E-27	M78590.1	EST_HUMAN	EST T00738 Fetal brain, Stratiogene (cat#936206) Homo sapiens cDNA clone HFBCF07
10395	23317	36798	1.32	2.0E-27	M78590.1	EST_HUMAN	EST T00738 Fetal brain, Stratiogene (cat#936206) Homo sapiens cDNA clone HFBCF07
11302	24252	37778	2.97	2.0E-27	AU121685.1	EST_HUMAN	AU121685 MAMMAT Homo sapiens cDNA clone MAMMA1000746 5'
11816	14935		19.93	2.0E-27	AA555345.1	EST_HUMAN	nk01b10.s1 NCI_CGAP_Prl1 Homo sapiens cDNA clone IMAGE:1000699 similar to gb:M17886 60S ACIDIC RIBOSOMAL PROTEIN P1 (HUMAN);

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Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
436	13510		2.28	1.0E-27	AL163246.2	NT	Homo sapiens chromosome 21 segment HS21C046
998	14049	27002	1.58	1.0E-27	AB028898.1	NT	Homo sapiens DNA, DLEC1 to ORCTL4 gene region, section 1/2 (DLEC1, ORCTL3, ORCTL4 genes, complete cds)
1707	14738	27720	0.95	1.0E-27	4827059	NT	Homo sapiens xylulokinase (H. influenzae) homolog (XYLB) mRNA
4108	17142		1.08	1.0E-27	BE350127.1	EST_HUMAN	h09g01.x1 NCL_CGAP_Kid13 Homo sapiens cDNA clone IMAGE:3146256 3' similar to contains MER29.b3
6094	19751	33028	5.21	1.0E-27	6006855	NT	MER29 repetitive element;
7054	20076	33384	2.01	1.0E-27	F30158.1	EST_HUMAN	Homo sapiens Retina-derived POU-domain factor-1 (RPF-1), mRNA
7054	20076	33385	2.01	1.0E-27	F30158.1	EST_HUMAN	HSPD20461 HM3 Homo sapiens cDNA clone s4000095C10
8957	21923	35351	0.71	1.0E-27	AB007923.1	NT	HSPD20461 HM3 Homo sapiens cDNA clone s4000095C10
9337	22302		2.33	1.0E-27	BE079780.1	EST_HUMAN	Homo sapiens mRNA for KIAA0454 protein, partial cds
10080	23007	36478	2.7	1.0E-27	D87449.1	NT	RC8-BT0627-140200-011-E08 BT0627 Homo sapiens cDNA
12016	24893	38490	3.73	1.0E-27	AF111093.1	NT	Human mRNA for KIAA0260 gene, partial cds
143	13245		2.16	9.0E-28	BE348399.1	EST_HUMAN	Bos taurus latrophilin 3 splice variant bbah mRNA, complete cds
311	13403	26329	2.84	9.0E-28	AU126260.1	EST_HUMAN	h1w7c11.x1 NCL_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3183188 3' similar to TR:Q07314 Q07314
4817	17834	30732	1.08	9.0E-28	P50447	SWISSPROT	SECRETED NEUREXIN III-ALPHA-C PRECURSOR, [3] TR:Q07280 TR:Q07313;
12222	25059		3.71	9.0E-28	BF377859.1	EST_HUMAN	AU126260 NT2RP1 Homo sapiens cDNA clone NT2RP1000443 5'
12553	25817		1.9	8.0E-28	AW157571.1	EST_HUMAN	ALPHA-1-ANTITRYPSIN PRECURSOR (ALPHA-1 PROTEASE INHIBITOR) (ALPHA-1-ANTIPROTEINASE)
1185	14228	27182	8.96	7.0E-28	AU142750.1	EST_HUMAN	CM2-TN0140-070900-372-g01 TN0140 Homo sapiens cDNA
11520	24461	38012	2.43	7.0E-28	11417866	NT	au83h08.x1 Schneider fetal brain 00004 Homo sapiens cDNA clone IMAGE:2782911 3' similar to TR:C60302 O60302 KIAA0555 PROTEIN, contains element MER22 repetitive element;
12181	25029		2.98	7.0E-28	AV733348.1	EST_HUMAN	AU142750 Y79AA1 Homo sapiens cDNA clone Y79AA1000824 5'
9271	22237		1.09	6.0E-28	AF016052.1	NT	Homo sapiens gamma-glutamyltransferase-like activity 1 (GGTLA1), mRNA
12806	25433		3.82	6.0E-28	AA504562.1	EST_HUMAN	AV735348 CB Homo sapiens cDNA clone CBFAKA12 5'
318	13410		3.1	5.0E-28	A1921003.1	EST_HUMAN	Homo sapiens zinc finger protein ZNF191 (ZNF191) gene, complete cds
4035	17073	29973	1.52	5.0E-28	R79762.1	EST_HUMAN	aa60e03.1 NCL_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:825340 5' similar to contains Alu repetitive element; contains element PTR5 repetitive element;
2633	15632	28657	1.48	4.0E-28	AW195066.1	EST_HUMAN	w018c07.x1 NCL_CGAP_Pan1 Homo sapiens cDNA clone IMAGE:2455692 3' similar to contains THR.b1 THR repetitive element;
2989	16047	28957	1.18	4.0E-28	4505316	NT	y08f10.1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:146443 5'
3125	16182	28092	1.93	4.0E-28	BE409100.1	EST_HUMAN	x133c09.x1 NCL_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2895504 3' similar to SW:GG95_HUMAN Q08379 GOLGIN-95;
							Homo sapiens myosin phosphatase, target subunit 1 (MYPT1), mRNA
							601300703F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3635305 5'

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7551	20514	33872	2.45	4.0E-28	AI198941.1	EST_HUMAN	qf66f10.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1755019 3' similar to gb:M19503 LINE-1 REVERSE TRANSCRIPTASE HOMOLOG (HUMAN);
11213	24166		3.51	4.0E-28	AF029308.1	NT	Homo sapiens chromosome 9 duplication of the T cell receptor beta locus and tyrosinogen gene families
11349	24299		38.65	4.0E-28	AB038241.1	NT	Felis catus GAPDH mRNA for glyceraldehyde-3-phosphate dehydrogenase, complete cds
11364	20514	33872	3.87	4.0E-28	AI198941.1	EST_HUMAN	qf66f10.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1755019 3' similar to gb:M19503 LINE-1 REVERSE TRANSCRIPTASE HOMOLOG (HUMAN);
12599	25301		1.86	4.0E-28	AW854244.1	EST_HUMAN	RC3-CT0254-240400-210-F12 CT0254 Homo sapiens cDNA
1288	14323		2.61	3.0E-28	AF155382.1	NT	Homo sapiens metalloprotease-like, disintegrin-like, cysteine-rich protein 2 epsilon (ADAM22) mRNA, complete cds
9179	22145	35572	1.94	3.0E-28	BF354030.1	EST_HUMAN	MR3-HT0713-280500-013-009 HT0713 Homo sapiens cDNA
11282	24232	37758	2.14	3.0E-28	U53588.1	NT	Homo sapiens MHC class 1 region
12628	25315		2.92	3.0E-28	AI831901.1	EST_HUMAN	wj98f07.x1 NCI_CGAP_Lym12 Homo sapiens cDNA clone IMAGE:2410885 3' similar to contains Alu repetitive element/contains element HGR repetitive element ;
89	13205	26129	11.64	2.0E-28	BE062167.1	EST_HUMAN	RC1-BT0254-220300-019-c05 BT0254 Homo sapiens cDNA
1047	14093	27045	4.14	2.0E-28	4501912	NT	Homo sapiens a disintegrin and metalloprotease domain 23 (ADAM23) mRNA
1169	14210	27164	12.37	2.0E-28	Y11107.3	NT	Homo sapiens ITGB4 gene for integrin beta 4 subunit, exons 3-41
2485	15489	28513	2.27	2.0E-28	AI348634.1	EST_HUMAN	qo35f06.x1 NCI_CGAP_Lu5 Homo sapiens cDNA clone IMAGE:1910483 3' similar to contains L1.b2.L1 repetitive element ;
3373	16423	29348	0.76	2.0E-28	AL163209.2	NT	Homo sapiens chromosome 21 segment HS21C009
8440	19505	32756	1.48	2.0E-28	BF224402.1	EST_HUMAN	hr76c03.x1 NCI_CGAP_Kid1 Homo sapiens cDNA clone IMAGE:3134404 3' similar to contains LOR1.b1 LOR1 repetitive element ;
6464	19529		6.46	2.0E-28	BF212905.1	EST_HUMAN	601814196f1 NIH_MGC_54 Homo sapiens cDNA clone IMAGE:4048751 5'
8378	21348	34760	0.76	2.0E-28	AF005273.1	NT	Sus scrofa domestica submaxillary apomucin mRNA, complete cds
9943	22870		8.68	2.0E-28	AW972305.1	EST_HUMAN	EST384394 IMAGE resequences, MAGL Homo sapiens cDNA
11936	24817	38414	1.92	2.0E-28	AF224669.1	NT	Homo sapiens mannosidase, beta A, lysosomal (MANBA) gene, and ubiquitin-conjugating enzyme E2D 3 (UBE2D3) genes, complete cds
12609	25308		2.06	2.0E-28	H06376.1	EST_HUMAN	yf79c09.1 Soares infant brain 1N1B Homo sapiens cDNA clone IMAGE:44300 5'
1474	14507	27481	3.15	1.0E-28	D38044.1	NT	Human gene for Ah-receptor, exon 7-9
2229	15243	28268	1.84	1.0E-28	BF333236.1	EST_HUMAN	QV1-BT0821-120900-360-b03 BT0821 Homo sapiens cDNA
2692	15668	28705	0.92	1.0E-28	AF000995.1	NT	Homo sapiens ubiquitous TPR motif, Y isoform (UTY) mRNA, alternative transcript 2, complete cds
4985	18000	30889	0.64	1.0E-28	AV732194.1	EST_HUMAN	AV732194 HTF Homo sapiens cDNA clone HTFBIH05 5'
8193	21163		8.03	1.0E-28	11429885	NT	Homo sapiens similar to ribosomal protein L12 (H. sapiens) (LOC883091), mRNA
8352	21321		3.37	1.0E-28	8922763	NT	Homo sapiens hypothetical protein FLJ10968 (FLJ10968), mRNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9833	22577	36027	4.47	1.0E-28	AA308744.1	EST_HUMAN	EST179615 HCC cell line (metastasis to liver in mouse) II Homo sapiens cDNA 5' end similar to similar to retroviral LTR
10235	23160	36648	6.47	1.0E-28	4758431	NT	Homo sapiens gamma-glutamyltransferase-like activity 1 (GGT1A1), mRNA
10235	23160	36649	6.47	1.0E-28	4758431	NT	Homo sapiens gamma-glutamyltransferase-like activity 1 (GGT1A1), mRNA
12186	25033		4.36	1.0E-28	AA054182.1	EST_HUMAN	z51a01.1 Soares retina N2b-4HR Homo sapiens cDNA clone IMAGE:380448 5'
12931	25716		2.58	1.0E-28	AL163247.2	NT	Homo sapiens chromosome 21 segment HS21 C047
13037	25918	31302	3.46	9.0E-29	AW663987.1	EST_HUMAN	h176p06.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2978266 3'
12713	25367		3.12	8.0E-29	Q00130	SWISSPROT	HYPOTHETICAL GENE 50 PROTEIN
1606	14638	27615	1.04	7.0E-29	AW966447.1	EST_HUMAN	EST378521 IMAGE resequences, MAGI Homo sapiens cDNA
3564	19610		0.9	7.0E-29	BE254708.1	EST_HUMAN	601114990F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3355387 5'
13086	25616		9.37	7.0E-29	AJ132352.1	NT	Rattus norvegicus mRNA for 45 kDa secretory protein, partial
597	13664	26578	6.67	6.0E-29	AI936748.1	EST_HUMAN	wp69b01.x1 NC1_CGAP_Brn25 Homo sapiens cDNA clone IMAGE:2466985 3' similar to TR.O15475
12489	25234		8.12	6.0E-29	BE940436.1	EST_HUMAN	O15475 UNNAMED HERV-H PROTEIN : contains LTR7.b1 LTR7 repetitive element ;
12574	25284		1.97	6.0E-29	BF568097.1	EST_HUMAN	RC3-JT0082-210800-021-c05 UT0062 Homo sapiens cDNA
5033	18047		1.34	5.0E-29	AL163203.2	NT	602184092F1 NIH_MGC_42 Homo sapiens cDNA clone IMAGE:4300079 5'
9083	22049		8.5	5.0E-29	AW887541.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C003
							RC3-OT0091-170300-011-c12 OT0091 Homo sapiens cDNA
3246	16301		1.33	4.0E-29	AI752367.1	EST_HUMAN	cn15c02.x1 Normal Human Trabecular Bone Cells Homo sapiens cDNA clone NHTBC_cn15c02 random
6125	19203		5.91	4.0E-29	BE164930.1	EST_HUMAN	QV1-HT0471-280300-121-a05 HT0471 Homo sapiens cDNA
							wd35g06.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2330170 3' similar to contains
8417	21386	34794	0.92	4.0E-29	AI678101.1	EST_HUMAN	MER29.12 MER29 repetitive element ;
8417	21386	34795	0.92	4.0E-29	AI678101.1	EST_HUMAN	MER29.12 MER29 repetitive element ;
9097	22063	35488	2.97	4.0E-29	JO4988.1	NT	Human 90 KD heat shock protein gene, complete cds
2379	15387	28411	0.94	3.0E-29	U87847.1	NT	Human beta-galactosidase alpha2,6-sialyltransferase (SIAT1) mRNA, exon U
4444	17470	30359	1.61	3.0E-29	AB042297.1	NT	Homo sapiens PTS gene for 6-pyruvoyl-tetrahydropterin synthase, complete cds
4764	17784	30880	0.94	3.0E-29	BF332356.1	EST_HUMAN	QV1-BT0821-120900-360-b03 BT0821 Homo sapiens cDNA
6040	19122	32327	0.77	3.0E-29	BE314018.1	EST_HUMAN	601152657F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:3508627 5'
9085	22051	35473	2.19	3.0E-29	D38044.1	NT	Human gene for Ah-receptor, exon 7-9
							xv17f03.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2813405 3' similar to contains Alu
9655	22598	36047	1.97	3.0E-29	AW303317.1	EST_HUMAN	repetitive element; contains MER19.12 MER19 repetitive element ;
9889	22842		2.2	3.0E-29	AL163246.2	NT	Homo sapiens chromosome 21 segment HS21C046

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1518	14550		1.02	7.0E-30	BE091133.1	EST_HUMAN	PIM4-BT0724-150400-004-d11 BT0724 Homo sapiens cDNA
1571	14604		1.4	6.0E-30	X51755.1	NT	Human lambda-immunoglobulin constant region complex (germline)
1788	14817	27802	1.8	6.0E-30	D25303.1	NT	Human mRNA for Integrin alpha subunit, complete cds
3204	16259	29178	2.51	6.0E-30	BE008026.1	EST_HUMAN	QV0-BN0147-280400-214-f12 BN0147 Homo sapiens cDNA
4791	16259	29178	1.02	6.0E-30	BE008026.1	EST_HUMAN	QV0-BN0147-280400-214-f12 BN0147 Homo sapiens cDNA
10905	23825	37337	0.74	6.0E-30	AF177227.1	NT	Homo sapiens CTCL tumor antigen se20-10 mRNA, partial cds
13054	14604		4.35	6.0E-30	X51755.1	NT	Human lambda-immunoglobulin constant region complex (germline)
4041	17079	29979				EST_HUMAN	ig92g03.x1 NCI_CGAP_CLL1 Homo sapiens cDNA clone IMAGE:2116276 3' similar to contains Alu repetitive element
5310	25746		32.98	5.0E-30	AI399992.1	EST_HUMAN	Human acylate hydratase (ACO2) gene, exon 7
11233	24186		4.98	5.0E-30	U87931.1	NT	Homo sapiens chromosome 21 segment HS21C078
11489	24432	37981	2.21	5.0E-30	AL163278.2	NT	Homo sapiens chromosome 21 segment HS21C010
11489	24432	37982	2.03	5.0E-30	AL163210.2	NT	Homo sapiens chromosome 21 segment HS21C010
2153	15169	28185	2.03	5.0E-30	AL163210.2	NT	Homo sapiens chromosome 21 segment HS21C010
2153	15169	28186	1.79	4.0E-30	AW937471.1	EST_HUMAN	QV3-DT0043-080200-080-006 DT0043 Homo sapiens cDNA
7035	18367	31254	1.79	4.0E-30	AW937471.1	EST_HUMAN	QV3-DT0043-080200-080-006 DT0043 Homo sapiens cDNA
9256	22222	35652	0.55	4.0E-30	P11369	SWISSPROT	RETROVIRUS-RELATED POL POLYPROTEIN [CONTAINS: REVERSE TRANSCRIPTASE; ENDONUCLEASE]
1154	14196		2.5	4.0E-30	AW812488.1	EST_HUMAN	CM1-ST0181-091199-035-08 ST0181 Homo sapiens cDNA
3770	16812	29721	4.51	3.0E-30	AI335551.1	EST_HUMAN	qq93c05.x1 Soares_tet_fetus_Nb2HF8_9w Homo sapiens cDNA clone IMAGE:1938920 3' similar to contains MER29.b2 MER29 repetitive element
7470	20436	33793	1.03	3.0E-30	AF128893.1	NT	Homo sapiens telomerase reverse transcriptase (TERT) gene, exons 1-8
8284	21253		0.5	3.0E-30	T18882.1	EST_HUMAN	b12056t Testis 1 Homo sapiens cDNA clone b12056
8831	21798		0.52	3.0E-30	AF078779.1	NT	Rattus norvegicus putative four repeat ion channel mRNA, complete cds
10800	23721		0.44	3.0E-30	AF078779.1	NT	Rattus norvegicus putative four repeat ion channel mRNA, complete cds
10832	23852		2.18	3.0E-30	BE350127.1	EST_HUMAN	h09g01.x1 NCI_CGAP_K1d13 Homo sapiens cDNA clone IMAGE:3146256 3' similar to contains MER29.b3 MER29 repetitive element
10932	23852	37366	0.52	3.0E-30	AB032669.1	NT	Homo sapiens mRNA for KIAA1143 protein, partial cds
11541	24482	38034	0.52	3.0E-30	AB032669.1	NT	Homo sapiens mRNA for KIAA1143 protein, partial cds
676	13739	26666	5.69	3.0E-30	P34056	SWISSPROT	TRANSCRIPTION FACTOR AP-2
1086	14130		1.57	2.0E-30	AW867316.1	EST_HUMAN	CM0-CT0307-310100-158-h03 CT0307 Homo sapiens cDNA
1475	14508	27482	3.03	2.0E-30	F08688.1	EST_HUMAN	HSC23F051 normalized infant brain cDNA Homo sapiens cDNA clone c-23f05
2127	15721	28738	5.36	2.0E-30	BE175877.1	EST_HUMAN	RC5-HT0582-110400-013-H08 HT0582 Homo sapiens cDNA
2930	15988	28909	11.19	2.0E-30	BE765332.1	EST_HUMAN	IL2-NT0101-280700-116-E04 NT0101 Homo sapiens cDNA
			6.11	2.0E-30	AF114165.1	NT	Homo sapiens Y-linked zinc finger protein (ZFY) gene, complete cds

Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3803	16843	29751	2.1	2.0E-30	AW206581.1	EST_HUMAN	U1-H-B11-af-c-12-0-U1.s1 NCL_CGAP_Sub3 Homo sapiens cDNA clone IMAGE:2722558 3'
4812	17829	30726	1.76	2.0E-30	BE298945.1	EST_HUMAN	G01119860F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3029438 5'
4812	17829	30727	1.76	2.0E-30	BE298945.1	EST_HUMAN	G01119860F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3029438 5'
6822	19872	33269	0.71	2.0E-30	BF306337.1	EST_HUMAN	G01893208F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4138983 5'
8820	21787	35211	0.69	2.0E-30	AA019103.1	EST_HUMAN	ze88c10.r1 Soares retina N2b-4HR Homo sapiens cDNA clone IMAGE:363186 5'
8882	21849	35270	7.02	2.0E-30	C16939.1	EST_HUMAN	C18839 Human placenta cDNA (TFujivara) Homo sapiens cDNA clone GEN-570C01 5'
8882	21948	35371	3.99	2.0E-30	BE870617.1	EST_HUMAN	7e37c12.x1 NCL_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3284662 3' similar to SW:DHSA_HUMAN P31040 SUCCINATE DEHYDROGENASE [UBIQUINONE] FLAVOPROTEIN SUBUNIT PRECURSOR ;
8882	21948	35372	3.99	2.0E-30	BE870617.1	EST_HUMAN	7e37c12.x1 NCL_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3284662 3' similar to SW:DHSA_HUMAN P31040 SUCCINATE DEHYDROGENASE [UBIQUINONE] FLAVOPROTEIN SUBUNIT PRECURSOR ;
10356	23280	36756	3.88	2.0E-30	AW971568.1	EST_HUMAN	EST383657 IMAGE resequences, MAGI, Homo sapiens cDNA ha33d06.x1 NCL_CGAP_Kid12 Homo sapiens cDNA clone IMAGE:2875489 3' similar to contains THR.b3 THR repetitive element ;
10442	23364	36854	8.55	2.0E-30	AW470791.1	EST_HUMAN	CT1839 Human placenta cDNA (TFujivara) Homo sapiens cDNA clone GEN-570C01 5'
286	13381	26309	19.55	1.0E-30	C18939.1	EST_HUMAN	CT1839 Human placenta cDNA (TFujivara) Homo sapiens cDNA clone IMAGE:2910981 3' similar to contains hd30b04.x1 Soares_NFL_T_OBC_S1 Homo sapiens cDNA clone IMAGE:868599 3'
539	13610	26529	7.04	1.0E-30	AW468897.1	EST_HUMAN	MER1.13 MER1 MER1 repetitive element ; Homo sapiens chromosome 21 segment HS21C003
717	13779	26713	1.23	1.0E-30	AL163203.2	NT	ac77b08.s1 Stratagene lung (#937210) Homo sapiens cDNA clone IMAGE:868599 3'
2222	15238	28260	3.82	1.0E-30	AA664377.1	EST_HUMAN	G0202560F1 NCL_CGAP_Bmt87 Homo sapiens cDNA clone IMAGE:4157891 5'
2469	15473	28496	2.39	1.0E-30	BF347728.1	EST_HUMAN	EST186868 HCC cell line (metastasis to liver in mouse) II Homo sapiens cDNA 5' end
3067	16124	29037	1.12	1.0E-30	AA315045.1	EST_HUMAN	G01809932F1 NIH_MGC_18 Homo sapiens cDNA clone IMAGE:4040694 5'
7995	20934	34328	2.08	1.0E-30	BF183230.1	EST_HUMAN	GHR220532 Chromosome 22 exon Homo sapiens cDNA clone C22_728 5'
12862	25941		11.93	1.0E-30	H55593.1	EST_HUMAN	yf99b08.r1 Soares infant brain 1N1B Homo sapiens cDNA clone IMAGE:30566 5' similar to gb:X12953 RAS- RELATED PROTEIN RAB-2 (HUMAN);
8667	21635	35059	0.92	9.0E-31	R18214.1	EST_HUMAN	yf99b08.r1 Soares infant brain 1N1B Homo sapiens cDNA clone IMAGE:30566 5' similar to gb:X12953 RAS- RELATED PROTEIN RAB-2 (HUMAN);
8667	21635	35057	0.92	9.0E-31	R18214.1	EST_HUMAN	RELATD PROTEIN RAB-2 (HUMAN);
8971	21937		1.79	9.0E-31	Z38293.1	EST_HUMAN	HSC05F032 normalized Infant brain cDNA Homo sapiens cDNA clone c-05103 3'
8973	21939	35364	0.49	9.0E-31	AF078779.1	NT	Rattus norvegicus putative four repeat ion channel mRNA, complete cds
1078	14123	27075	1.82	8.0E-31	8923389	NT	Homo sapiens hypothetical protein FLJ20420 (FLJ20420), mRNA
2423	15430		5.96	8.0E-31	AL163208.2	NT	Homo sapiens chromosome 21 segment HS21C008
4955	17970	30880	1.12	8.0E-31	P23275	SWISSPROT	OLFACTORY RECEPTOR 15 (OR3)
4955	17970	30861	1.12	8.0E-31	P23275	SWISSPROT	OLFACTORY RECEPTOR 15 (OR3)

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
712	13774		1.99	7.0E-31	AA372637.1	EST_HUMAN	EST84555 Colon adenocarcinoma IV Homo sapiens cDNA 5' and
2676	15672	28691	2.38	7.0E-31	BE326517.1	EST_HUMAN	hw05a11.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3182012 3'
2676	15672	28692	2.38	7.0E-31	BE326517.1	EST_HUMAN	hw05a11.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3182012 3'
8744	21712	35133	0.99	7.0E-31	AF208541.1	NT	Homo sapiens V1-vascular vasopressin receptor AVPR1A gene, promoter region and partial cds
8744	21712	35134	0.99	7.0E-31	AF208541.1	NT	Homo sapiens V1-vascular vasopressin receptor AVPR1A gene, promoter region and partial cds
9621	22565		0.92	7.0E-31	BE408811.1	EST_HUMAN	601304125F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3638310 5'
12711	25366	31771	5.66	7.0E-31	X51755.1	NT	Human lambda-immunoglobulin constant region complex (germline)
3691	16734		3.06	6.0E-31	AF223391.1	NT	Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced
8493	21481		7.57	8.0E-31	AF055086.1	NT	Homo sapiens MHC class 1 region
8674	21642	35087	0.7	6.0E-31	BE350127.1	EST_HUMAN	h09g01.x1 NCI_CGAP_Kid13 Homo sapiens cDNA clone IMAGE:3146256 3' similar to contains MER29.b3 MER29 repetitive element
11090	24050	37573	1.86	6.0E-31	AU119105.1	EST_HUMAN	AU119105 HEMBA1 Homo sapiens cDNA clone HEMBA1005050 5'
12325	25127	31848	2.27	6.0E-31	AW372868.1	EST_HUMAN	RC5-BT0377-091289-031-D12 BT0377 Homo sapiens cDNA
12456	25764		2.08	6.0E-31	BE894488.1	EST_HUMAN	601433087F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3918524 5'
194	13295	26222	2.83	5.0E-31	M60694.1	NT	Homo sapiens type I DNA topoisomerase gene, exon 8
194	13295	26223	2.83	5.0E-31	M60694.1	NT	Homo sapiens type I DNA topoisomerase gene, exon 8
8788	21755		1.46	5.0E-31	BF056540.1	EST_HUMAN	7106104.x1 NCI_CGAP_GC8 Homo sapiens cDNA clone IMAGE:3443479 3' similar to TR:Q13537 Q13537
598	13865		3.45	4.0E-31	AJ271735.1	NT	SIMILAR TO POGO ELEMENT. contains L1.1 L1 repetitive element
						NT	Homo sapiens Xq pseudautosomal region; segment 1/2
1615	14647	27622	1.01	4.0E-31	Q10473	SWISSPROT	POLYPEPTIDE N-ACETYL GALACTOSAMINYLTRANSFERASE (PROTEIN-UDP
1834	14961		2.09	4.0E-31	AL163280.2	NT	ACETYL GALACTOSAMINYLTRANSFERASE (UDP-GALNAC:POLYPEPTIDE, N-
2800	15792		1.98	4.0E-31	5730038	NT	ACETYL GALACTOSAMINYLTRANSFERASE (GALNAC-T1)
10900	23820	37329	0.43	4.0E-31	AF084464.1	NT	Homo sapiens citromosome 21 segment HS21C080
						NT	Homo sapiens SET domain and mariner transposase fusion gene (SETMAR) mRNA
2603	15603	28625	0.98	3.0E-31		NT	Rattus norvegicus GTP-binding protein RRM2 (Ram2) mRNA, complete cds
						NT	Homo sapiens SEC63, endoplasmic reticulum translocan component (S. cerevisiae) like (SEC63L), mRNA
7562	20525	33883	6.73	3.0E-31	4826853	NT	Homo sapiens NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 8 (19kD, ASH) (NDUFB8) mRNA
7736	20891	34055	1.28	3.0E-31	11420329	NT	Homo sapiens hypothetical protein FLJ10842 (FLJ10842), mRNA
8501	21469		2.35	3.0E-31	AL163206.2	NT	Homo sapiens chromosome 21 segment HS21C008
9939	22868	36328	4.66	3.0E-31	D14523.1	NT	Horse mRNA for ferritin L-chain, complete cds
10961	23881	37394	0.52	3.0E-31	AA421242.1	EST_HUMAN	z06604.t1 Scores_NHT Homo sapiens cDNA clone IMAGE:731047 5'

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10995	23961	37486	3.17	3.0E-31	P11174	SWISSPROT	40S RIBOSOMAL PROTEIN S15 (RIG PROTEIN)
11487	24430		6.84	3.0E-31	BF035327.1	EST_HUMAN	601458331F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3802086 5'
1932	14956	27953	1.33	2.0E-31	AW638171.1	EST_HUMAN	QV2.LT0051-260300-111-103 LT0051 Homo sapiens cDNA
2224	15238	28262	0.98	2.0E-31	AI393388.1	EST_HUMAN	tg44g05.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2111672 3'
2347	15356	28379	2.93	2.0E-31	AL119245.1	EST_HUMAN	DKFZp761G1513.J1 761 (synonym: hamy2) Homo sapiens cDNA clone DKFZp761G1513 5'
							aa8811.s1 Stratagene fetal retina 937202 Homo sapiens cDNA clone IMAGE:838413 3' similar to contains
							THR.12 THR repetitive element:
2447	15452	28473	5.67	2.0E-31	AA458824.1	EST_HUMAN	UI-H-B13-akb-f-09-0-U1.s1 NCL_CGAP_Sub5 Homo sapiens cDNA clone IMAGE:2733833 3'
5347	18452	31323	0.72	2.0E-31	AW444496.1	EST_HUMAN	h09g01.x1 NCL_CGAP_Kid13 Homo sapiens cDNA clone IMAGE:3146256 3' similar to contains MER29.B3
5798	18890	32072	2.86	2.0E-31	BE350127.1	EST_HUMAN	MER29 repetitive element:
9431	22395		2.71	2.0E-31	AA877764.1	EST_HUMAN	m0604.s1 NCL_CGAP_Cot10 Homo sapiens cDNA clone IMAGE:1161055 3' similar to TR:Q13537 Q13537
9562	22524	35973	4.13	2.0E-31	7681535	NT	MER37 TRANSPOSABLE ELEMENT, COMPLETE CONSENSUS SEQUENCE.:
10268	23191	36877	1.13	2.0E-31	AV710948.1	EST_HUMAN	Homo sapiens B9 protein (B9), mRNA
10266	23191	36678	1.13	2.0E-31	AV710948.1	EST_HUMAN	AV710948 Cu Homo sapiens cDNA clone CUAALB07 5'
10435	23357	36844	2.57	2.0E-31	BE408611.1	EST_HUMAN	601304125F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3638310 5'
10435	23357	36845	2.57	2.0E-31	BE408611.1	EST_HUMAN	601304125F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3638310 5'
12427	25195		1.91	2.0E-31	AF148512.1	NT	Homo sapiens hexokinase II gene, promoter region
12566	25987		3.94	2.0E-31	AI114527.1	EST_HUMAN	HA1110 Human fetal liver cDNA library Homo sapiens cDNA
17	13137	26036	11.03	1.0E-31	U93163.1	NT	Homo sapiens MAGE-B2 (MAGE-B2), MAGE-B3 (MAGE-B3), MAGE-B4 (MAGE-B4), and MAGE-B1 (MAGE-B1) genes, complete cds
1671	14703	27678	3.34	1.0E-31	O96371	SWISSPROT	OLFACTORY RECEPTOR 2C1
1671	14703	27679	3.34	1.0E-31	O96371	SWISSPROT	OLFACTORY RECEPTOR 2C1
1671	14703	27680	3.34	1.0E-31	O96371	SWISSPROT	OLFACTORY RECEPTOR 2C1
4666	17687	30571	1.35	1.0E-31	AL134376.1	EST_HUMAN	DKFZp547B235.J1 547 (synonym: hfbt1) Homo sapiens cDNA clone DKFZp547B235 5'
4666	17687	30572	1.35	1.0E-31	AL134376.1	EST_HUMAN	DKFZp547B235.J1 547 (synonym: hfbt1) Homo sapiens cDNA clone DKFZp547B235 5'
5365	18470	31341	3.75	1.0E-31	AW391679.1	EST_HUMAN	MR3-S10220-151299-028-008_1 ST0220 Homo sapiens cDNA
6266	19329	32559	2.31	1.0E-31	AF048727.1	NT	Homo sapiens minisatellite ceb1 repeat region
							Bos taurus xenobiotic/medium-chain fatty acid:CoA ligase form XL-III mRNA, nuclear mRNA encoding
7506	20471	33831	1.08	1.0E-31	AF126145.1	NT	mitochondrial protein, complete cds
8132	21069	34468	0.76	1.0E-31	BE972818.1	EST_HUMAN	601652052F1 NIH_MGC_82 Homo sapiens cDNA clone IMAGE:3935293 5'
10596	23518	37009	0.68	1.0E-31	U93163.1	NT	Homo sapiens MAGE-B2 (MAGE-B2), MAGE-B3 (MAGE-B3), MAGE-B4 (MAGE-B4), and MAGE-B1 (MAGE-B1) genes, complete cds

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11261	24213	37737	4.66	1.0E-31	AI086434.1	EST_HUMAN	qf21h03.x1 NCI_CGAP_Bm25 Homo sapiens cDNA clone IMAGE:1760709 3' similar to TR:Q16595 Q16595 FRATAXIN.
12103	24974	38571	1.5	1.0E-31	U66081.1	NT	Human germline T-cell receptor beta chain TCRBV17S1A1T, TCRBV2S1, TCRBV10S1P, TCRBV28S1P, TCRBV19S1P, TCRBV15S1, TCRBV11S1A1T, HVB relic, TCRBV28S1P, TCRBV34S1, TCRBV14S1, TCRBV3S1, TCRBV4S1A1T, TRY4, TRY5, TRY6, TRY7, TRY8, TCRBD1, TCRBJ1S1, TCRBJ1S2.>
6795	19849	33134	2.13	9.0E-32	AV723976.1	EST_HUMAN	AV723976 HTB Homo sapiens cDNA clone HTBAA.G01 5'
7598	20559	33919	0.53	9.0E-32	L31770.1	NT	Bos taurus vacuolar H+-ATPase subunit mRNA, complete cds
7848	20795		0.85	9.0E-32	11430822	NT	Homo sapiens hypothetical protein FLJ11284 (FLJ11284), mRNA
2090	15107	28126	3.05	8.0E-32	AI067770.1	EST_HUMAN	oz15a09.x1 Soares_fetal_liver_spleen_INFLS_S1 Homo sapiens cDNA clone IMAGE:1675384 3'
5559	18656	31601	0.89	8.0E-32	AW997214.1	EST_HUMAN	RC2-BN0048-200300-015-e04 BN0048 Homo sapiens cDNA
4896	17913	30803	1.16	7.0E-32	P62581	SWISSPROT	NUCLEAR ENVELOPE PORE MEMBRANE PROTEIN POM 121 (PORE MEMBRANE PROTEIN OF 121 KD) (P145)
12405	25178		7.66	7.0E-32	X17283.1	NT	Human chromosome 22 immunoglobulin V(K) gene, part with 5' breakpoint between orphion and neighbouring non-amplified region
2742	15736	28752	1.2	6.0E-32	AI478104.1	EST_HUMAN	Im34a10.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2159994 3' similar to contains MER29.13 MER29 repetitive element;
7591	20552		1.29	6.0E-32	BE888016.1	EST_HUMAN	601511530F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3913087 5'
1035	14081	27032	17.73	5.0E-32	AF116827.1	NT	Homo sapiens PRO1181 mRNA, complete cds
931	13984		1.85	4.0E-32	AL163246.2	NT	Homo sapiens chromosome 21 segment HS21C046
7861	20805	34181	3.03	4.0E-32	11432574	NT	Homo sapiens AT-binding transcription factor 1 (ATBF1), mRNA
7861	20805	34182	3.03	4.0E-32	11432574	NT	Homo sapiens AT-binding transcription factor 1 (ATBF1), mRNA
8702	21670		1	4.0E-32	BE084410.1	EST_HUMAN	RC4-BT0311-141199-011-h06 BT0311 Homo sapiens cDNA
456	13629	26459	3.32	3.0E-32	Y17293.1	NT	Homo sapiens FLI1 gene, partial
1448	14481	27458	9.76	3.0E-32	AV731500.1	EST_HUMAN	AV731500 HTF Homo sapiens cDNA clone HTFAK.C07 5'
9749	22690	36147	19.67	3.0E-32	AV758634.1	EST_HUMAN	AV758634 BM Homo sapiens cDNA clone BMFBH12 5'
9749	22690	36148	19.67	3.0E-32	AV758634.1	EST_HUMAN	AV758634 BM Homo sapiens cDNA clone BMFBH12 5'
11270	24222	37747	2.81	3.0E-32	AA777621.1	EST_HUMAN	z65a07.s1 Soares_fetal_liver_spleen_INFLS_S1 Homo sapiens cDNA clone IMAGE:448500 3' similar to contains THR13 THR repetitive element;
11550	24491		1.46	3.0E-32	BF036327.1	EST_HUMAN	60145831F1 NIH_MGC_86 Homo sapiens cDNA clone IMAGE:3862086 5'
12430	25197		6.4	3.0E-32	BE279086.1	EST_HUMAN	601156285F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3139701 5'
12788	18336	31283	3.46	3.0E-32	5174574	NT	Homo sapiens myeloid/lymphoid or mixed-lineage leukemia (trithorax (Drosophila) homolog); translocated to, 4 (MLLT4) mRNA

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12786	18336	31284	3.46	3.0E-32	5174574	NT	Homo sapiens myeloid/lymphoid or mixed-lineage leukemia (t(11q24;q24) translocation; translocated to, 4 (MLL1) mRNA
12937	25517		4.33	3.0E-32	BE279086.1	EST_HUMAN	601156285F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3139701 5'
4918	17935	30827	0.97	2.0E-32	BE296613.1	EST_HUMAN	601173631F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3529159 5'
6381	19449	32690	0.87	2.0E-32	M35418.1	NT	Human cell 12-lipoxygenase mRNA, complete cds
6624	19682	32959	6.86	2.0E-32	Z38133.1	NT	H. sapiens mRNA for myosin
6624	19682	32960	6.86	2.0E-32	Z38133.1	NT	H. sapiens mRNA for myosin
8621	21589	35006	2.19	2.0E-32	AA114294.1	EST_HUMAN	zr66c08.r1 Stratagene HeLa cell s3 937216 Homo sapiens cDNA clone IMAGE:563150 5'
8621	21589	35007	2.19	2.0E-32	AA114294.1	EST_HUMAN	zr66c08.r1 Stratagene HeLa cell s3 937216 Homo sapiens cDNA clone IMAGE:563150 5'
13049	25589	31683	4.17	2.0E-32	AV736449.1	EST_HUMAN	AV736449 CB Homo sapiens cDNA clone CBFB/A08 5'
13049	25589	31684	4.17	2.0E-32	AV736449.1	EST_HUMAN	AV736449 CB Homo sapiens cDNA clone CBFB/A08 5'
3110	16167		1.07	1.0E-32	BE743299.1	EST_HUMAN	601573207F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3834433 5'
7256	19891	33289	6.73	1.0E-32	11439789	NT	Homo sapiens chromosome 11 open reading frame 9 (C11ORF9), mRNA
8943	21909	35334	6.78	1.0E-32	AA720574.1	EST_HUMAN	hw21g02.s1 NCI_CGAP_GCB0 Homo sapiens cDNA clone IMAGE:1241138 3' similar to contains THR.13
3493	16540		5.7	9.0E-33	BE327112.1	EST_HUMAN	THR repetitive element;
6560	19620		3.43	9.0E-33	AF223391.1	NT	hw07c05.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3182216 3' similar to TR:O88539 O88539
9140	22106	35532	1.82	9.0E-33	BF347229.1	EST_HUMAN	WW DOMAIN BINDING PROTEIN 11.;
11150	24110		4.08	9.0E-33	AL163280.2	NT	Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced
63	13182	26098	2.4	7.0E-33	5031736	NT	602021164F1 NCI_CGAP_Bm87 Homo sapiens cDNA clone IMAGE:4156670 5'
63	13182	26099	2.4	7.0E-33	5031736	NT	Homo sapiens chromosome 21 segment HS21C080
2169	15185	28206	2.43	7.0E-33	AI590115.1	EST_HUMAN	Homo sapiens short-chain alcohol dehydrogenase family member (HEP27) mRNA
2657	15654		7.82	7.0E-33	AV730056.1	EST_HUMAN	Homo sapiens short-chain alcohol dehydrogenase family member (HEP27) mRNA
2841	14737	27719	1.62	7.0E-33	AV730015.1	EST_HUMAN	Homo sapiens short-chain alcohol dehydrogenase family member (HEP27) mRNA
3256	16310		16.32	7.0E-33	AW971307.1	EST_HUMAN	tot12b09.x1 NCI_CGAP_U12 Homo sapiens cDNA clone IMAGE:2178809 3' similar to contains OFR.H OFR
9298	22264		1.07	7.0E-33	X54890.1	NT	repetitive element;
11178	24134	37864	2.89	7.0E-33	BF347229.1	EST_HUMAN	AV730056 HTF Homo sapiens cDNA clone HTFAVE06 5'
11578	24516	38071	2.65	7.0E-33	AW971568.1	EST_HUMAN	AV730015 HTF Homo sapiens cDNA clone HTFANF08 5'
12409	26182	31819	3.85	7.0E-33	AA601416.1	EST_HUMAN	EST383395 IMAGE resequences, MAGI. Homo sapiens cDNA
							Human hLRP mRNA for leukocyte common antigen-related peptide (protein-tyrosine phosphate) (EC 3.1.3.48)
							3.1.3.48)
							602021164F1 NCI_CGAP_Bm87 Homo sapiens cDNA clone IMAGE:4156670 5'
							EST383357 IMAGE resequences, MAGI. Homo sapiens cDNA
							not6h01.s1 NCI_CGAP_Phet Homo sapiens cDNA clone IMAGE:1100881 3' similar to contains L1.11 L1
							repetitive element;

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Table 4
Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3749	16791		0.69	6.0E-33	AL163285.2	NT	Homo sapiens chromosome 21 segment HS21C085
6185	19280	32494	1.09	6.0E-33	F30631.1	EST_HUMAN	HSPD21201 HM3 Homo sapiens cDNA clone s4000107H06
6185	19280	32495	1.09	6.0E-33	F30631.1	EST_HUMAN	HSPD21201 HM3 Homo sapiens cDNA clone s4000107H06
8925	21891	35319	7.52	6.0E-33	J04038.1	NT	Human glyceraldehyde-3-phosphate dehydrogenase (GAPDH) gene, complete cds
9050	22016	35440	3.18	6.0E-33	11429198	NT	Homo sapiens similar to RAD23 (S. cerevisiae) homolog B (H. sapiens) (LOC63277), mRNA
10371	23294	36769	1.73	6.0E-33	6755609	NT	Mus musculus SRY-box containing gene 6 (Sox6), mRNA
10371	23294	36770	1.73	6.0E-33	6755609	NT	Mus musculus SRY-box containing gene 6 (Sox6), mRNA
1792	14821		1.63	6.0E-33	BF373515.1	EST_HUMAN	QV1-FT0189-100700-271-a02 FT0169 Homo sapiens cDNA
1898	14923		1.27	6.0E-33	11141884	NT	Homo sapiens solute carrier family 5 (choline transporter), member 7 (SLC5A7), mRNA
1914	14938	27933	1.31	6.0E-33	4507208	NT	Homo sapiens spermidine synthase (SRM) mRNA
1914	14938	27934	1.31	6.0E-33	4507208	NT	Homo sapiens spermidine synthase (SRM) mRNA
2280	15293		1.49	6.0E-33	AL163285.2	NT	Homo sapiens chromosome 21 segment HS21C085
4087	17121	30015	1.28	6.0E-33	AB014598.1	NT	Homo sapiens mRNA for KIAA0699 protein, partial cds
8823	19877	33166	51.92	6.0E-33	AA189080.1	EST_HUMAN	z45006.s1 Stratagene INT neuron (#837233) Homo sapiens cDNA clone IMAGE:632627 3' similar to contains Alu repetitive element;
10610	23532	37027	0.85	6.0E-33	AW264879.1	EST_HUMAN	xq33f11.x1 NCI_CGAP_Lu28 Homo sapiens cDNA clone IMAGE:2752461 3'
10610	23532	37028	0.85	6.0E-33	AW264879.1	EST_HUMAN	xq33f11.x1 NCI_CGAP_Lu28 Homo sapiens cDNA clone IMAGE:2752461 3'
1130	14173		0.87	6.0E-33	AL163207.2	NT	Homo sapiens chromosome 21 segment HS21C007
2135	15152	28167	1.53	6.0E-33	4758987	NT	Homo sapiens RAB1, member RAS oncogene family (RAB1) mRNA
2428	15435		2.92	6.0E-33	AA626621.1	EST_HUMAN	ab51b1.1 Stratagene lung carcinoma 937218 Homo sapiens cDNA clone IMAGE:844317 5' similar to contains Alu repetitive element; contains MER28 b2 MER28 repetitive element;
2562	15554	28574	2.35	6.0E-33	AL163210.2	NT	Homo sapiens chromosome 21 segment HS21C070
4509	17534	30418	1.65	6.0E-33	AW293349.1	EST_HUMAN	UI-H-B12-ah1-c-03-O-J1.s1 NCI_CGAP_Sub4 Homo sapiens cDNA clone IMAGE:2727149 3'
5477	18578	31487	21.96	6.0E-33	AA053063.1	EST_HUMAN	z171a08.1 Stratagene colon (#937204) Homo sapiens cDNA clone IMAGE:510038 5' similar to gb:X12871_maf1 HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN A1 (HUMAN);
6532	19595	32857	2.14	6.0E-33	8393994	NT	Homo sapiens polymerase (DNA directed), alpha (POLA), mRNA
6532	19595	32858	2.14	6.0E-33	8393994	NT	Homo sapiens polymerase (DNA directed), alpha (POLA), mRNA
1091	14135		6.18	6.0E-33	BE350127.1	EST_HUMAN	h09g01.x1 NCI_CGAP_Kid13 Homo sapiens cDNA clone IMAGE:3146256 3' similar to contains MER29.b3 MER29 repetitive element;
1092	14135		4.81	6.0E-33	BE350127.1	EST_HUMAN	h09g01.x1 NCI_CGAP_Kid13 Homo sapiens cDNA clone IMAGE:3146256 3' similar to contains MER29.b3 MER29 repetitive element;
2456	15894		0.91	6.0E-33	AV647851.1	EST_HUMAN	AV647851 GLC Homo sapiens cDNA clone GLC8CF09 3'
10806	23727	37228	1.02	6.0E-33	AA861510.1	EST_HUMAN	ak32b12.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1407847 3' similar to TR:Q13579 Q13579 MARINER TRANSPOSASE ;

Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
18	13138		0.63	2.0E-33	AI160189.1	EST_HUMAN	kb67g03.x1 Soares_fetal_heart_NbHH19W Homo sapiens cDNA clone IMAGE:1705204 3' similar to contains ORF.11 ORF repetitive element;
105	13138		2.93	2.0E-33	AI160189.1	EST_HUMAN	kb67g03.x1 Soares_fetal_heart_NbHH19W Homo sapiens cDNA clone IMAGE:1705204 3' similar to contains ORF.11 ORF repetitive element;
4449	17475		4.22	2.0E-33	BE159039.1	EST_HUMAN	MR0-HT0405-160300-202-d08 HT0405 Homo sapiens cDNA
5021	18035	30920	9.82	2.0E-33	AA626683.1	EST_HUMAN	ab51g11.1r1 Stratiogene lung carcinoma 937218 Homo sapiens cDNA clone IMAGE:844388 5' similar to gb:X00734_cds1 TUBULIN BETA-5 CHAIN (HUMAN);
5129	18138	31015	2.58	2.0E-33	11421332	NT	Homo sapiens hypothetical protein SIRP-b2 (SIRP-b2), mRNA
5129	18138	31016	2.58	2.0E-33	11421332	NT	Homo sapiens hypothetical protein SIRP-b2 (SIRP-b2), mRNA
6563	19623	32888	1	2.0E-33	AI277492.1	EST_HUMAN	q96d01.x1 Soares_NHMPu_S1 Homo sapiens cDNA clone IMAGE:1880161 3'
9456	22420		2.29	2.0E-33	AI062256.1	EST_HUMAN	oz21d03.x1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:1675973 3' similar to gb:M28536 TRANSLATIONAL INITIATION FACTOR 2 BETA SUBUNIT (HUMAN);
10979	23899	37411	0.9	2.0E-33	11421332	NT	Homo sapiens hypothetical protein SIRP-b2 (SIRP-b2), mRNA
10979	23899	37412	0.9	2.0E-33	11421332	NT	Homo sapiens hypothetical protein SIRP-b2 (SIRP-b2), mRNA
9	13129		2.05	1.0E-33	AF003528.1	NT	Homo sapiens X-linked anhidrotic ectodermal dysplasia protein gene (EDA), exon 2 and flanking repeat regions
5669	18764	31934	0.7	1.0E-33	AF199420.1	NT	Homo sapiens F-box protein FBL4 (FBL4) mRNA, complete cds
7637	20597	33961	1.18	1.0E-33	M13975.1	NT	Homo sapiens protein kinase C beta-1 type (PRKCB1) mRNA, complete cds
10381	26010		0.79	1.0E-33	U60822.1	NT	Human dystrophin (DMD) gene, exons 7, 8 and 9, and partial cds
11377	24324	37853	1.72	1.0E-33	AV744220.1	EST_HUMAN	AV744220 CB Homo sapiens cDNA clone QB0AAA11 5'
11650	24587	38157	1.79	1.0E-33	AW998818.1	EST_HUMAN	QV3-BN0047-230200-102-b03 BN0047 Homo sapiens cDNA
11973	24851	38448	2.59	1.0E-33	U60822.1	NT	Human dystrophin (DMD) gene, exons 7, 8 and 9, and partial cds
12685	25352		1.98	1.0E-33	AI927191.1	EST_HUMAN	wo88c06.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2462410 3'
12852	13129		3.4	1.0E-33	AF003528.1	NT	Homo sapiens X-linked anhidrotic ectodermal dysplasia protein gene (EDA), exon 2 and flanking repeat regions
4844	17665		1.17	9.0E-34	BE156575.1	EST_HUMAN	PM4-HT0352-181199-001-D02 HT0352 Homo sapiens cDNA
13069	25903		3.44	9.0E-34	AJ271735.1	NT	Homo sapiens Xq pseudautosomal region: segment 1/2
2181	15196	28216	0.93	8.0E-34	8922751	NT	Homo sapiens hypothetical protein FLJ10900 (FLJ10900), mRNA
8077	21014	34414	0.49	8.0E-34	BE098882.1	EST_HUMAN	MR4-BT0399-200100-001-h03 BT0399 Homo sapiens cDNA
1439	14472	27449	2.93	7.0E-34	T70845.1	EST_HUMAN	yt15e05.r1 Soares_fetal_liver_spleen_1NFLS Homo sapiens cDNA clone IMAGE:108320 5'
10359	14472	27449	0.6	7.0E-34	T70845.1	EST_HUMAN	yt15e05.r1 Soares_fetal_liver_spleen_1NFLS Homo sapiens cDNA clone IMAGE:108320 5'
12479	25227		1.69	7.0E-34	H12868.1	EST_HUMAN	yt14c70.r1 Soares_placenta_Nb2HP Homo sapiens cDNA clone IMAGE:148722 5'
471	13543	26471	2.11	6.0E-34	U10991.1	NT	Human G2 protein mRNA, partial cds
471	13543	26472	2.11	6.0E-34	U10991.1	NT	Human G2 protein mRNA, partial cds

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Table 4
Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
12287	25103	31836	1.86	6.0E-34	U03686.1	NT	Mus musculus DAB/2J hair-specific (hach-1) gene
1897	14922		2.36	5.0E-34	7706500	NT	Homo sapiens Npw38-binding protein NpwBP (LOC51729), mRNA
5101	18111	30883	4.68	5.0E-34	U30883.1	NT	Human splicing factor SRP55-1 (SRP-56) mRNA, complete cds
9218	22184	35617	1.17	5.0E-34	AF078779.1	NT	Rattus norvegicus putative four repeat ion channel mRNA, complete cds
11016	23980	37506	2.03	5.0E-34	AB037856.1	NT	Homo sapiens mRNA for KIAA1435 protein, partial cds
11683	24521		1.49	5.0E-34	AL163209.2	NT	Homo sapiens chromosome 21 segment HS21C009
2014	16035	28046	1.71	4.0E-34	AI804667.1	EST_HUMAN	IG4-c06.x1 NCL_CGAP_P28 Homo sapiens cDNA clone IMAGE:2249194 3'
6223	18231	31106	0.64	4.0E-34	AW886262.1	EST_HUMAN	RC5-O10078-280300-022-D02 OT0078 Homo sapiens cDNA
9393	22358	35788	1.07	4.0E-34	BF209778.1	EST_HUMAN	601874950F1 NIH_MGC_54 Homo sapiens cDNA clone IMAGE:4102213 5'
6359	19428	32671	0.74	3.0E-34	M37277.1	NT	Human Ig germline H-chain D-region genes, partial cds
11486	24429		3.18	3.0E-34	BF036327.1	EST_HUMAN	601458531F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3862086 5'
9303	22268	35698	1.93	2.0E-34	AI678101.1	EST_HUMAN	w435g06.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2330170 3' similar to contains MER29.12 MER29 repetitive element
9303	22268	35699	1.93	2.0E-34	AI678101.1	EST_HUMAN	w435g06.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2330170 3' similar to contains MER29.12 MER29 repetitive element
11496	24439	37987	1.57	2.0E-34	P51805	SWISSPROT	PLEXIN 4 PRECURSOR (TRANSMEMBRANE PROTEIN SEX)
11496	24439	37988	1.57	2.0E-34	P51805	SWISSPROT	PLEXIN 4 PRECURSOR (TRANSMEMBRANE PROTEIN SEX)
1505	14538	27510	8.53	1.0E-34	P12236	SWISSPROT	ADP ATP CARRIER PROTEIN, LIVER ISOFORM T2 (ADP/ATP TRANSLOCASE 3) (ADENINE NUCLEOTIDE TRANSLOCATOR 3) (ANT 3)
3887	18730	28641	1.35	1.0E-34	AF003528.1	NT	Homo sapiens X-linked anhidrotic ectodermal dysplasia protein gene (EDA), exon 2 and flanking repeat regions
4098	17132	30025	0.81	1.0E-34	AY009397.1	NT	Homo sapiens WNT3 precursor (WNT3) mRNA, complete cds
4098	17132	30026	0.81	1.0E-34	AY009397.1	NT	Homo sapiens WNT3 precursor (WNT3) mRNA, complete cds
4606	17531		6.11	1.0E-34	BE071414.1	EST_HUMAN	RC2-BT0506-240400-016-H08 BT0506 Homo sapiens cDNA
8261	19334	32565	1.98	1.0E-34	BE074052.1	EST_HUMAN	601484430F1 NIH_MGC_69 Homo sapiens cDNA clone IMAGE:3886999 5'
6281	19334	32566	1.98	1.0E-34	BE074052.1	EST_HUMAN	601484430F1 NIH_MGC_69 Homo sapiens cDNA clone IMAGE:3886999 5'
9881	22634	36090	0.46	1.0E-34	P23286	SWISSPROT	OLFACTORY RECEPTOR-LIKE PROTEIN F5
10055	22982	36450	14.47	1.0E-34	AL038636.1	EST_HUMAN	DKFZp564A1663.1 564 (synonym: hfr2) Homo sapiens cDNA clone DKFZp564A1663 5'
11516	24457	38007	1.71	1.0E-34	BE781790.1	EST_HUMAN	601470592F1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:3873478 5'
11516	24457	38008	1.71	1.0E-34	BE781790.1	EST_HUMAN	601470592F1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:3873478 5'
11530	24471	38022	3.22	1.0E-34	11439598	NT	Homo sapiens nucleobindin 2 (NUCB2), mRNA
12654	25921		1.4	1.0E-34	AA807097.1	EST_HUMAN	cc31c11.s1 NCL_CGAP_G081 Homo sapiens cDNA clone IMAGE:1351318 3' similar to gb: X68203
12874	25507		4.01	1.0E-34	AL163210.2	NT	TYROSINE-PROTEIN KINASE RECEPTOR FLT4 PRECURSOR (HUMAN); Homo sapiens chromosome 21 segment HS21C010

Table 4
Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3659	16702	29617	1.25	9.0E-35	AW663302.1	EST_HUMAN	h177b06.y1 NCI_CGAP_GU1 Homo sapiens cDNA clone IMAGE:2968787 5'
227	13326		13.21	8.0E-35	6031180	NT	Homo sapiens prohibitin (PHB) mRNA
1751	14780	27765	4.47	8.0E-35	BF59937.1	EST_HUMAN	naa33a08.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:3258134 3' similar to TR:O75912
1751	14780	27766	4.47	8.0E-35	BF59937.1	EST_HUMAN	O75912 DIACYLGLYCEROL KINASE IOTA. ;
4902	17919	30811	2.91	8.0E-35	BF183195.1	EST_HUMAN	naa33a08.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:3258134 3' similar to TR:O75912
11049	24012	37537	1.84	8.0E-35	BE378480.1	EST_HUMAN	O75912 DIACYLGLYCEROL KINASE IOTA. ;
12402	25175		5.41	8.0E-35	BF669282.1	EST_HUMAN	601809588F1 NIH_MGC 44 Homo sapiens cDNA clone IMAGE:4040324 5'
6631	19689	32968	1.85	7.0E-35	11425417	NT	601236488F1 NIH_MGC 44 Homo sapiens cDNA clone IMAGE:3608513 5'
1411	14444	27416	0.93	6.0E-35	AA757115.1	EST_HUMAN	602184624T1 NIH_MGC 42 Homo sapiens cDNA clone IMAGE:4300660 3'
1985	15006	28009	2.85	6.0E-35	6005975	NT	Homo sapiens phosphatidylinositol glycan, class L (PIGL), mRNA
4083	17117	30012	0.76	6.0E-35	AW297191.1	EST_HUMAN	ah53h03.s1 Soares_testis_NHT Homo sapiens cDNA clone 1309397 3'
8229	21198	34605	3.66	6.0E-35	6005921	NT	Homo sapiens zinc finger protein 208 (ZNF208), mRNA
9058	22024	35447	0.51	6.0E-35	X94232.1	NT	UI-HBW0-ajd-4-09-0-UJ.s1 NCI_CGAP_Sub6 Homo sapiens cDNA clone IMAGE:2731433 3'
9058	22024	35448	0.51	6.0E-35	X94232.1	NT	Homo sapiens triple functional domain (PTPRF interacting) (TRIO), mRNA
10025	22952	36420	0.68	6.0E-35	AB002364.1	NT	H. sapiens mRNA for novel T-cell activation protein
10263	23188	36672	3.04	6.0E-35	AB037786.1	NT	H. sapiens mRNA for KIAA1365 protein, partial cds
1722	14752	27737	61.6	5.0E-35	X63392.1	NT	Human mRNA for KIAA1365 protein, partial cds
2795	15787	28805	0.9	5.0E-35	AB007866.2	NT	H. sapiens immunoglobulin kappa light chain variable region L14
3021	16079	28000	1.47	5.0E-35	6912639	NT	Homo sapiens mRNA for KIAA0406 protein, partial cds
							Homo sapiens Ring1 and YY1 binding protein (RYBP), mRNA
							Homo sapiens cdk2 kinase (CLK2), propin', cole1, glucocorticoidase (GBA), and metaxin genes, complete cds; metaxin pseudogene and glucocorticoidase pseudogene; and thrombospondin3 (THBS3) gene, partial cds
4438	17464	30354	2.05	5.0E-35	AF023268.1	NT	TCBAP1D3842 Pediatric pre-B cell acute lymphoblastic leukemia Baylor-HGSC project=TCBA Homo
4742	17762	30656	0.99	5.0E-35	BE246085.1	EST_HUMAN	sapiens cDNA clone TCBAP3842
8626	21493		4.74	5.0E-35	BE830982.1	EST_HUMAN	sapiens cDNA clone TCBAP3842
8552	21520	34939	2.2	5.0E-35	AI208765.1	EST_HUMAN	601431984F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3817229 5'
8552	21520	34940	2.2	5.0E-35	AI208765.1	EST_HUMAN	q38c05.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1837448 3' similar to
11512	24453		2.39	5.0E-35	AA001786.1	EST_HUMAN	q38c05.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1837448 3' similar to
1429	14463	27440	19.86	4.0E-35	BE257907.1	EST_HUMAN	SW:Y249_HUMAN Q92539 HYPOTHETICAL PROTEIN KIAA0249. ;
							q38c05.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1837448 3' similar to
							SW:Y249_HUMAN Q92539 HYPOTHETICAL PROTEIN KIAA0249. ;
							zh84f12.r1 Soares_fetal_liver_spleen_1N1FLS_S1 Homo sapiens cDNA clone IMAGE:428015 5'
							601109719F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3350405 5'

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Table 4
Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1835	14862	27859	7.51	4.0E-35	H91193.1	EST_HUMAN	y198a07.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA IMAGE:241236 5' similar to contains PTR5 repetitive element;
4844	17881		0.63	4.0E-35	AF003528.1	NT	Homo sapiens X-linked anhidrotic ectodermal dysplasia protein gene (EDA), exon 2 and flanking repeat regions
5145	18154		0.93	4.0E-35	BE409102.1	EST_HUMAN	601300705F1 NIH_MGC 21 Homo sapiens cDNA clone IMAGE:3635401 5'
7418	20383		1.81	4.0E-35	BE360127.1	EST_HUMAN	h09g01.x1 NCL_CGAP_Kid13 Homo sapiens cDNA clone IMAGE:3146256 3' similar to contains MIER29.b3 MER29 repetitive element;
8863	21830	35253	8.37	4.0E-35	AL046598.1	EST_HUMAN	DKFZp434L148_r1 434 (synonym: hies3) Homo sapiens cDNA clone DKFZp434L148 5'
1582	14816	27598	21.76	3.0E-35	BE268182.1	EST_HUMAN	601125280F1 NIH_MGC_8 Homo sapiens cDNA clone IMAGE:3345603 5'
2338	15349		3.36	3.0E-35	AF224492.1	NT	Homo sapiens phospholipid scramblase 1 gene, complete cds
5413	18516	31393	27.9	3.0E-35	BF433100.1	EST_HUMAN	7n25a09.x1 NCL_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3665361 3' similar to TR:Q9QZH7
5413	18516	31394	27.9	3.0E-35	BF433100.1	EST_HUMAN	Q9QZH7 F-BOX PROTEIN FBL2;
9844	22780		1.71	3.0E-35	AF223391.1	NT	7n25a09.x1 NCL_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3665361 3' similar to TR:Q9QZH7 Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced
10535	23457	36954	0.93	3.0E-35	AW003063.1	EST_HUMAN	wr03a05.x1 NCL_CGAP_GC8 Homo sapiens cDNA clone IMAGE:2480432 3' similar to SW:POL1_HUMAN P10266 RETROVIRUS-RELATED POL POLYPROTEIN [CONTAINS: REVERSE TRANSCRIPTASE];
108	15832	26146	0.83	2.0E-35	N88965.1	EST_HUMAN	K6932F Human fetal heart, Lambda ZAP Express Homo sapiens cDNA clone K6932 5' similar to
1192	14232	27188	1.39	2.0E-35	T11909.1	EST_HUMAN	REPEATITIVE ELEMENT
2227	15241	28266	5.04	2.0E-35	AB018413.1	NT	A971F Heart Homo sapiens cDNA clone A971
2693	15689	28706	1	2.0E-35	AW66005.1	EST_HUMAN	Homo sapiens mRNA for Gab2, complete cds
3323	16374	29294	0.93	2.0E-35	6912459	NT	h188a12.x1 Soares NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2979166 3' similar to
3323	16374	29295	0.93	2.0E-35	6912459	NT	SW:TR12_HUMAN Q14669 THYROID RECEPTOR INTERACTING PROTEIN 12;
3570	16815		1.06	2.0E-35	AB020702.1	NT	Homo sapiens Grb2-associated binder 2 (KIAA0571), mRNA
3930	16970	29883	1.42	2.0E-35	BE247575.1	EST_HUMAN	Homo sapiens mRNA for KIAA0895 protein, partial cds
3930	16970	29884	1.42	2.0E-35	BE247575.1	EST_HUMAN	TCBAP2E 4328 Pediatric pre-B cell acute lymphoblastic leukemia Baylor-HGSC project=TCBA Homo sapiens cDNA clone TCBAP4328
4697	17718		2.65	2.0E-35	H49239.1	EST_HUMAN	TCBAP2E 4328 Pediatric pre-B cell acute lymphoblastic leukemia Baylor-HGSC project=TCBA Homo sapiens cDNA clone TCBAP4328
5662	18768	31928	1.8	2.0E-35	BF332417.1	EST_HUMAN	y191a12.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:274079 5'
							QV6-BT0701-210400-199-b04 BT0701 Homo sapiens cDNA

Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7311	20282	33622	0.65	2.0E-35	BE832636.1	EST_HUMAN	CM2-MT0125-280700-297-G02 MT0125 Homo sapiens cDNA
7311	20282	33623	0.65	2.0E-35	BE832636.1	EST_HUMAN	CM2-MT0125-280700-297-G02 MT0125 Homo sapiens cDNA
11148	24108	37634	11.23	2.0E-35	X5947.1	NT	H. sapiens PROS-27 mRNA
12158	16374	29294	2.39	2.0E-35	6912459	NT	Homo sapiens Grb2-associated binder 2 (KIAA0571), mRNA
12158	16374	29295	2.39	2.0E-35	6912459	NT	Homo sapiens Grb2-associated binder 2 (KIAA0571), mRNA
12340	25138	31851	1.47	2.0E-35	BE904978.1	EST_HUMAN	Homo sapiens cDNA clone IMAGE:3898699 5'
12340	25138	31852	1.47	2.0E-35	BE904978.1	EST_HUMAN	601498774F1 NIH_MGC_70 Homo sapiens cDNA clone IMAGE:3898699 5'
12854	25462		7.88	2.0E-35	AL163210.2	NT	Homo sapiens chromosome 21 segment HS21C010
12973	15832	26148	1.72	2.0E-35	N88965.1	EST_HUMAN	K6932F Human fetal heart, Lambda ZAP Express Homo sapiens cDNA clone K6932 5' similar to REPETITIVE ELEMENT
48	13168	26073	5.26	1.0E-35	AA631949.1	EST_HUMAN	frnc16 Regional genomic DNA specific cDNA library Homo sapiens cDNA clone CR12-1
48	13168	26074	5.26	1.0E-35	AA631949.1	EST_HUMAN	frnc16 Regional genomic DNA specific cDNA library Homo sapiens cDNA clone CR12-1
753	13814	26756	95.25	1.0E-35	AW389473.1	EST_HUMAN	IL2-ST0162-131089-006-d12 ST0162 Homo sapiens cDNA
753	13814	26757	95.25	1.0E-35	AW389473.1	EST_HUMAN	IL2-ST0162-131089-006-d12 ST0162 Homo sapiens cDNA
910	13965		0.99	1.0E-35	T87947.1	EST_HUMAN	y89a01.r1 Soares fetal liver spleen cDNA library Homo sapiens cDNA clone IMAGE:115752 5' similar to SP-A44282 A44282 RETROVIRUS-RELATED POLYPROTEIN - HUMAN ;
2549	15550	28571	3.02	1.0E-35	7705994	NT	Homo sapiens hypothetical protein (LOC51233), mRNA
2778	15770	28790	1.85	1.0E-35	BE350127.1	EST_HUMAN	Homo sapiens hypothetical protein (LOC51233), mRNA
2778	15770	28791	1.85	1.0E-35	BE350127.1	EST_HUMAN	Homo sapiens hypothetical protein (LOC51233), mRNA
3177	16232	29148	3.44	1.0E-35	AV650422.1	EST_HUMAN	MER29 repetitive element;
3177	16232	29149	3.44	1.0E-35	AV650422.1	EST_HUMAN	MER29 repetitive element;
4452	17478	30365	4.04	1.0E-35	7656005	NT	MER29 repetitive element;
4452	17478	30366	4.04	1.0E-35	7656005	NT	MER29 repetitive element;
5583	18684	31653	1.54	1.0E-35	11526238	NT	MER29 repetitive element;
7189	18420	31221	0.59	1.0E-35	AW808865.1	EST_HUMAN	AV650422 GLC Homo sapiens cDNA clone GLOCCE06 3'
7189	18420	31222	0.59	1.0E-35	AW808865.1	EST_HUMAN	AV650422 GLC Homo sapiens cDNA clone GLOCCE06 3'
7725	20681	34045	0.83	1.0E-35	AB033105.1	NT	AV650422 GLC Homo sapiens cDNA clone GLOCCE06 3'
7903	20846	34231	0.94	1.0E-35	11418002	NT	AV650422 GLC Homo sapiens cDNA clone GLOCCE06 3'
9900	25699	36312	3.17	1.0E-35	AU158595.1	EST_HUMAN	Mus musculus activin receptor interacting protein 1 (Arip1-pending), mRNA
9900	25699	36313	3.17	1.0E-35	AU158595.1	EST_HUMAN	Mus musculus activin receptor interacting protein 1 (Arip1-pending), mRNA
10942	23862	37377	0.83	1.0E-35	BF585994.1	EST_HUMAN	Mus musculus activin receptor interacting protein 1, subunit B (p60) (CHAF1B), mRNA
							Homo sapiens chromatin assembly factor 1, subunit B (p60) (CHAF1B), mRNA
							MR1-ST0111-111199-011-d07 ST0111 Homo sapiens cDNA
							MR1-ST0111-111199-011-d07 ST0111 Homo sapiens cDNA
							Homo sapiens mRNA for KIAA1279 protein, partial cds
							Homo sapiens KIAA0645 gene product (KIAA0645), mRNA
							AU158595 PLACE3 Homo sapiens cDNA clone PLACE3000382 3'
							AU158595 PLACE3 Homo sapiens cDNA clone PLACE3000382 3'
							naa06d06.x1 NCI_CGAP_P128 Homo sapiens cDNA clone IMAGE:3254051 3' similar to TR:O31341
							O31341 BETA-GALACTOSIDASE ;

Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10942	23862	37378	0.63	1.0E-35	BF569594.1	EST_HUMAN	hna06406.x1 NCL CGAP_P128 Homo sapiens cDNA clone IMAGE:3254051 3' similar to TR:O31341
12052	24925	38522	1.72	1.0E-35	AB028980.1	NT	O31341 BETA-GALACTOSIDASE
12052	24925	38523	1.72	1.0E-35	AB028980.1	NT	Homo sapiens mRNA for KIAA1057 protein, partial cds
12057	24930		1.59	1.0E-35	AI525119.1	EST_HUMAN	Homo sapiens mRNA for KIAA1057 protein, partial cds
12188	25887		1.71	1.0E-35	11418274	NT	prommer-7 D01.1 b1 tumor Homo sapiens cDNA 5'
12320	16550	28571	1.42	1.0E-35	7705994	NT	Homo sapiens fibulin 1 (FBLN1), mRNA
12404	25177		1.77	1.0E-35	11418110	NT	Homo sapiens hypothetical protein (LOC61233), mRNA
12747	25398		1.97	1.0E-35	BE792832.1	EST_HUMAN	Homo sapiens casein kinase 1, epsilon (CSNK1E), mRNA
4011	17050	29856	2.35	9.0E-36	AW821707.1	EST_HUMAN	601584833F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3838985 5'
6123	19201	32425	0.75	8.0E-36	X78479.1	NT	RC3-ST0315-180200-013-f12 ST0315 Homo sapiens cDNA
9585	25547	35998	0.61	8.0E-36	AA348480.1	EST_HUMAN	B bovis BBSc mRNA for scinderin
10516	23438		0.45	8.0E-36	7706259	NT	EST 54938 Hippocampus II Homo sapiens cDNA 5' end similar to endogenous retrovirus 9, 5' LTR
2942	16000	28923	1.68	7.0E-36	AW857579.1	EST_HUMAN	Homo sapiens CGI-03 protein (LOC51605), mRNA
3135	16192		4.05	7.0E-36	4557498	NT	CM1-CT0315-091299-063-007 CT0315 Homo sapiens cDNA
7916	20859	34247	6.21	7.0E-36	U06672.1	NT	Homo sapiens C-terminal binding protein 2 (CTBP2), mRNA
7916	20859	34248	6.21	7.0E-36	U06672.1	NT	Human carcinoembryonic antigen gene family member 12 (CGM12) gene, exons L and LN
12558	25278	31778	2.01	7.0E-36	AF052051.1	NT	Human carcinoembryonic antigen gene family member 12 (CGM12) gene, exons L and LN
2021	15042	28053	4.16	6.0E-36	7706622	NT	Homo sapiens glutathione transferase A4 gene, exon 1
2427	16434		5.3	6.0E-36	AB035346.1	NT	Homo sapiens minijun 2 (NINJ2), mRNA
3653	16696	29611	1.88	6.0E-36	BF515101.1	EST_HUMAN	Homo sapiens TCL6 gene, exon 12
5404	18507	31384	5.66	6.0E-36	AI435189.1	EST_HUMAN	U1H-BW1-anv-c-12-0-U1.s1 NCL CGAP_Sub7 Homo sapiens cDNA clone IMAGE:3083542 3'
7316	20287	33629	3.48	6.0E-36	AW780143.1	EST_HUMAN	tr83b06.x1 Soares NSF F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:2126195 3' similar to
8999	21965	35390	2.51	6.0E-36	AF208161.1	NT	gbM11949 PANCREATIC SECRETORY TRYPSIN INHIBITOR PRECURSOR (HUMAN);
10585	23507		0.6	6.0E-36	C16927.1	EST_HUMAN	h06h02.x1 NCL CGAP_Co14 Homo sapiens cDNA clone IMAGE:3036627 3' similar to SW:IMA2_HUMAN
11874	24756	38339	3.51	6.0E-36	AI380499.1	EST_HUMAN	P52292 IMPORTIN ALPHA-2 SUBUNIT
12963	25804	31526	1.9	6.0E-36	BE737154.1	EST_HUMAN	Homo sapiens synctin precursor, mRNA, complete cds
138	13243	26173	12.86	5.0E-36	AJ271735.1	NT	C16927 Clontech human aorta polyA+ mRNA (#6572) Homo sapiens cDNA clone GEN-535C11 5'
2761	15763	26773	12.8	5.0E-36	BE388436.1	EST_HUMAN	tr95c09.x1 NCL CGAP_CLL1 Homo sapiens cDNA clone IMAGE:2107024 3' similar to contains MER9.b2
3026	16669	29581	1.32	6.0E-36	AL163209.2	NT	MER9 repetitive element
							601305064F1 NIH_MGC_39 Homo sapiens cDNA clone IMAGE:3639782 5'
							Homo sapiens Xq pseudautosomal region; segment 1/2
							601285567F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3607289 5'
							Homo sapiens chromosome 21 segment HS21C009

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Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4827	17844	30743	1.21	5.0E-36	5729729	NT	Homo sapiens API5-like 1 (API5L1), mRNA
4827	17844	30744	1.21	5.0E-36	5729729	NT	Homo sapiens API5-like 1 (API5L1), mRNA
8070	21007	34405	0.77	5.0E-36	11079227	NT	Homo sapiens N-ethylmaleimide-sensitive factor (NSF), mRNA
12156	13243	26173	2.97	5.0E-36	AJ271735.1	NT	Homo sapiens Xq pseudautosomal region, segment 1/2
12455	25214	31832	3.03	5.0E-36	11417862	NT	Homo sapiens calcineurin binding protein 1 (KIAA0330), mRNA
1228	14266	27223	1.24	4.0E-36	BE010038.1	EST_HUMAN	PM3-BN0176-100400-001-g04 BN0176 Homo sapiens cDNA
							RETROVIRUS-RELATED POL POLYPROTEIN [CONTAINS: REVERSE TRANSCRIPTASE];
1436	14469	27447	0.99	4.0E-36	P10266	SWISSPROT	ENDONUCLEASE
1652	14684	27658	1.63	4.0E-36	BE382574.1	EST_HUMAN	601298574F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:3628386 5'
2231	15245		1.64	4.0E-36	AW247772.1	EST_HUMAN	2820020.5prime NIH_MGC_7 Homo sapiens cDNA clone IMAGE:2820020 5'
3365	16415	29340	0.65	4.0E-36	BE389299.1	EST_HUMAN	601282266F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3604168 5'
3365	16415	29341	0.65	4.0E-36	BE389299.1	EST_HUMAN	601282266F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3604168 5'
4786	17804	30696	0.71	4.0E-36	AL163204.2	NT	Homo sapiens chromosome 21 segment HS21C004
5804	18895		0.96	4.0E-36	RE4023.1	EST_HUMAN	y1905.r1 Soares placenta Nb2-IP Homo sapiens cDNA clone IMAGE:139713 5'
6173	19248	32481	2.48	4.0E-36	11497041	NT	Homo sapiens a disintegrin and metalloproteinase domain 22 (ADAM22), transcript variant 3, mRNA
7915	20858	34246	1.74	4.0E-36	M33320.1	NT	Human platelet Glycoprotein IIb (GPIIb) gene, exons 2-29
8901	21867	35290	1.2	4.0E-36	D87675.1	NT	Homo sapiens DNA for amyloid precursor protein, complete cds
8901	21867	35291	1.2	4.0E-36	D87675.1	NT	Homo sapiens DNA for amyloid precursor protein, complete cds
11332	24282	37806	1.8	4.0E-36	AA400370.1	EST_HUMAN	zu66c10.r1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:743250 5'
12471	25220		1.86	4.0E-36	11420516	NT	Homo sapiens nuclear factor of activated T-cells, cytoplasmic 2 (NFATC2), mRNA
12515	25768		8.26	4.0E-36	AV753629.1	EST_HUMAN	AV753629 TP Homo sapiens cDNA clone TPCABH01 5'
697	13759	26691	3.9	3.0E-36	AF099810.1	NT	Homo sapiens neurexin III-alpha gene, partial cds
1497	14530	27502	0.97	3.0E-36	AF110239.1	NT	Homo sapiens calcium/calmodulin-stimulated cyclic nucleotide phosphodiesterase (PDE1A) gene, partial cds
1497	14530	27503	0.97	3.0E-36	AF110239.1	NT	Homo sapiens calcium/calmodulin-stimulated cyclic nucleotide phosphodiesterase (PDE1A) gene, partial cds
4530	17554	30442	6.81	3.0E-36	10181139	NT	Mus musculus junctophilin 1 (Jp1-pending), mRNA
3184	16239	29157	2.17	2.0E-36	BE256267.1	EST_HUMAN	601106343F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3342706 5'
4996	18011	30898	8.63	2.0E-36	AW880376.1	EST_HUMAN	QV0-OT0030-240300-174-h04 OT0030 Homo sapiens cDNA
5563	18660	31606	2.52	2.0E-36	AF267747.1	NT	Mus musculus p47-phox gene, complete cds
5948	19034	32227	3.85	2.0E-36	T08756.1	EST_HUMAN	EST06648 Infant Brain, Bonto Soares Homo sapiens cDNA clone HIBBJ28 5' end
6728	19784	33063	12.4	2.0E-36	T69629.1	EST_HUMAN	y44a07.r1 Siratagene liver (#637224) Homo sapiens cDNA clone IMAGE:33508 5'
9743	22684	36138	0.82	2.0E-36	BF512794.1	EST_HUMAN	UI-H-BW1-amu-a-11-o-UI.st NCJ CGAP_Sub7 Homo sapiens cDNA clone IMAGE:3071132 3'
9907	22728	36184	0.57	2.0E-36	4507848	NT	Homo sapiens ubiquitin specific protease 13 (isopeptidase T-3) (USP13) mRNA

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Table 4
Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9907	22728	36185	0.57	2.0E-36	4507848	NT	Homo sapiens ubiquitin specific protease 13 (isopeptidase T-3) (USP13) mRNA
886	13941	26899	2.74	1.0E-36	BE409310.1	EST_HUMAN	601300988F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3636480 5'
2155	15171	28189	1.06	1.0E-36	BE146523.1	EST_HUMAN	RC1-HT0217-131199-021-H07 HT0217 Homo sapiens cDNA
2155	15171	28190	1.06	1.0E-36	BE146523.1	EST_HUMAN	RC1-HT0217-131199-021-H07 HT0217 Homo sapiens cDNA
2212	15227	28249	1.35	1.0E-36	BF673761.1	EST_HUMAN	602136463F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4272866 5'
3355	16408		1.34	1.0E-36	AF156982.1	NT	Homo sapiens human endogenous retrovirus W, provC8-19 protease (pro) gene, partial cds
5818	18908	32092	0.82	1.0E-36	AL044446.1	EST_HUMAN	DKFZ434G022_r1 434 (synonym: htes3) Homo sapiens cDNA clone DKFZ434G022 5'
6003	19086	32286	1.3	1.0E-36	4827084	NT	Homo sapiens zinc finger protein 147 (estradiol-responsive finger protein) (ZNF147) mRNA
6307	19378		3.86	1.0E-36	AI867714.1	EST_HUMAN	wb37c12.x1 NCL_CGAP_G06 Homo sapiens cDNA clone IMAGE:2307862 3' similar to contains Alu repetitive element;
6529	19592	32852	1.34	1.0E-36	R25012.1	EST_HUMAN	yg36g10.r1 Soares infant brain 1N1B Homo sapiens cDNA clone IMAGE:34529 5' similar to SP:CAHP_HUMAN P35219 CARBONIC ANHYDRASE-RELATED PROTEIN;
6529	19592	32853	1.34	1.0E-36	R25012.1	EST_HUMAN	yg36g10.r1 Soares infant brain 1N1B Homo sapiens cDNA clone IMAGE:34529 5' similar to SP:CAHP_HUMAN P35219 CARBONIC ANHYDRASE-RELATED PROTEIN;
6639	19892	33187	0.7	1.0E-36	AL120542.1	EST_HUMAN	DKFZ6761A229_r1 781 (synonym: hamy2) Homo sapiens cDNA clone DKFZ6761A229 5'
8293	21262	34671	2.77	1.0E-36	AA148034.1	EST_HUMAN	z651a12.r1 Stratagene endothelial cell 937223 Homo sapiens cDNA clone IMAGE:590398 5'
8293	21262	34672	2.77	1.0E-36	AA148034.1	EST_HUMAN	z651a12.r1 Stratagene endothelial cell 937223 Homo sapiens cDNA clone IMAGE:590398 5'
8388	21357	34784	1.15	1.0E-36	AA420467.1	EST_HUMAN	nc60e08.r1 NCL_CGAP_P1 Homo sapiens cDNA clone IMAGE:745670
8388	21357	34785	1.15	1.0E-36	AA420467.1	EST_HUMAN	nc60e08.r1 NCL_CGAP_P1 Homo sapiens cDNA clone IMAGE:745670
8520	21488	34902	0.48	1.0E-36	AU141688.1	EST_HUMAN	AU141688 THYRO1 Homo sapiens cDNA clone THYRO1001033 5'
8520	21488	34903	0.48	1.0E-36	AU141688.1	EST_HUMAN	AU141688 THYRO1 Homo sapiens cDNA clone THYRO1001033 5'
9384	22349	35781	2.72	1.0E-36	AW103658.1	EST_HUMAN	xe82607.x1 NCL_CGAP_Bm35 Homo sapiens cDNA clone IMAGE:2614357 3'
10473	23395	36892	3.95	1.0E-36	BF364166.1	EST_HUMAN	QV3-NN1023-010800-199-h01 NN1023 Homo sapiens cDNA
10691	23613	37107	0.65	1.0E-36	AW855868.1	EST_HUMAN	RC3-CT0279-040500-017-a10 CT0279 Homo sapiens cDNA
10691	23613	37108	0.65	1.0E-36	AW855868.1	EST_HUMAN	RC3-CT0279-040500-017-a10 CT0279 Homo sapiens cDNA
11294	24244	37771	2.84	1.0E-36	AW897636.1	EST_HUMAN	CM3-NN0061-140400-147-h12 NN0061 Homo sapiens cDNA
11709	24674	38251	2.88	1.0E-36	AW504143.1	EST_HUMAN	UIHF-BN0-ale-c-03-0-JUL1 NIH_MGC_50 Homo sapiens cDNA clone IMAGE:3079277 5'
12338	25136		5.51	1.0E-36	11418177	NT	Homo sapiens Ran GTPase activating protein 1 (RANGAP1) mRNA
12777	25414		4.97	1.0E-36	AL163213.2	NT	Homo sapiens chromosome 21 segment HS21C013
13034	25579		4.02	1.0E-36	AF202723.1	NT	Homo sapiens Sad1 unc-84 domain protein 2 (SUN2) mRNA, partial cds
7607	20568	33929	2.3	9.0E-37	AW009277.1	EST_HUMAN	ws80807.x1 NCL_CGAP_Cc3 Homo sapiens cDNA clone IMAGE:2504245 3'
7607	20568	33930	2.3	9.0E-37	AW009277.1	EST_HUMAN	ws80807.x1 NCL_CGAP_Cc3 Homo sapiens cDNA clone IMAGE:2504245 3'
3366	16416	29342	1.17	8.0E-37	4757979	NT	Homo sapiens chimerin (chimaerin) 2 (CHN2) mRNA
6320	18428		1.8	8.0E-37	BE698077.1	EST_HUMAN	CM0-UT0003-050800-503-609 UT0003 Homo sapiens cDNA

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Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5927	19013	32205	3.73	8.0E-37	BE350127.1	EST_HUMAN	h09g01.x1 NCL_CGAP_Kid13 Homo sapiens cDNA clone IMAGE:3146256 3' similar to contains MER29.b3 MER29 repetitive element;
5927	19013	32206	3.73	8.0E-37	BE350127.1	EST_HUMAN	h09g01.x1 NCL_CGAP_Kid13 Homo sapiens cDNA clone IMAGE:3146256 3' similar to contains MER29.b3 MER29 repetitive element;
5977	19062	32263	6.05	8.0E-37	AW840840.1	EST_HUMAN	RC1-CN0008-210100-012-a09_1 CN0008 Homo sapiens cDNA
8216	21185	34595	6.98	8.0E-37	X87344.1	NT	H sapiens DMA, DMB, HLA-Z1, IPP2, LMP2, TAP1, LMP7, TAP2, DOB, DQB2 and RING8, 9, 13 and 14 genes
1289	14324		2.33	7.0E-37	AL042800.1	EST_HUMAN	DKFZp434E0422_r1 434 (synonym: htes3) Homo sapiens cDNA clone DKFZp434E0422 5'
1759	14788	27773	0.92	7.0E-37	AF111167.2	NT	Homo sapiens jun dimerization protein gene, partial cds; cfos gene, complete cds; and unknown gene
1759	14788	27774	0.92	7.0E-37	AF111167.2	NT	Homo sapiens jun dimerization protein gene, partial cds; cfos gene, complete cds; and unknown gene
5161	18170	31049	1.56	7.0E-37	AW988923.1	EST_HUMAN	EST380899 IMAGE resequences, MAGJ Homo sapiens cDNA
11109	24069	37591	8.45	7.0E-37	AI817700.1	EST_HUMAN	wk25b11.x1 NCL_CGAP_Bm25 Homo sapiens cDNA clone IMAGE:2413341 3' similar to contains PTR5.12 PTR5 repetitive element;
11241	24194	37712	1.93	7.0E-37	AI536702.1	EST_HUMAN	hm87g03.x1 NCL_CGAP_Bm25 Homo sapiens cDNA clone IMAGE:2165140 3' similar to contains L1.b3 L1 repetitive element;
8782	21749	35171	0.59	8.0E-37	AF169689.1	NT	Homo sapiens protocadherin alpha 10 alternate isoform (PCDH-alpha10) mRNA, complete cds
12903	25487		3.98	6.0E-37	AF202723.1	NT	Homo sapiens Sad1 unc-84 domain protein 2 (SUN2) mRNA, partial cds
6212	19286	32518	4.33	5.0E-37	AA307123.1	EST_HUMAN	EST178035 Cdon carcinoma (HCC) cell line Homo sapiens cDNA 5' end
6212	19286	32519	4.33	5.0E-37	AA307123.1	EST_HUMAN	EST178035 Cdon carcinoma (HCC) cell line Homo sapiens cDNA 5' end
9109	22075	35501	0.88	5.0E-37	AV750211.1	EST_HUMAN	AV750211 NPC Homo sapiens cDNA clone NPCBGH09 5'
11265	24217		3.87	5.0E-37	7657117	NT	Homo sapiens glycine C-acetyltransferase (2-amino-3-ketobutyrate-CoA ligase) [GCAT], mRNA
12333	25193		6.43	5.0E-37	AF149773.1	NT	Homo sapiens NOD1 protein (NOD1) gene, exons 1, 2, and 3
2431	15438	28455	2.41	4.0E-37	AA702704.1	EST_HUMAN	z190b04.s1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:448015 3'
4914	17831	30729	1.05	4.0E-37	M10976.1	NT	Human endogenous retroviral DNA (4-1), complete retroviral segment
5268	18275		0.93	4.0E-37	N62051.1	EST_HUMAN	EST52g10 WATM1 Homo sapiens cDNA clone 52g10 similar to human STS G04101
6419	19486	32735	0.69	4.0E-37	AW794602.1	EST_HUMAN	RC8-UM0014-210200-021-H05 UM0014 Homo sapiens cDNA
9711	22684	35121	0.57	4.0E-37	AA843806.1	EST_HUMAN	ak09c02.s1 Soares_parathyroid_tumor_NbHPA Homo sapiens cDNA clone IMAGE:1405442 3'
2033	15052	28068	3.07	3.0E-37	AL048956.1	EST_HUMAN	DKFZp434L2418_r1 434 (synonym: htes3) Homo sapiens cDNA clone DKFZp434L2418
2033	15052	28069	3.07	3.0E-37	AL048956.1	EST_HUMAN	DKFZp434L2418_r1 434 (synonym: htes3) Homo sapiens cDNA clone DKFZp434L2418
2519	15522		1.74	3.0E-37	AW981150.1	EST_HUMAN	EST373222 IMAGE resequences, MAGF Homo sapiens cDNA
2876	16034		3.71	3.0E-37	AW981150.1	EST_HUMAN	EST373222 IMAGE resequences, MAGF Homo sapiens cDNA
5064	19049	32250	0.73	3.0E-37	AL138274.1	EST_HUMAN	DKFZp547G067_r1 547 (synonym: hbr1) Homo sapiens cDNA clone DKFZp547G067 5'

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7804	20754	34130	0.75	3.0E-37	A1748952.1	EST_HUMAN	at34c05.x1 Barstead colon HPLRB7 Homo sapiens cDNA clone IMAGE:2373866 3' similar to TR:Q13537
381	13494	26426	3.06	2.0E-37	D88780.1	NT	Q13537 SIMILAR TO POGO ELEMENT. ;
381	13494	26427	3.06	2.0E-37	D88780.1	NT	Homo sapiens mRNA for AML1, complete cds
1082	14126	27078	2.49	2.0E-37	AU131202.1	EST_HUMAN	Homo sapiens mRNA for AML1, complete cds
1082	14126	27080	2.49	2.0E-37	AU131202.1	EST_HUMAN	AU131202 NT2RP3 Homo sapiens cDNA clone NT2RP3002166 5'
1981	15002	28005	2.43	2.0E-37	AL163247.2	NT	AU131202 NT2RP3 Homo sapiens cDNA clone NT2RP3002166 5'
3908	16948	29859	5.24	2.0E-37	4503210	NT	Homo sapiens chromosome 21 segment HS21C047
5462	18564		0.74	2.0E-37	BF035327.1	EST_HUMAN	Homo sapiens cytochrome P450, subfamily XXV1A (steroid 27-hydroxylase, cerebrotendinous xanthomatosis), polypeptide 1 (CYP27A1b) mRNA
6896	19753	33030	0.85	2.0E-37	BF035327.1	EST_HUMAN	601458531F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3862086 5'
6816	19870	33159	3.92	2.0E-37	AA346720.1	EST_HUMAN	Homo sapiens mouse thiamin pyrophosphokinase homolog (TPK1), mRNA
8329	21298	34713	0.51	2.0E-37	BE537764.1	EST_HUMAN	EST52931 Fetal heart II Homo sapiens cDNA 5' end
8329	21298	34714	0.51	2.0E-37	BE537764.1	EST_HUMAN	601067534F1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3453657 5'
8372	21341	34752	3.33	2.0E-37	BF204032.1	EST_HUMAN	601067534F1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3453657 5'
11885	24766	38353	8.89	2.0E-37	AF176013.1	NT	601869157F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4111406 5'
12738	25607		1.51	2.0E-37	11417972	NT	Homo sapiens J domain containing protein 1 isoform b (JDPT1) mRNA, complete cds
13074	25607		4.68	2.0E-37	11417972	NT	Homo sapiens pascadillo (zebrafish) homolog 1, containing BRCT domain (PES1), mRNA
2099	15116	28138	5.41	1.0E-37	AL163281.2	NT	Homo sapiens pascadillo (zebrafish) homolog 1, containing BRCT domain (PES1), mRNA
3985	17025	29936	4.56	1.0E-37	AF180011.1	NT	Homo sapiens chromosome 21 segment HS21C081
4191	17222	30111	1.09	1.0E-37	BE872365.1	EST_HUMAN	Homo sapiens ribonuclease III (RN3) mRNA, complete cds
4978	17993	30882	2.21	1.0E-37	BF371719.1	EST_HUMAN	601448619F1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3852652 5'
6119	19197		1.01	1.0E-37	7305350	NT	QVQ-FN0180-280700-318-c10 FN0180 Homo sapiens cDNA
8557	21525	34943	0.7	1.0E-37	BE548032.1	EST_HUMAN	Mus musculus obgolin (Obg), mRNA
9087	22053	35476	3.45	1.0E-37	AA171408.1	EST_HUMAN	601072419F1 NIH_MGC_12 Homo sapiens cDNA clone IMAGE:3458308 5'
10971	23691	37405	0.44	1.0E-37	AV730743.1	EST_HUMAN	zp21b02.r1 Stragene neuroepithelium (#637231) Homo sapiens cDNA clone IMAGE:610059 5' similar to contains L1 L2 L1 repetitive element ;
11058	24019	37542	2.07	1.0E-37	M22878.1	NT	AV730743 HTF Homo sapiens cDNA clone HTFAHG10 5'
12646	25329		4.28	1.0E-37	BE771814.1	EST_HUMAN	Human somatic cytochrome c (HC1) processed pseudogene, complete cds
5872	19981	32150	1.67	9.0E-38	10048482	NT	GM3-FT0096-140700-243-d07 FT0096 Homo sapiens cDNA
1226	14284	27221	1.85	8.0E-38	11436955	NT	Rattus norvegicus multidomain presynaptic cytomatrix protein Piccolo (LOC56768), mRNA
2506	15509	28536	2.16	8.0E-38	BF348221.1	EST_HUMAN	Homo sapiens Gfb2-associated binder 2 (KIA00571), mRNA
12698	14284	27221	1.44	8.0E-38	11436955	NT	602018401F1 NC1 CGAP_Bm67 Homo sapiens cDNA clone IMAGE:4153992 5'
3055	16112	29027	1.88	6.0E-38	BF033033.1	EST_HUMAN	Homo sapiens Gfb2-associated binder 2 (KIA00571), mRNA
							601455722F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3859348 5'

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5670	18765	31935	1.48	6.0E-38	11425114	NT	Homo sapiens zinc finger protein ZNF287 (ZNF287), mRNA
5670	18765	31936	1.48	6.0E-38	11425114	NT	Homo sapiens zinc finger protein ZNF287 (ZNF287), mRNA
7650	20513	33871	0.51	6.0E-38	8923130	NT	Homo sapiens hypothetical protein FLJ20128 (FLJ20128), mRNA
7613	20573	33936	0.74	6.0E-38	AJ010999.1	NT	Homo sapiens mRNA for potassium channel Kv4.2
7613	20573	33937	0.74	6.0E-38	AJ010999.1	NT	Homo sapiens mRNA for potassium channel Kv4.2
12189	25035		3.19	6.0E-38	11435947	NT	Homo sapiens chromosome 12 open reading frame 3 (C12ORF3), mRNA
12677	25347	31765	18.01	6.0E-38	AB002059.1	NT	Homo sapiens DNA for Human P2X1, complete cds
13052	25793	31616	1.66	6.0E-38	11418164	NT	Homo sapiens adenylosuccinate lyase (ADSL), mRNA
728	13789	26724	1.28	5.0E-38	AW971819.1	EST_HUMAN	EST388908 IMAGE resequences, MAGL Homo sapiens cDNA
2460	15464	28487	1.24	5.0E-38	AJ237740.1	NT	Homo sapiens RIBLIR gene (partial), exon 8
7228	20250	33594	1.8	5.0E-38	BE871610.1	EST_HUMAN	601450148F1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3654074 5'
119	13228	26154	3.65	4.0E-38	Z25466.1	NT	B.taurus mitochondrial aspartate aminotransferase mRNA, complete CDS
119	13228	26155	3.65	4.0E-38	Z25466.1	NT	B.taurus mitochondrial aspartate aminotransferase mRNA, complete CDS
2110	15127		3.98	3.0E-38	AF003530.1	NT	Homo sapiens homeobox protein CDX4 (CDX4) gene, complete cds and flanking repeat regions
3710	16753		1.24	3.0E-38	7549807	NT	Homo sapiens HIRA interacting protein 4 (dnaj-llike) (HIRAP4), mRNA
3869	19908	29817	1.68	3.0E-38	P63538	SWISSPROT	SSU72 PROTEIN
3869	19908	29818	1.68	3.0E-38	P63538	SWISSPROT	SSU72 PROTEIN
6917	25671	33284	7.83	3.0E-38	AL163300.2	NT	Homo sapiens chromosome 21 segment HS21C100
7455	20421	33776	0.6	3.0E-38	AW302461.1	EST_HUMAN	xv04d01.x1 NCL CGAP_Brn53 Homo sapiens cDNA clone IMAGE:2827009 3'
7832	20780		0.57	3.0E-38	AA378327.1	EST_HUMAN	EST91188 Synovial sarcoma Homo sapiens cDNA 5' end
7844	20791	34167	6.28	3.0E-38	BF373664.1	EST_HUMAN	CM3-FT0181-140700-241-607 FT0181 Homo sapiens cDNA
8997	21963	35388	1.97	3.0E-38	H85494.1	EST_HUMAN	yv88604.r1 Soares melanocyte 2NBHM Homo sapiens cDNA clone IMAGE:249775 5'
8997	21963	35389	1.97	3.0E-38	H85494.1	EST_HUMAN	yv88604.r1 Soares melanocyte 2NBHM Homo sapiens cDNA clone IMAGE:249775 5'
10331	23255		2.06	3.0E-38	AL163248.2	NT	Homo sapiens chromosome 21 segment HS21C048
12909	18333	31171	1.46	3.0E-38	11435947	NT	Homo sapiens chromosome 12 open reading frame 3 (C12ORF3), mRNA
52	13172	28081	2.54	2.0E-38	AL163248.2	NT	Homo sapiens chromosome 21 segment HS21C048
1380	14414	27384	2.28	2.0E-38	5902097	NT	Homo sapiens SMT3 (suppressor of mit two 3, yeast) homolog 2 (SMT3H2), mRNA
1653	14685	27659	2.07	2.0E-38	AA437553.1	EST_HUMAN	zw30d01.r1 Soares ovary tumor NBHOT Homo sapiens cDNA clone IMAGE:770785 5' similar to
1653	14685	27660	2.07	2.0E-38	AA437553.1	EST_HUMAN	SW:MA12_RABIT P45701 MANNOSYL-OLIGOSACCHARIDE ALPHA-1,2-MANNOSIDASE ;
2418	15425	28448	1.11	2.0E-38	W76571.1	EST_HUMAN	zw30d01.r1 Soares ovary tumor NBHOT Homo sapiens cDNA clone IMAGE:770785 5' similar to
						EST_HUMAN	zdc66g09.r1 Soares_fetal NBHT_HNF19W Homo sapiens cDNA clone IMAGE:345664 5'
5271	18160	31040	0.79	2.0E-38	AA437181.1	EST_HUMAN	zw61d09.r1 Soares testis NHT Homo sapiens cDNA clone IMAGE:758129 5' similar to TR:G817957

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5807	18897	32079	0.61	2.0E-38	Z26634.2	NT	Homo sapiens mRNA for ankyrin B (440 kDa)
5807	18897	32080	0.61	2.0E-38	Z26634.2	NT	Homo sapiens mRNA for ankyrin B (440 kDa)
7888	20927	34322	1.27	2.0E-38	AV721103.1	EST_HUMAN	AV721103 HTB Homo sapiens cDNA clone HTBARH11 5'
8828	21795		5.59	2.0E-38	BE169980.1	EST_HUMAN	MR3-HT0487-150200-113-g01 HT0487 Homo sapiens cDNA
9246	22122	35642	0.55	2.0E-38	F06450.1	EST_HUMAN	HSC18F031 normalized infant brain cDNA Homo sapiens cDNA clone c-18F03
9316	22281	35711	1.21	2.0E-38	AF069755.1	NT	Homo sapiens orphan G protein-coupled receptor HG20 (HG20) mRNA, complete cds
9576	22538		1.04	2.0E-38	BE22255.1	EST_HUMAN	hu09g02.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3166130 3' similar to TR:O02710 O02710 GAG POLYPROTEIN.
10816	23736	37239	1.74	2.0E-38	D63479.2	NT	Homo sapiens mRNA for KIAA0145 protein, partial cds
11819	24702	38284	4.62	2.0E-38	BE12790.1	EST_HUMAN	QV2-HT0698-080800-283-a05 HT0698 Homo sapiens cDNA
11955	24834	38429	3.66	2.0E-38	AF190501.1	NT	Homo sapiens leucine-rich repeat-containing G protein-coupled receptor 6 (LGR6) mRNA, partial cds
11955	24834	38430	3.66	2.0E-38	AF190501.1	NT	Homo sapiens leucine-rich repeat-containing G protein-coupled receptor 6 (LGR6) mRNA, partial cds
12240	25071		3.39	2.0E-38	AV726988.1	EST_HUMAN	AV726988 HTC Homo sapiens cDNA clone HTCAHX07 5'
12242	25072		2.13	2.0E-38	AB012723.1	NT	Homo sapiens gene for kinesin-like protein, complete cds
12538	25262		2.51	2.0E-38	M55630.1	NT	Human topoisomerase I pseudogene 2
12548	25271	31810	6.8	2.0E-38	H55641.1	EST_HUMAN	GHR220580 Chromosome 22 exon Homo sapiens cDNA clone C22_788 5'
13065	25599		3	2.0E-38	11418248	NT	Homo sapiens sulfotransferase-related protein (SULTX3), mRNA
1095	14139		2.38	1.0E-38	AA401570.1	EST_HUMAN	z162b02.11 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:742539 5' similar to contains element MER19 repetitive element
2015	15036	28047	1.92	1.0E-38	4855288	NT	Homo sapiens guanine nucleotide binding protein-like 1 (GNL1), mRNA
2035	15054	28071	1.17	1.0E-38	7661969	NT	Homo sapiens KIAA0173 gene product (KIAA0173), mRNA
2502	15505	28532	2.01	1.0E-38	AF270831.1	NT	Homo sapiens cyclin K (CKNK) gene, exon 7
4182	17213	30101	0.99	1.0E-38	AB037863.1	NT	Homo sapiens mRNA for KIAA1442 protein, partial cds
4352	17379	30259	10.48	1.0E-38	AL169203.2	NT	Homo sapiens chromosome 21 segment HS21C003
4352	17379	30260	10.48	1.0E-38	AL169203.2	NT	Homo sapiens chromosome 21 segment HS21C003
4627	17648	30536	0.93	1.0E-38	8922543	NT	Homo sapiens chromosome 21 segment HS21C003
5143	18152	31032	0.77	1.0E-38	AA07526.1	EST_HUMAN	Homo sapiens hypothetical protein FLJ10600 (FLJ10600), mRNA
6143	19218	32447	6.58	1.0E-38	7305360	NT	7B44H06 Chromosome 7 Fetal Brain cDNA Library Homo sapiens cDNA clone 7B44H06
6143	19218	32448	6.58	1.0E-38	7305360	NT	Mus musculus otogelin (Otog), mRNA
7634	20594	33957	3.03	1.0E-38	AB014512.1	NT	Mus musculus otogelin (Otog), mRNA
9508	22471	35915	0.55	1.0E-38	11422250	NT	Homo sapiens mRNA for KIAA0512 protein, partial cds
							Homo sapiens hypothetical protein FLJ10600 (FLJ10600), mRNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9765	22706	36162	6.34	1.0E-38	BE350127.1	EST_HUMAN	h109g01.x1 NCI_CGAP_Kid13 Homo sapiens cDNA clone IMAGE:3148256 3' similar to contains MER28.b3
12401	25712		2.08	1.0E-38	AL163284.2	NT	MER29 repetitive element ;
56	13176	26087	5.73	8.0E-39	4502312	NT	Homo sapiens chromosome 21 segment HS21C084
1395	14429	27398	0.94	8.0E-39	4758229	NT	Homo sapiens ATPase, H+ transporting, lysosomal (vacuolar probin pump) 16kD (ATP6C) mRNA
1846	14872		1.54	8.0E-39	AI823404.1	EST_HUMAN	Homo sapiens estrogen receptor-binding fragment-associated gene 9 (EBAG9) mRNA
2105	15122	28142	5.19	7.0E-39	AL163227.2	NT	wh53f10.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2384481 3' similar to TR:P87890 P87890
11160	24118	37645	1.8	6.0E-39	BF331826.1	EST_HUMAN	POL PROTEIN ;
12981	25545		3.12	6.0E-39	BE670394.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C027
1009	14058	27010	1.43	5.0E-39	AF003528.1	NT	QV1-BT0631-040900-357-02 BT0631 Homo sapiens cDNA
2998	16056	28976	8.13	5.0E-39	AI750154.1	EST_HUMAN	7e34-c03.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3284356 3' similar to WP:R151.6
12689	25356		2.82	4.0E-39	AB015610.1	NT	CE00828 ;
552	13622	26542	20.77	4.0E-39	AB015610.1	NT	Homo sapiens X-linked anhidrotic ectodermal dysplasia protein gene (EDA), exon 2 and flanking repeat regions
3587	16632	29550	0.92	4.0E-39	AL163210.2	NT	at36b04.x1 Barstead colon HPLRB7 Homo sapiens cDNA clone IMAGE:2374063 3' similar to TR:Q15408
5928	19014	32207	0.65	4.0E-39	11422113	NT	Q15408 NEUTRAL PROTEASE LARGE SUBUNIT ; contains LTR7 t1 LTR7 repetitive element ;
5928	19014	32208	0.65	4.0E-39	11422113	NT	Homo sapiens hypothetical protein FLJ10803 (FLJ10803), mRNA
8411	21380	34786	1.14	4.0E-39	AA682949.1	EST_HUMAN	Chlorocebus aethiops mRNA for ribosomal protein S4X, complete cds
9884	22637	36092	0.61	4.0E-39	D84116.1	NT	Homo sapiens chromosome 21 segment HS21C010
9884	22637	36093	0.61	4.0E-39	D84116.1	NT	Homo sapiens EBNA-2 co-activator (100kD) (p100), mRNA
12704	25363		3.29	4.0E-39	11418177	NT	Homo sapiens EBNA-2 co-activator (100kD) (p100), mRNA
12819	25441		3.15	4.0E-39	BE936452.1	EST_HUMAN	ae82g04.s1 Stratagene schizo brain S11 Homo sapiens cDNA clone IMAGE:1020438 3' similar to contains OFR.b1 ORF repetitive element ;
49	13169	26075	14.8	3.0E-39	AA631949.1	EST_HUMAN	Homo sapiens DNA for prostacyclin synthase, exon 2
49	13169	26076	14.8	3.0E-39	AA631949.1	EST_HUMAN	Homo sapiens Ran GTPase activating protein 1 (RANGAP1), mRNA
49	13169	26077	14.8	3.0E-39	AA631949.1	EST_HUMAN	Homo sapiens Ran GTPase activating protein 1 (RANGAP1), mRNA
12233	25065	38163	6.14	3.0E-39	AI084557.1	EST_HUMAN	QV0-FN0063-260600-278-c08 FN0063 Homo sapiens cDNA
12233	25065	38164	6.14	3.0E-39	AI084557.1	EST_HUMAN	fmfc16 Regional genomic DNA specific cDNA library Homo sapiens cDNA clone CR12-1
							fmfc16 Regional genomic DNA specific cDNA library Homo sapiens cDNA clone CR12-1
							fmfc16 Regional genomic DNA specific cDNA library Homo sapiens cDNA clone CR12-1
							fmfc16 Regional genomic DNA specific cDNA library Homo sapiens cDNA clone CR12-1
							ox63at10.s1 Soares NIHMPu_S1 Homo sapiens cDNA clone IMAGE:1660986 3' similar to SW:GTR5_RAT
							P43427 GLUCOSE TRANSPORTER TYPE 5, SMALL INTESTINE ;
							ox63at10.s1 Soares NIHMPu_S1 Homo sapiens cDNA clone IMAGE:1660986 3' similar to SW:GTR5_RAT
							P43427 GLUCOSE TRANSPORTER TYPE 5, SMALL INTESTINE ;

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Table 4
Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
12282	25100		11.16	3.0E-39	H37903.1	EST_HUMAN	yp51c06.s1 Soares retina N2b4HR Homo sapiens cDNA clone IMAGE:190954 3'
898	13953		9.79	2.0E-39	BE409203.1	EST_HUMAN	601301607F1 NIH_MGC 21 Homo sapiens cDNA clone IMAGE:3636289 5'
913	13968		13.84	2.0E-39	AI625119.1	EST_HUMAN	promna-7.D01.r bvtumor Homo sapiens cDNA 5'
1033	14079		4.67	2.0E-39	AF000579.1	NT	Homo sapiens homogenisate 1,2-dioxygenase gene, complete cds
1532	14565		24.51	2.0E-39	AW372318.1	EST_HUMAN	PM0-BT0340-211299-003-d02 BT0340 Homo sapiens cDNA
1990	15011		3.62	2.0E-39	AA720574.1	EST_HUMAN	hw21g02.s1 NCI_CGAP_GCB0 Homo sapiens cDNA clone IMAGE:1241138 3' similar to contains THR.13
2636	15635	28017	2.3	2.0E-39	AL163248.2	NT	THR repetitive element;
4431	17458	30349	1.58	2.0E-39	BF370207.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C048
5568	18665	31624	4.2	2.0E-39	AA608880.1	EST_HUMAN	RC4-FN0037-290700-011-a10 FN0037 Homo sapiens cDNA
7594	20555	33915	2.34	2.0E-39	AA080867.1	EST_HUMAN	ng86103.s1 NCI_CGAP_P16 Homo sapiens cDNA clone IMAGE:941693
7776	20729	34101	0.61	2.0E-39	AL163202.2	NT	zn06102.1 Stratagene hNT neuron (#837233) Homo sapiens cDNA clone IMAGE:546651 5'
7776	20729	34102	0.61	2.0E-39	AL163202.2	NT	Homo sapiens chromosome 21 segment HS21C002
8653	21621	35041	0.56	2.0E-39	AF078779.1	NT	Homo sapiens chromosome 21 segment HS21C002
9851	22787		1.32	2.0E-39	AA884631.1	EST_HUMAN	Rattus norvegicus putative four repeat ion channel mRNA, complete cds
9984	22911		0.53	2.0E-39	AI686660.1	EST_HUMAN	am88c11.s1 Stratagene schizo brain S11 Homo sapiens cDNA clone IMAGE:1630196 3'
11781	24689	38271	2.56	2.0E-39	D86984.1	NT	tu35e03.x1 NCI_CGAP_P128-Homo sapiens cDNA clone IMAGE:2253052 3'
1516	14548	27520	3.52	1.0E-39	AJ008345.1	NT	Human mRNA for KIAA0209 gene, partial cds
1516	14548	27521	3.52	1.0E-39	AJ008345.1	NT	Homo sapiens KVLQ11 gene
1533	14566	27535	6.96	1.0E-39	7657020	NT	Homo sapiens KVLQ11 gene
4889	17710	30603	6.87	1.0E-39	AW951995.1	EST_HUMAN	Homo sapiens DKFZp434P211 protein (DKFZP434P211), mRNA
4889	17710	30604	6.87	1.0E-39	AW951995.1	EST_HUMAN	EST384065 IMAGE resequences, MAGB Homo sapiens cDNA
4731	17751	30643	8.48	1.0E-39	7657020	NT	EST364065 IMAGE resequences, MAGB Homo sapiens cDNA
5432	18534	31442	0.87	1.0E-39	11417342	NT	Homo sapiens DKFZp434P211 protein (DKFZP434P211), mRNA
5432	18534	31443	0.87	1.0E-39	11417342	NT	Homo sapiens sema domain, seven thrombospondin repeats (type 1 and type 1-like), transmembrane domain (TM) and short cytoplasmic domain, (semaphorin) 5A (SEMA5A), mRNA
5711	18805	31982	1.2	1.0E-39	T80876.1	EST_HUMAN	Homo sapiens sema domain, seven thrombospondin repeats (type 1 and type 1-like), transmembrane domain (TM) and short cytoplasmic domain, (semaphorin) 5A (SEMA5A), mRNA
5747	18841	32023	4.7	1.0E-39	AJ278170.1	NT	yd26g08.1 Soares fetal liver spleen 1NF1S Homo sapiens cDNA clone IMAGE:109402 5' similar to contains
5747	18841	32024	4.7	1.0E-39	AJ278170.1	NT	Alu repetitive element; contains LTR1 repetitive element;
7000	20126		1.88	1.0E-39	11436736	NT	Mus musculus mRNA for neuronal interacting factor X1 (NIX1) (Nix1 gene)
7589	20550	33911	2.1	1.0E-39	D78132.1	NT	Mus musculus mRNA for neuronal interacting factor X1 (NIX1) (Nix1 gene)
8910	21876	35302	0.96	1.0E-39	O46530	SWISSPROT	Homo sapiens tubby like protein 3 (TULP3), mRNA
							Homo sapiens mRNA for ras-related GTP-binding protein, complete cds
							RIBONUCLEASE K6 PRECURSOR (RNASE K6)

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
557	13627	26645	1.8	9.0E-40	5803210	NT	Homo sapiens UDP-glucose pyrophosphorylase 2 (UGP2), mRNA
1239	14275	27234	14.84	9.0E-40	4755145	NT	Homo sapiens AE-binding protein 1 (AEBP1), mRNA
1239	14275	27235	14.84	9.0E-40	4755145	NT	Homo sapiens AE-binding protein 1 (AEBP1), mRNA
1443	14478	27453	0.99	9.0E-40	4507512	NT	Homo sapiens tissue inhibitor of metalloproteinase 3 (Sorsby fundus dystrophy, pseudoinflammatory) (TIMP3), mRNA
3799	16839	29746	0.88	9.0E-40	4503784	NT	Homo sapiens fragile X mental retardation 1 (FMR1), mRNA
3997	18315	29643	4.05	9.0E-40	AB03070.1	NT	Homo sapiens mRNA for KIAA1244 protein, partial cds
4527	17401	30281	0.78	9.0E-40	4507848	NT	Homo sapiens ubiquitin specific protease 13 (isopeptidase T-3) (USP13), mRNA
3054	16111	29026	0.91	8.0E-40	AA078165.1	EST_HUMAN	7H15A04 Chromosome 7 HeLa cDNA Library/Homo sapiens cDNA clone 7H15A04
3945	16885		2.39	8.0E-40	BE396541.1	EST_HUMAN	601288958F1 NIH_MGC_8 Homo sapiens cDNA clone IMAGE:3619166 5'
7985	20924	34317	2.22	7.0E-40	U60325.1	NT	Human DNA polymerase gamma mRNA, nuclear gene encoding mitochondrial protein, complete cds
7985	20924	34318	2.22	7.0E-40	U60325.1	NT	Human DNA polymerase gamma mRNA, nuclear gene encoding mitochondrial protein, complete cds
11243	24196	37715	1.78	7.0E-40	AL163246.2	NT	Homo sapiens chromosome 21 segment HS21C046
2737	15731	28746	7.5	6.0E-40	AA361275.1	EST_HUMAN	ESTT0527 T-cell lymphoma Homo sapiens cDNA 5' end similar to zinc finger protein family
2737	15731	28747	7.5	6.0E-40	AA361275.1	EST_HUMAN	ESTT0527 T-cell lymphoma Homo sapiens cDNA 5' end similar to zinc finger protein family
6049	19130		2.05	6.0E-40	BE504788.1	EST_HUMAN	h240g01.x1 NCI_CGAP_G08 Homo sapiens cDNA clone IMAGE:3210480 3'
6270	19343		1.32	6.0E-40	7661999	NT	Homo sapiens KIAA0211 gene product (KIAA0211), mRNA
7121	20055	33359	3.38	6.0E-40	11439783	NT	Homo sapiens fatty acid desaturase 1 (FADS1), mRNA
7121	20055	33360	3.38	6.0E-40	11439783	NT	Homo sapiens fatty acid desaturase 1 (FADS1), mRNA
10336	23260	36738	9.47	6.0E-40	AV653028.1	EST_HUMAN	AV653028 GLC Homo sapiens cDNA clone GLCDGF04.3'
10336	23260	36739	9.47	6.0E-40	AV653028.1	EST_HUMAN	AV653028 GLC Homo sapiens cDNA clone GLCDGF04.3'
2612	16611	28635	1.12	5.0E-40	AL163285.2	NT	Homo sapiens chromosome 21 segment HS21C085
1894	14919	27915	3.21	4.0E-40	AI686005.1	EST_HUMAN	h91b01.x1 NCI_CGAP_P128 Homo sapiens cDNA clone IMAGE:2248873 3' similar to TR:O73505 O73505 POL PROTEIN ;
2117	15134		2.22	4.0E-40	AF003528.1	NT	Homo sapiens X-linked anhidrotic ectodermal dysplasia protein gene (EDA), exon 2 and flanking repeat regions
4415	17442	30333	8.57	4.0E-40	7662117	NT	Homo sapiens KIAA0433 protein (KIAA0433), mRNA
8218	21167	34597	0.44	4.0E-40	AU127831.1	EST_HUMAN	AU127831 NT2RP2 Homo sapiens cDNA clone NT2RP2002172 5'
8324	21293	34707	4.81	4.0E-40	AA742808.1	EST_HUMAN	n34e10.1 NCI_CGAP_B44 Homo sapiens cDNA clone IMAGE:1222122
9410	22375	35812	5.53	4.0E-40	BE009416.1	EST_HUMAN	PIMD-BN0167-070500-002-h12 BN0167 Homo sapiens cDNA

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Table 4
Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9410	22375	35813	5.53	4.0E-40	BE009416.1	EST_HUMAN	PMO-BN0167-070500-002-h12 BN0167 Homo sapiens cDNA
11071	24033	37557	1.66	4.0E-40	AW841885.1	EST_HUMAN	RC1-CN0017-120200-012-e04 CN0017 Homo sapiens cDNA
4158	17189	30077	1.02	3.0E-40	A1925949.1	EST_HUMAN	wh1207.x1 NCL_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2380549 3'
6607	19665	32840	0.86	3.0E-40	4506736	NT	Homo sapiens ribosomal protein S6 kinase, 70kD, polypeptide 1 (RPS8KB1) mRNA
6796	19850	33135	7.89	3.0E-40	11417342	NT	Homo sapiens sema domain, seven thrombospondin repeats (type 1 and type 1-like), transmembrane domain (TM) and short cytoplasmic domain, (semaphorin) 5A (SEMA5A), mRNA
8724	21692	35118	3.94	3.0E-40	5454167	NT	Homo sapiens HBV associated factor (XAP4) mRNA
9320	22885	35715	1.23	3.0E-40	AF078779.1	NT	Rattus norvegicus putative four repeat ion channel mRNA, complete cds
9566	22528	35977	1.34	3.0E-40	AF078779.1	NT	Rattus norvegicus putative four repeat ion channel mRNA, complete cds
11597	24535	38092	9.3	3.0E-40	6005813	NT	Homo sapiens serine threonine protein kinase (NDR), mRNA
325	13416		4.59	2.0E-40	A1223036.1	EST_HUMAN	q552n08.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1838847 3'
795	13854		29.29	2.0E-40	AW303868.1	EST_HUMAN	xc24e10.x1 NCL_CGAP_U14 Homo sapiens cDNA clone IMAGE:2761098 3' similar to SW:RSS_MOUSE
1842	14868		1.77	2.0E-40	AV731601.1	EST_HUMAN	P97461 40S RIBOSOMAL PROTEIN S5.;
1951	14974	27973	1.94	2.0E-40	4506188	NT	AV731601 HTF Homo sapiens cDNA clone HTFAZE05 5'
1951	14974	27974	1.94	2.0E-40	4506188	NT	Homo sapiens proteasome (prosome, macropain) subunit, alpha type, 7 (PSMA7) mRNA, and translated products
2085	15102	28119	1.01	2.0E-40	A1988562.1	EST_HUMAN	Homo sapiens proteasome (prosome, macropain) subunit, alpha type, 7 (PSMA7) mRNA, and translated products
2179	15194	28215	1.84	2.0E-40	5453592	NT	w90a11.x1 NCL_CGAP_GC6 Homo sapiens cDNA clone IMAGE:2514716 3' similar to TR:Q91929 Q91929
2700	15696		1.79	2.0E-40	BE275632.1	EST_HUMAN	ZINC FINGER PROTEIN.;
3143	19200	29111	4.44	2.0E-40	5453592	NT	Homo sapiens adenyl cyclase-associated protein 2 (CAP2) mRNA
4937	17963	30845	1.7	2.0E-40	AL163280.2	NT	601121567F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3345784 5'
4937	17963	30846	1.7	2.0E-40	AL163280.2	NT	Homo sapiens adenyl cyclase-associated protein 2 (CAP2) mRNA
5237	18245	31117	1.12	2.0E-40	4505880	NT	Homo sapiens chromosome 21 segment HS21C080
884	13939		1.63	1.0E-40	AA225989.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C080
2629	15628	28653	1.47	1.0E-40	BF038881.1	EST_HUMAN	Homo sapiens plasminogen (PLG) mRNA
2698	15692		1.54	1.0E-40	BE018348.1	EST_HUMAN	nc09a09.s1 NCL_CGAP_P11 Homo sapiens cDNA clone IMAGE:1007608
2747	15740	28756	1.36	1.0E-40	BF541030.1	EST_HUMAN	601460375F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3663803 5'
2747	15740	28757	1.36	1.0E-40	BF541030.1	EST_HUMAN	601460375F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3663803 5'
3309	16362		1.58	1.0E-40	4507142	NT	bb78a10.y1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3048570 5' similar to TR:Q9Z168 Q9Z168
4640	17661	30549	4.18	1.0E-40	4508012	NT	SYNTAXIN 17.;
							602068604F1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:4067736 5'
							602068604F1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:4067736 5'
							Homo sapiens sorting nexin 3 (SNX3) mRNA
							Homo sapiens zinc finger protein 200 (ZNF200) mRNA, and translated products

Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6384	19452	32695	0.73	1.0E-40	W92708.1	EST_HUMAN	zh7811.s1 Soares fetal_liver_spleen_INFLS_S1 Homo sapiens cDNA clone IMAGE:418317 3'
6384	19452	32696	0.73	1.0E-40	W92708.1	EST_HUMAN	zh7811.s1 Soares fetal_liver_spleen_INFLS_S1 Homo sapiens cDNA clone IMAGE:418317 3'
7283	20265	33599	1.92	1.0E-40	AA573201.1	EST_HUMAN	h42804.s1 NCI_CGAP_AA1 Homo sapiens cDNA clone IMAGE:996167 3'
7283	20265	33600	1.92	1.0E-40	AA573201.1	EST_HUMAN	h42804.s1 NCI_CGAP_AA1 Homo sapiens cDNA clone IMAGE:996167 3'
7443	20409	33761	0.84	1.0E-40	P28808	SWISSPROT	POL POLYPROTEIN [CONTAINS: PROTEASE, REVERSE TRANSCRIPTASE; RIBONUCLEASE H]
11262	24214	37738	2.42	1.0E-40	AU149345.1	EST_HUMAN	AU149345 NT2RM4 Homo sapiens cDNA clone NT2RM4002122 3'
12659	25847		14.2	1.0E-40	BF334112.1	EST_HUMAN	MR2-CT0222-21 1089-002-e10 CT0222 Homo sapiens cDNA
12813	25822		1.64	1.0E-40	Z00015.1	NT	H.sapiens Y(k) gene low repetitive L-family member (cos 20)
8254	21223	34633	1.59	8.0E-41	AL163203.2	NT	Homo sapiens chromosome 21 segment HS21C003
829	15852	26840	1.81	7.0E-41	AI934384.1	EST_HUMAN	wp04h04.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2463895 3'
829	15852	26841	1.81	7.0E-41	AI934384.1	EST_HUMAN	wp04h04.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2463895 3'
5337	18442	31195	0.95	7.0E-41	11545770	NT	Homo sapiens hypothetical protein FLJ13188 (FLJ13188), mRNA
6124	19202	32426	2.97	7.0E-41	11419208	NT	Homo sapiens a disintegrin and metalloproteinase domain 22 (ADAM22), mRNA
6488	19553	32803	1.08	7.0E-41	11433010	NT	Homo sapiens IQ motif containing GTPase activating protein 1 (IQGAP1), mRNA
7186	18417	31218	0.88	7.0E-41	U72335.1	NT	Human platelet activating factor acetylhydrolase, brain isoform, 45 kDa subunit (LIS1) gene, exons 3 and 4
11763	24891	38272	2.6	7.0E-41	4758445	NT	Homo sapiens guanine nucleotide binding protein 10 (GNG10) mRNA
13072	25844		10.83	7.0E-41	11417972	NT	Homo sapiens pascadillo (zbratfish) homolog 1, containing BRCT domain (PES1), mRNA
280	13375	26304	0.65	6.0E-41	AB037163.1	NT	Homo sapiens DSCR5b mRNA, complete cds
2120	15137	28157	1.67	6.0E-41	7957042	NT	Homo sapiens Down syndrome candidate region 1 (DSOR1), mRNA
8304	21273	34684	1.59	6.0E-41	BF513783.1	EST_HUMAN	UHL-BW1-amp-b-03-0-U1.s1 NCI_CGAP_Sub7 Homo sapiens cDNA clone IMAGE:3070421 3'
1819	14846	27838	1.75	5.0E-41	T82628.1	EST_HUMAN	yc03e10.s1 Stragene lung (#937210) Homo sapiens cDNA clone IMAGE:79628 3'
4134	17166		1.03	5.0E-41	4885636	NT	Homo sapiens target of myb1 (chicken) homolog (TOM1), mRNA
6698	19755		2.06	5.0E-41	BE07042.1	EST_HUMAN	PM4-BT0341-251199-002-F11 BT0341 Homo sapiens cDNA
391	13468		1.73	4.0E-41	BE156318.1	EST_HUMAN	QV0-HT0367-150200-114-g09 HT0367 Homo sapiens cDNA
1100	14144	27084	1.16	4.0E-41	AU116344.1	EST_HUMAN	AU116344 HEMBA1 Homo sapiens cDNA clone HEMBA1005683 5'
1408	14441	27411	9.16	4.0E-41	AI027117.1	EST_HUMAN	ow45e06.s1 Soares parathyroid_tumor_NbHPA Homo sapiens cDNA clone IMAGE:1649794 3' similar to TR:000597 000597 CYTOCHROME C-LIKE POLYPEPTIDE; contains LTR5.b1 LTR5 repetitive element;
1408	14441	27412	9.16	4.0E-41	AI027117.1	EST_HUMAN	ow45e06.s1 Soares parathyroid_tumor_NbHPA Homo sapiens cDNA clone IMAGE:1649794 3' similar to TR:000597 000597 CYTOCHROME C-LIKE POLYPEPTIDE; contains LTR5.b1 LTR5 repetitive element;
1420	14453	27427	2.75	4.0E-41	AB008681.1	NT	Homo sapiens gene for activin receptor type IIB, complete cds

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Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1641	14673	27646	6.9	4.0E-41	AI500406.1	EST_HUMAN	Im96c04.x1 NCI_CGAP_Brn28 Homo sapiens cDNA clone IMAGE:2166968 3' similar to contains ORF.b1 ORF repetitive element;
2869	15958	28876	3.56	4.0E-41	AJ228041.1	NT	Homo sapiens 959 kb contig between AML1 and CBR1 on chromosome 21q22; segment 1/3
2899	15958	28877	3.66	4.0E-41	AJ228041.1	NT	Homo sapiens 959 kb contig between AML1 and CBR1 on chromosome 21q22; segment 1/3
4168	17199	30085	2.26	4.0E-41	X62685.1	NT	H. sapiens DNase I hypersensitive site (HSS-3) enhancer element
6658	19715		1.31	4.0E-41	AV758295.1	EST_HUMAN	AV758295 BM Homo sapiens cDNA clone BMFBHC08 5'
10052	22879	38446	8.41	4.0E-41	BF304883.1	EST_HUMAN	601888096F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4122119 5'
11981	24858		11.56	4.0E-41	AV710480.1	EST_HUMAN	AV710480 Cu Homo sapiens cDNA clone CUAAC007 5'
947	14000	28952	2.61	3.0E-41	AB030176.1	NT	Homo sapiens PAD-H19 mRNA for peptidylarginine deiminase type II, complete cds Homo sapiens DNA, DLEC1 to ORCTL4 gene region, section 1/2 (DLEC1, ORCTL3, ORCTL4 genes, complete cds)
4362	17389	30271	2.6	3.0E-41	AB026698.1	NT	Homo sapiens mRNA for KIAA1327 protein, partial cds
5148	18157		1.15	3.0E-41	AB037748.1	NT	H. sapiens mRNA for putative p64 ClCP protein
5569	18666	31623	9.46	3.0E-41	X87699.1	NT	Homo sapiens mRNA for KIAA1387 protein, partial cds
6518	19581	32839	1.61	3.0E-41	AB037808.1	NT	EST64683 Jurkat T-cells VI Homo sapiens cDNA 5' end
7473	20439	33797	0.62	3.0E-41	AA356168.1	EST_HUMAN	YJ75408.H Soares breast 2NBHBS1 Homo sapiens cDNA clone IMAGE:154575 5'
8072	21009	34407	0.52	3.0E-41	R54785.1	EST_HUMAN	QVQ-BN0040-170300-160-H08 BN0040 Homo sapiens cDNA
12116	24986	38587	3.46	3.0E-41	AW994941.1	EST_HUMAN	QVQ-BN0040-170300-160-H08 BN0040 Homo sapiens cDNA
12116	24986	38588	3.46	3.0E-41	AW994941.1	EST_HUMAN	QVQ-BN0040-170300-160-H08 BN0040 Homo sapiens cDNA
12195	25040		1.49	3.0E-41	AA609768.1	EST_HUMAN	af17710.s1 Soares testis_NHT Homo sapiens cDNA clone IMAGE:1031947 3'
1841	14895	27570	15.21	2.0E-41	U43701.1	NT	Human ribosomal protein L23a mRNA, complete cds
1975	14996	27998	2.16	2.0E-41	AA331940.1	EST_HUMAN	EST35818 Embryo, 8 week I Homo sapiens cDNA 5' end
2228	15242	28267	1.37	2.0E-41	D86962.1	NT	Human mRNA for KIAA0207 gene, complete cds
2276	15289	28314	4.43	2.0E-41	X89631.1	NT	G. gorilla DNA for ZNF80 gene homolog
2839	14695	27570	7.99	2.0E-41	U43701.1	NT	Human ribosomal protein L23a mRNA, complete cds
3851	16891	29795	0.9	2.0E-41	5032106	NT	Homo sapiens son of sevenless (Drosophila) homolog 1 (SOS1) mRNA
4652	17673	30560	1.13	2.0E-41	AL163287.2	NT	Homo sapiens chromosome 21 segment HS21C087
4652	17673	30561	1.13	2.0E-41	AL163287.2	NT	Homo sapiens chromosome 21 segment HS21C067
5617	18713	31871	0.61	2.0E-41	AA584575.1	EST_HUMAN	not2607.st1 NCI_CGAP_Phe1 Homo sapiens cDNA clone IMAGE:1100460 3' similar to gb:X52851_mel PEPTIDYL-PROLYL CIS-TRANS ISOMERASE A (HUMAN);
6782	19637	33121	0.85	2.0E-41	4504778	NT	Homo sapiens Integrin, beta 8 (ITGB8) mRNA
7935	20877	34267	6.36	2.0E-41	AF038404.1	NT	Homo sapiens homolog of Nedd5 (Nedd5) mRNA, complete cds
8148	21085	34484	0.6	2.0E-41	11422047	NT	Homo sapiens origin recognition complex, subunit 5 (yeast homolog)-like (ORCL), mRNA
8403	21372	34780	1.63	2.0E-41	M96944.1	NT	Human B-cell specific transcription factor (BSAP) mRNA, complete cds
8403	21372	34781	1.63	2.0E-41	M96944.1	NT	Human B-cell specific transcription factor (BSAP) mRNA, complete cds

Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8433	21402	34815	1.47	2.0E-41	AA328285.1	EST_HUMAN	EST131723 Embryo, 12 week 1 Homo sapiens cDNA 5' end
9326	22281	35721	1.61	2.0E-41	P52742	SWISSPROT	ZINC FINGER PROTEIN 135
9772	22713	36167	0.72	2.0E-41	11417118	NT	Homo sapiens KIAA0433 protein (KIAA0433), mRNA
9772	22713	36168	0.72	2.0E-41	11417118	NT	Homo sapiens KIAA0433 protein (KIAA0433), mRNA
11815	24700	38281	2.21	2.0E-41	AA372837.1	EST_HUMAN	EST84555 Colon adenocarcinoma IV Homo sapiens cDNA 5' end
3219	16274	29197	1.33	1.0E-41	BE869735.1	EST_HUMAN	601445847F1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3849803 5'
3219	16274	29198	1.33	1.0E-41	BE869735.1	EST_HUMAN	601445847F1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3849803 5'
4598	17619	30512	7.8	1.0E-41	6678468	NT	Mus musculus tubulin alpha 6 (Tuba6), mRNA
7026	18358	31278	0.49	1.0E-41	H99079.1	EST_HUMAN	yc18b03.s1 Soares melanocyte 2N6HM Homo sapiens cDNA clone IMAGE:262061 3'
9773	22714	36169	1.73	1.0E-41	A1217868.1	EST_HUMAN	qf75c10.x1 Soares testis_NHT Homo sapiens cDNA clone IMAGE:1756858 3'
11494	24437	37986	1.56	1.0E-41	AW847812.1	EST_HUMAN	IL3-CT0213-190200-040-F09 CT0213 Homo sapiens cDNA
12332	25132		2.72	1.0E-41	11526291	NT	Homo sapiens hypothetical protein FLJ20454 (FLJ20454), mRNA
8865	21832		1.06	9.0E-42	BE179191.1	EST_HUMAN	RCO-HT0813-210300-032-g01 HT0813 Homo sapiens cDNA
9529	22492	35939	3.08	9.0E-42	11560151	NT	Homo sapiens hypothetical C2H2 zinc finger protein FLJ22504 (FLJ22504), mRNA
9529	22492	36840	3.08	9.0E-42	11560151	NT	Homo sapiens hypothetical C2H2 zinc finger protein FLJ22504 (FLJ22504), mRNA
463	13536	26462	6.85	8.0E-42	AF003530.1	NT	Homo sapiens homeobox protein CDX4 (CDX4) gene, complete cds and flanking repeat regions
2118	16135	28155	1.18	8.0E-42	AB028898.1	NT	Homo sapiens DNA, DLEC1 to ORCTL4 gene region, section 1/2 (DLEC1, ORCTL3, ORCTL4 genes, complete cds)
5197	18208	31080	1.06	8.0E-42	6679031	NT	Mus musculus neural precursor cell expressed, developmentally down-regulated gene 1 (Nedd1), mRNA
12376	25850		28	8.0E-42	AA493898.1	EST_HUMAN	h07c02.s1 NCL_CGAP_Thyl1 Homo sapiens cDNA clone IMAGE:943586 similar to TR:G434304 G434304 367BP EXPRESSED SEQUENCE TAG MRNA:
12364	25726		1.55	8.0E-42	AW08062.1	EST_HUMAN	xc97a04.x1 NCL_CGAP_Bm35 Homo sapiens cDNA clone IMAGE:2592174 3' similar to contains OFR:12
932	13985		1.46	7.0E-42	AL163285.2	NT	OFR repetitive element:
8814	21781		0.6	7.0E-42	R10963.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C085
9599	22603	35052	1.67	7.0E-42	A1204358.1	EST_HUMAN	yf38g04.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:129174 5'
11508	24450	38000	3.47	7.0E-42	AA569592.1	EST_HUMAN	qf58g12.x1 Soares testis_NHT Homo sapiens cDNA clone IMAGE:1754278 3'
11508	24450	38001	3.47	7.0E-42	AA569592.1	EST_HUMAN	n123g07.s1 NCL_CGAP_P11 Homo sapiens cDNA clone IMAGE:914652
1873	14898	27896	3.35	6.0E-42	AF012872.1	NT	n123g07.s1 NCL_CGAP_P11 Homo sapiens cDNA clone IMAGE:914652
1873	14898	27896	3.35	6.0E-42	AF012872.1	NT	Homo sapiens phosphatidylinositol 4-kinase 230 (p14K230) mRNA, complete cds
2297	15309		5.49	6.0E-42	AW238656.1	EST_HUMAN	Homo sapiens phosphatidylinositol 4-kinase 230 (p14K230) mRNA, complete cds xp28f08.x1 NCL_CGAP_HN10 Homo sapiens cDNA clone IMAGE:2741799 3' similar to contains L1.11 L1 repetitive element:

Table 4

Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5039	18052		1.46	6.0E-42	AI284770.1	EST_HUMAN	qu24h09.x1 NCI_CGAP_Br12 Homo sapiens cDNA clone IMAGE:1965761 similar to contains Alu repetitive element;
5543	18640	31580	1.6	6.0E-42	AB028990.1	NT	Homo sapiens mRNA for KIAA1067 protein, partial cds
5805	18640	31580	1.37	6.0E-42	AB028990.1	NT	Homo sapiens mRNA for KIAA1067 protein, partial cds
136	13241		5.99	5.0E-42	AJ271735.1	NT	Homo sapiens Xq pseudautosomal region; segment 1/2
438	13512	29443	1.7	5.0E-42	BE217913.1	EST_HUMAN	h31611.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3175052 3'
487	13560		4.65	5.0E-42	5730038	NT	Homo sapiens SET domain and mariner transposase fusion gene (SETMAR) mRNA
488	13561		1.37	5.0E-42	5730038	NT	Homo sapiens SET domain and mariner transposase fusion gene (SETMAR) mRNA
6844	19897	33191	1.07	5.0E-42	11433063	NT	Homo sapiens ubiquitin protein ligase E3A (human papilloma virus E6-associated protein, Angelman syndrome) (UBE3A), mRNA
6844	19897	33192	1.07	5.0E-42	11433063	NT	Homo sapiens ubiquitin protein ligase E3A (human papilloma virus E6-associated protein, Angelman syndrome) (UBE3A), mRNA
6971	20194	33522	2.61	5.0E-42	11417957	NT	Homo sapiens myotubularin related protein 3 (MTMR3), mRNA
7409	20376	33727	1.6	5.0E-42	AF071599.1	NT	Homo sapiens multifunctional calmodulin-dependent protein kinase II delta2 isoform mRNA, complete cds
8110	21047	34447	0.51	5.0E-42	4826977	NT	Homo sapiens reelin (RELN) mRNA
9131	22097	35524	2.98	5.0E-42	AB037715.1	NT	Homo sapiens mRNA for KIAA1294 protein, partial cds
10970	23890	37403	0.48	5.0E-42	11431168	NT	Homo sapiens 3-hydroxyanthranilate 3,4-dioxygenase (HAAO), mRNA
10970	23890	37404	0.48	5.0E-42	11431168	NT	Homo sapiens 3-hydroxyanthranilate 3,4-dioxygenase (HAAO), mRNA
12087	24959	38555	3.28	5.0E-42	X98411.1	NT	H. sapiens mRNA for myosin-IE
12087	24959	38556	3.28	5.0E-42	X98411.1	NT	H. sapiens mRNA for myosin-IE
754	13815	26758	23.04	4.0E-42	AF055066.1	NT	Homo sapiens MHC class 1 region
754	13815	26759	23.04	4.0E-42	AF055066.1	NT	Homo sapiens MHC class 1 region
1067	14112	27082	2.03	4.0E-42	AF18011.1	NT	Homo sapiens ribonuclease III (RN3) mRNA, complete cds
4223	17252	30139	1.24	4.0E-42	X59417.1	NT	H. sapiens PROS-27 mRNA
4255	17284	30166	1.12	4.0E-42	AF248219.1	NT	Homo sapiens SNARE protein kinase SNAK mRNA, complete cds
4277	17306	30185	4.28	4.0E-42	4506496	NT	Homo sapiens regulatory factor X, 4 (influences HLA class II expression) (RFX4) mRNA
4613	17634	30525	10.99	4.0E-42	4508008	NT	Homo sapiens zinc finger protein 177 (ZNF177) mRNA
5290	18295	31155	1	4.0E-42	AL163203.2	NT	Homo sapiens chromosome 21 segment HS21C003
5290	18296	31156	1	4.0E-42	AL163203.2	NT	Homo sapiens chromosome 21 segment HS21C003
10850	23770	37269	0.54	4.0E-42	AW371201.1	EST_HUMAN	CMO-B70282-171299-127-b03 B70282 Homo sapiens cDNA
11010	23975	37499	1.88	4.0E-42	AW818630.1	EST_HUMAN	RC1-ST0278-040400-018-h11 ST0278 Homo sapiens cDNA
11010	23976	37600	1.88	4.0E-42	AW818630.1	EST_HUMAN	RC1-ST0278-040400-018-h11 ST0278 Homo sapiens cDNA
11741	24626	38205	2.69	4.0E-42	BF038327.1	EST_HUMAN	601458531F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3862086 5'

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Table 4
Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1479	14512	27488	4.08	2.0E-42	BF376834.1	EST_HUMAN	RC0-TN0079-110900-024-g07 TN0079 Homo sapiens cDNA
2402	15409	28433	0.93	2.0E-42	AV690218.1	EST_HUMAN	AV690218 GKC Homo sapiens cDNA clone GK08B08 5'
2422	15429		3.65	2.0E-42	AW898344.1	EST_HUMAN	RC3-NN0070-270400-011-h10 NN0070 Homo sapiens cDNA
2432	15439	28456	3.27	2.0E-42	AW250059.1	EST_HUMAN	2819293.3prime NIH_MGC_7 Homo sapiens cDNA clone IMAGE:2819293 3'
5850	18940	32124	11.89	2.0E-42	AW955368.1	EST_HUMAN	EST367438 IMAGE resequences, MAGC Homo sapiens cDNA
5850	18940	32125	11.89	2.0E-42	AW955368.1	EST_HUMAN	EST367438 IMAGE resequences, MAGC Homo sapiens cDNA
5836	19894	32971	0.73	2.0E-42	M29145.1	NT	Human hepatocyte growth factor (HGF) mRNA, complete cds
6916	19968	33263	0.77	2.0E-42	A062586.1	EST_HUMAN	ow83d05.x1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:1653417 3'
10201	23126	36612	1.17	2.0E-42	BE539819.1	EST_HUMAN	601061284F1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3447620 5'
10415	23337	36822	0.61	2.0E-42	P81649	SWISSPROT	RIBONUCLEASE K3 (RNAASE K3)
10415	23337	36823	0.61	2.0E-42	P81649	SWISSPROT	RIBONUCLEASE K3 (RNAASE K3)
10974	23894	37408	0.82	2.0E-42	AW834834.1	EST_HUMAN	RC0-LT0001-150200-032-411 LT0001 Homo sapiens cDNA
12045	24919	38515	1.48	2.0E-42	AL163246.2	NT	Homo sapiens chromosome 21 segment HS21C046
735	13795	28734	2.47	1.0E-42	X57147.1	NT	Human endogenous retrovirus pH1.1 (ERV9)
1043	14089	27042	0.76	1.0E-42	AW298809.1	EST_HUMAN	UHH-B11-afn-e-04-0-UJ.s1 NCI_CGAP_Sub3 Homo sapiens cDNA clone IMAGE:2721871 3'
1103	14147	27057	1.27	1.0E-42	AJ251818.1	NT	Homo sapiens partial C9 gene for complement component C9, exon 1
1103	14147	27058	1.27	1.0E-42	AJ251818.1	NT	Homo sapiens partial C9 gene for complement component C9, exon 1
1247	15862	27248	12.69	1.0E-42	AF067166.1	NT	Homo sapiens NADH-ubiquinone oxidoreductase AGGG subunit precursor homolog mRNA, nuclear gene encoding mitochondrial protein, complete cds
1247	15862	27249	12.69	1.0E-42	AF067166.1	NT	Homo sapiens NADH-ubiquinone oxidoreductase AGGG subunit precursor homolog mRNA, nuclear gene encoding mitochondrial protein, complete cds
1711	14741	27725	2.08	1.0E-42	11423219	NT	Homo sapiens rec (LOC51201), mRNA
2046	15085	28085	1.05	1.0E-42	AF110296.1	NT	Homo sapiens PDN1 gene, exon 17
2551	15553	28573	1.88	1.0E-42	5174458	NT	Homo sapiens major histocompatibility complex, class II, DM alpha (HLA-DMA) mRNA
2975	16033	28956	10.93	1.0E-42	4805524	NT	Homo sapiens origin recognition complex, subunit 5 (yeast homolog)-like (ORC5L) mRNA, and translated products
3721	16784	29875	2.43	1.0E-42	7662027	NT	Homo sapiens KIAA0285 gene product (KIAA0285), mRNA
3948	16988	29903	1.02	1.0E-42	AL163287.2	NT	Homo sapiens chromosome 21 segment HS21C067
4274	17303	30183	1.85	1.0E-42	AL163280.2	NT	Homo sapiens chromosome 21 segment HS21C080
4824	17645	30533	0.77	1.0E-42	AW813617.1	EST_HUMAN	RC3-ST0197-161095-012-a03 ST0197 Homo sapiens cDNA
4776	17796	30688	2.44	1.0E-42	5803122	NT	Homo sapiens proteasome inhibitor (Pi31), mRNA
4776	17796	30688	2.44	1.0E-42	5803122	NT	Homo sapiens proteasome inhibitor (Pi31), mRNA
4813	17830	30728	5.31	1.0E-42	4506758	NT	Homo sapiens ryanodine receptor 3 (RYR3) mRNA
4897	18012	30899	0.78	1.0E-42	Z48120.1	EST_HUMAN	HS00FF071 normalized infant brain cDNA Homo sapiens cDNA clone c-0ff07

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Table 4
Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10446	23368	36859	4.15	9.0E-43	4757969	NT	Homo sapiens chromodomain protein, Y chromosome-like (CDYL) mRNA
653	13719	26641	14	8.0E-43	AV736824.1	EST_HUMAN	AV736824 CB Homo sapiens cDNA clone CBLAKH08 5'
653	13719	26642	14	8.0E-43	AV736824.1	EST_HUMAN	AV736824 CB Homo sapiens cDNA clone CBLAKH08 5'
701	13763	26695	4.8	8.0E-43	8923276	NT	Homo sapiens hypothetical protein FLJ20297 (FLJ20297), mRNA
701	13763	26696	4.8	8.0E-43	8923276	NT	Homo sapiens hypothetical protein FLJ20297 (FLJ20297), mRNA
701	13763	26697	4.8	8.0E-43	8923276	NT	Homo sapiens hypothetical protein FLJ20297 (FLJ20297), mRNA
5783	18875	32057	0.78	8.0E-43	H19952.1	EST_HUMAN	y08e11.1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:148172 5'
3655	16998	29613	7.28	7.0E-43	AW246442.1	EST_HUMAN	2822251 SpRime NIH_MGC_7 Homo sapiens cDNA clone IMAGE:2822251 5'
9121	22087		3.41	7.0E-43	AU936748.1	EST_HUMAN	wp69b01.x1 NCI_CGAP_Brn26 Homo sapiens cDNA clone IMAGE:2466985 3' similar to TR:O15475
1347	14382		14.15	6.0E-43	AA491890.1	EST_HUMAN	O15475 UNNAMED HERV-H PROTEIN, contains LTR7.b1 LTR7 repetitive element;
2598	15599		2.91	6.0E-43	AV708201.1	EST_HUMAN	RIBOSOMAL PROTEIN L30 (HUMAN);
8444	19509	32759	2.19	6.0E-43	9955973	NT	AV708201 ADC Homo sapiens cDNA clone ADCACC10 5'
7083	20027	33331	1.91	6.0E-43	AW468897.1	EST_HUMAN	Homo sapiens ATP-binding cassette, sub-family C (CFTR/MRP), member 3 (ABCC3), transcript variant NRP3B, mRNA
10210	23135	36622	2.31	6.0E-43	AA195154.1	EST_HUMAN	hd30b04.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2910991 3' similar to contains
11437	24380		2.08	6.0E-43	AL119158.1	EST_HUMAN	zr35e08.r1 Soares_NHMPu_S1 Homo sapiens cDNA clone IMAGE:665410 5' similar to TR:G528641
144	13247		1.8	5.0E-43	AL163213.2	NT	G529641 DB1, COMPLETE CDS, contains element PTR7 repetitive element;
503	13575	26495	3.96	5.0E-43	AA382780.1	EST_HUMAN	DKFZp761L1712_r1 761 (synonym: hamy2) Homo sapiens cDNA clone DKFZp761L1712 5'
2869	16919	28840	1.63	5.0E-43	AV732576.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C013
8438	20021	33323	1.15	5.0E-43	AI613509.1	EST_HUMAN	EST166033 Testis 1 Homo sapiens cDNA 5' end
7087	20021	33323	0.65	5.0E-43	AI613509.1	EST_HUMAN	AV732578 HTF Homo sapiens cDNA clone HTFANCO6 5'
8528	21496	34910	0.7	5.0E-43	AA442271.1	EST_HUMAN	tw22e07.x1 NCI_CGAP_Brn52 Homo sapiens cDNA clone IMAGE:2260462 3'
8528	21496	34911	0.7	5.0E-43	AA442271.1	EST_HUMAN	tw22e07.x1 NCI_CGAP_Brn52 Homo sapiens cDNA clone IMAGE:2260462 3'
9231	22197		0.69	5.0E-43	H74277.1	EST_HUMAN	zr54e03.r1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:757420 5'
9719	22747	36198	4.22	5.0E-43	AA465288.1	EST_HUMAN	zr54e03.r1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:757420 5'
10763	23684	37190	2.35	5.0E-43	AI733244.1	EST_HUMAN	y449g12.r1 Soares fetal liver spleen 1N1LS Homo sapiens cDNA clone IMAGE:229510 5'
10802	23723	37225	1.45	5.0E-43	AL049110.1	EST_HUMAN	aa33d08.r1 NCI_CGAP_GC81 Homo sapiens cDNA clone IMAGE:8715055 5'
11115	24075	37598	4.88	5.0E-43	AW863007.1	EST_HUMAN	aa33d08.r1 NCI_CGAP_GC81 Homo sapiens cDNA clone IMAGE:8715055 5'
11786	23941	37463	3.48	5.0E-43	X15804.1	NT	aa33d08.r1 NCI_CGAP_GC81 Homo sapiens cDNA clone IMAGE:1569810 3' similar to TR:P80591 P80591
							PV14 GENE.
							DKFZp434D0119_r1 434 (synonym: htes2) Homo sapiens cDNA clone DKFZp434D0119
							MR2-SN0007-290400-004-c02 SN0007 Homo sapiens cDNA
							Human mRNA for alpha-actinin

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Table 4
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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
974	15816	26979	3.95	4.0E-43	AF003528.1	NT	Homo sapiens X-linked anhidrotic ectodermal dysplasia protein gene (EDA), exon 2 and flanking repeat regions
5331	18437	31189	1.18	4.0E-43	AI056338.1	EST_HUMAN	oy47n03.x1 NCL CGAP_Brn23 Homo sapiens cDNA clone IMAGE:1869013 3'
6505	19569	32821	0.78	4.0E-43	8986009	NT	Homo sapiens glycy-tRNA synthetase (GARS), mRNA
7337	20308		1.94	4.0E-43	11416793	NT	Homo sapiens probocadherin beta 6 (PCDH6), mRNA
8518	21486	34900	5.73	4.0E-43	AI244341.1	EST_HUMAN	q76a02.x1 NCL CGAP_Kid3 Homo sapiens cDNA clone IMAGE:1865354 3' similar to contains MER10.13
8518	21486	34901	5.73	4.0E-43	AI244341.1	EST_HUMAN	q76a02.x1 NCL CGAP_Kid3 Homo sapiens cDNA clone IMAGE:1865354 3' similar to contains MER10.13
10678	23600	37095	1.39	4.0E-43	6005967	NT	MER10 repetitive element:
12306	25115		6.35	4.0E-43	R20950.1	EST_HUMAN	Homo sapiens zinc finger protein 161 (ZNF161), mRNA
1218	14256		3.85	3.0E-43	AF223391.1	NT	yg06b05.r1 Soares infant brain 1N1B Homo sapiens cDNA clone IMAGE:31363 5' similar to contains MER10 repetitive element:
1704	14734	27716	1.63	3.0E-43	X97869.1	NT	Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced
3586	16631	29549	1.32	3.0E-43	S69002.1	NT	H. sapiens gene encoding La autoantigen
4319	17348	30232	1.02	3.0E-43	AA548154.1	EST_HUMAN	AML1-EVI1-1=AML1-EVI1 fusion protein (rearranged translocation) [human, leukemic cell line SKH1, mRNA
5003	18017	30904	0.98	3.0E-43	AB037856.1	NT	Mutant, 5938 nt
5424	18527	31405	0.51	3.0E-43	M59259.1	NT	nk55d06.a1 NCL CGAP_P17 Homo sapiens cDNA clone IMAGE:1017419
5424	18527	31406	0.51	3.0E-43	M59259.1	NT	Homo sapiens mRNA for KIAA1435 protein, partial cds
5996	19090	32277	0.9	3.0E-43	D34613.1	NT	Human carcinoembryonic antigen (CEA) gene, exon 6
6492	19557	32807	1.86	3.0E-43	7305360	NT	Human TBXAS1 gene for thromboxane synthase, promoter region and exon 1
6492	19557	32808	1.86	3.0E-43	7305360	NT	Mus musculus obogelin (Obog), mRNA
6890	19942	33238	4.38	3.0E-43	U65487.1	NT	Mus musculus obogelin (Obog), mRNA
8503	21471		8.69	3.0E-43	AA458824.1	EST_HUMAN	Human ribosomal RNA upstream binding transcription factor (UBTF) gene, partial cds
9172	22138	35594	1.82	3.0E-43	7661721	NT	aa88f11.a1 Stragene fetal retina 937202 Homo sapiens cDNA clone IMAGE:838413 3' similar to contains THR.12 THR repetitive element:
10223	23148	36637	0.6	3.0E-43	11420217	NT	Homo sapiens hypothetical protein (HSA011916), mRNA
185	13285		9.29	2.0E-43	AI190784.1	EST_HUMAN	Homo sapiens similar to ornithine carbamoyltransferase (H. sapiens) (LOC883649), mRNA
6620	19678	32955	0.95	2.0E-43	BE222778.1	EST_HUMAN	q081cd09.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1733968 3' similar to contains PTR7.13
							PTR7 PTR7 repetitive element:
							hu33a08.x1 NCL CGAP_Brn41 Homo sapiens cDNA clone IMAGE:3173750 3' similar to contains element
							MER40 repetitive element:

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Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6620	19678	32956	0.95	2.0E-43	BE222778.1	EST_HUMAN	hu53a08.x1 NCI_CGAP_Brm41 Homo sapiens cDNA clone IMAGE:3173750 3' similar to contains element
7491	20456	33814	1.07	2.0E-43	AW207390.1	EST_HUMAN	MER40 repetitive element;
8651	21619		9.34	2.0E-43	U43701.1	NT	U1H-B11-af-a-09-0-U1.s1 NCI_CGAP_Sub3 Homo sapiens cDNA clone IMAGE:2721712 3'
11532	24473		2.86	2.0E-43	T03007.1	EST_HUMAN	Human ribosomal protein L28a mRNA, complete cds
1657	14989	27664	4.13	1.0E-43	AF154836.1	NT	FB1G5 Fetal brain, Stragene Homo sapiens cDNA clone FB1G5 3' end similar to LINE-1
1657	14989	27665	4.13	1.0E-43	AF154836.1	NT	Homo sapiens Ras-like GTP-binding protein (RAB27A) gene, exons 1b and 2
1717	14747	27733	2.13	1.0E-43	AL163284.2	NT	Homo sapiens Ras-like GTP-binding protein (RAB27A) gene, exons 1b and 2
2734	15728	28742	5.67	1.0E-43	BF348283.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C084
5484	18584	31496	0.77	1.0E-43	4885544	NT	602022313.F1 NCI_CGAP_Brm67 Homo sapiens cDNA clone IMAGE:4157666 5'
6764	19818	33098	6.3	1.0E-43	4507168	NT	Homo sapiens pyruvate dehydrogenase kinase, isoenzyme 3 (PDK3) mRNA
6764	19818	33099	6.3	1.0E-43	4507168	NT	Homo sapiens Sp4 transcription factor (SP4) mRNA
7159	18391	31235	1.67	1.0E-43	R19761.1	EST_HUMAN	yg40a01.r1 Soares infant brain 1N1B Homo sapiens cDNA clone IMAGE:34732 5' similar to
8264	21233	34644	0.97	1.0E-43	AF175265.1	NT	SP-BD38_MOUSE P28666 BRAIN PROTEIN DN38;
8401	21370		3.15	1.0E-43	AF189490.1	NT	Homo sapiens vacuolar sorting protein 35 (VPS35) mRNA, complete cds
9189	22155	35584	30.83	1.0E-43	AW983676.1	EST_HUMAN	Homo sapiens 8q22.1 region and MTGB (CBFA2T1) gene, partial cds
10654	23576	37073	0.82	1.0E-43	AW983228.1	EST_HUMAN	EST375749 MAGC resequences, MAGB Homo sapiens cDNA
11311	24281	37787	5.9	1.0E-43	A1984861.1	EST_HUMAN	EST366299 MAGC resequences, MAGB Homo sapiens cDNA
11693	24658	38236	3.35	1.0E-43	11424378	NT	wr67n01.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2494705 3'
12244	25074		2.8	1.0E-43	AL137864.1	EST_HUMAN	Homo sapiens calcium channel, voltage-dependent, alpha 1E subunit (CACNA1E) mRNA
12745	25394	31757	2.24	1.0E-43	A1675416.1	EST_HUMAN	DKFZp761D1015.1 761 (synonym: hamy2) Homo sapiens cDNA clone DKFZp761D1015 5'
891	13946	26904	7.09	8.0E-44	A1222985.1	EST_HUMAN	wb99504.x1 NCI_CGAP_P28 Homo sapiens cDNA clone IMAGE:2313775 3'
891	13946	26905	7.09	8.0E-44	A1222985.1	EST_HUMAN	Homo sapiens cadherin EGF LAG sever-pass G-type receptor 1 (CELSR1) mRNA
8884	21850	35271	2.88	8.0E-44	X94354.1	NT	qh23g01.x1 Soares NFL_T_GBC S1 Homo sapiens cDNA clone IMAGE:1845552 3'
10702	23624	37120	0.47	8.0E-44	11423497	NT	qh23g01.x1 Soares NFL_T_GBC S1 Homo sapiens cDNA clone IMAGE:1845552 3'
10702	23624	37121	0.47	8.0E-44	11423497	NT	H. sapiens DNA for Cone cGMP-PDE gene
11499	24442	37993	3.93	8.0E-44	Y10498.2	NT	Homo sapiens small proline-rich protein 2C (SPRR2C) mRNA
11995	24872	38469	2.24	8.0E-44	L29139.1	NT	Homo sapiens small proline-rich protein 2C (SPRR2C) mRNA
12495	25237	31801	2.95	8.0E-44	11527389	NT	Homo sapiens myosin mRNA for thymidine kinase, partial
12536	25577	31698	1.53	8.0E-44	11418086	NT	Homo sapiens polymerase (RNA) II (DNA directed) polypeptide F (POLR2F) mRNA
12870	25755	31516	2.88	8.0E-44	11418099	NT	Homo sapiens putative nuclear protein (HRIHFB2122) mRNA
13029	25577	31698	1.58	8.0E-44	11418086	NT	Homo sapiens protein kinase C, alpha binding protein (PRKCABP), mRNA
							Homo sapiens putative nuclear protein (HRIHFB2122), mRNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
660	13726		0.87	7.0E-44	R06035.1	EST_HUMAN	ye89e01.11 Soares fetal liver spleen TNF α Homo sapiens cDNA clone IMAGE:124920 5'
2243	15257	28283	0.95	7.0E-44	5031896	NT	Homo sapiens LIM domain-containing preferred translocation partner in lipoma (LPP) mRNA
2977	16035	26957	2.68	7.0E-44	AF048729.1	NT	Homo sapiens minisatellite ms32 repeat region
2977	16035	28958	2.68	7.0E-44	AF048729.1	NT	Homo sapiens minisatellite ms32 repeat region
3876	16915	28824	2.55	7.0E-44	AL163284.2	NT	Homo sapiens chromosome 21 segment HS21C084
4270	17299	30177	1.07	7.0E-44	AF231919.1	NT	Homo sapiens chromosome 21 unknown mRNA
4270	17299	30178	1.07	7.0E-44	AF231919.1	NT	Homo sapiens chromosome 21 unknown mRNA
5168	18177	31055	1.04	7.0E-44	AF111168.2	NT	Homo sapiens serine palmitoyl transferase, subunit II gene, complete cds; and unknown genes
8526	21494	34908	5.87	7.0E-44	AU159839.1	EST_HUMAN	AU159839 Y79AA1 Homo sapiens cDNA clone Y79AA1000496 3'
6223	19297	32531	0.55	6.0E-44	Z20946.1	EST_HUMAN	HSAADAEYU P. Human foetal Brain Whole tissue Homo sapiens cDNA
12070	24943	38536	1.83	6.0E-44	AW954050.1	EST_HUMAN	EST366120 MAGC resequences, MAGC Homo sapiens cDNA
303	13397		3.9	5.0E-44	AJ289880.1	NT	Homo sapiens KIAA0851 gene (partial), X13 gene and LZTFL1 gene
332	13421		2.88	5.0E-44	AJ289880.1	NT	Homo sapiens KIAA0851 gene (partial), X13 gene and LZTFL1 gene
8220	21189	34598	3.85	5.0E-44	AJ58523.1	EST_HUMAN	tr40d02.x1 NCL_CGAP_Bn25 Homo sapiens cDNA clone IMAGE:2170083 3' similar to contains OFR.11
9739	22767		2.65	5.0E-44	AU124571.1	EST_HUMAN	OFR OFR repetitive element
3426	16473	29392	3.2	4.0E-44	AL163303.2	NT	AU124571 NT2RM4 Homo sapiens cDNA clone NT2RM4000218 5'
5050	18062		1.02	4.0E-44	AJ495225.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C103
7711	20668	34035	0.68	4.0E-44	BE883178.1	EST_HUMAN	(f11d02.x1 NCL_CGAP_Pan1 Homo sapiens cDNA clone IMAGE:2130147 3'
8614	21582	34998	0.84	4.0E-44	L21948.1	NT	(601508601F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3910152 5'
9230	22196		0.49	4.0E-44	BE176618.1	EST_HUMAN	Human fibrillin (FBN1) locus polymorphism
11569	24508	38065	8.23	4.0E-44	U90878.1	NT	RC3-HT0585-010400-023-808 HT0585 Homo sapiens cDNA
1801	14829		0.95	3.0E-44	6912477	NT	Homo sapiens carboxyl terminal LIM domain protein (CLIM1) mRNA, complete cds
2537	15539	28562	0.95	3.0E-44	BE880626.1	EST_HUMAN	Homo sapiens karyopherin alpha 6 (Importin alpha 7) (KPNA6), mRNA
3114	16171	29081	6.12	3.0E-44	AA169851.1	EST_HUMAN	(601491529F1 NIH_MGC_69 Homo sapiens cDNA clone IMAGE:3893839 5'
3905	16945	29858	1.71	3.0E-44	AA337234.1	EST_HUMAN	zpt18p05.11 Stratagene fetal retina 937202 Homo sapiens cDNA clone IMAGE:608777 5'
8074	21011	34410	0.55	3.0E-44	BE884820.1	EST_HUMAN	EST42299 Endometrial tumor Homo sapiens cDNA 5' end similar to similar to alpha-1-antitrypsinase F
9877	22830	36284	0.58	3.0E-44	AF005273.1	NT	(601510547F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3912010 5'
1051	14097	27047	1.04	2.0E-44	4826635	NT	Sus scrofa domestica submaxillary apomucin mRNA, complete cds
1051	14097	27048	1.04	2.0E-44	4826635	NT	Homo sapiens DEADH (Asp-Glu-Ala-Asp/His) box polypeptide 1 (DDX1) mRNA
1212	14250	27208	2.52	2.0E-44	5803200	NT	Homo sapiens DEADH (Asp-Glu-Ala-Asp/His) box polypeptide 1 (DDX1) mRNA
1212	14250	27209	2.52	2.0E-44	5803200	NT	Homo sapiens transmembrane trafficking protein (TMP21), mRNA
1315	14350	27318	5.49	2.0E-44	AF133588.1	NT	Homo sapiens transmembrane trafficking protein (TMP21), mRNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1370	14404	27374	1.05	2.0E-44	BE465325.1	EST_HUMAN	hw14g08.x1 NCL CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3182938 3' similar to SW:OXYB_HUMAN P22059 OXYSTEROL-BINDING PROTEIN. ;
2161	15177	28198	2.57	2.0E-44	AF070851.1	NT	Homo sapiens tissue-type bone marrow zinc finger protein 4 mRNA, complete cds
2618	16616		2.01	2.0E-44	5901933	NT	Homo sapiens adaptor-related protein complex 4, sigma 1 subunit (CLAPS4), mRNA
3484	16530	29455	1.18	2.0E-44	D87675.1	NT	Homo sapiens DNA for amyloid precursor protein, complete cds
4900	17621	30514	1.6	2.0E-44	AW864379.1	EST_HUMAN	PM4-SN0016-12000-003-q04 SN0016 Homo sapiens cDNA
6214	19288	32521	1.59	2.0E-44	11449801	NT	Homo sapiens chemokine (C-C motif) receptor 8 (CCR8), mRNA
7037	18389	31256	1.73	2.0E-44	AF038988.1	NT	Homo sapiens general transcription factor 2-1 (GTF2) mRNA, alternatively spliced product, complete cds
7645	20605	33970	3.8	2.0E-44	11419228	NT	Homo sapiens glutamate receptor, metabotropic 3 (GRM3), mRNA
7645	20605	33971	3.8	2.0E-44	11419228	NT	Homo sapiens glutamate receptor, metabotropic 3 (GRM3), mRNA
8771	21738	35158	0.72	2.0E-44	7706370	NT	Homo sapiens vesicle transport-related protein (KIAA0917), mRNA
8771	21738	35159	0.72	2.0E-44	7706370	NT	Homo sapiens vesicle transport-related protein (KIAA0917), mRNA
8966	21932	35357	1.83	2.0E-44	BE389038.1	EST_HUMAN	601286314F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3613588 5'
12152	25010		1.44	2.0E-44	BE244902.1	EST_HUMAN	TCBAP1E2785 Pediatric pre-B cell acute lymphoblastic leukemia Baylor-HGSC project=TCBA Homo sapiens cDNA clone TCBAP2795
12695	25898		1.32	2.0E-44	4828883	NT	Homo sapiens neuronal cell adhesion molecule (NRCAM) mRNA
13047	25597		1.58	2.0E-44	11526293	NT	Homo sapiens cat eye syndrome chromosome region, candidate 1 (CECR1), mRNA
54	13174	26084	7.78	1.0E-44	7657334	NT	Homo sapiens Missshapen/NIK-related kinase (MINK), mRNA
54	13174	26085	7.78	1.0E-44	7657334	NT	Homo sapiens Missshapen/NIK-related kinase (MINK), mRNA
582	13650	28564	1.85	1.0E-44	AW853132.1	EST_HUMAN	RC1-CT0249-030300-028-h12 CT0249 Homo sapiens cDNA
1202	14241		1.85	1.0E-44	AW894803.1	EST_HUMAN	RC1-BN0039-110300-012-501 BN0039 Homo sapiens cDNA
1577	14610		7.03	1.0E-44	AL183303.2	NT	Homo sapiens chromosome 21 segment HS21G103
2233	15247	28270	4.49	1.0E-44	AA434554.1	EST_HUMAN	zw53d02.11 Scores_total_fetus_Nb2HF8_9w Homo sapiens cDNA clone IMAGE:773763 5' similar to contains THR_13 THR repetitive element ;
2233	15247	28271	4.49	1.0E-44	AA434554.1	EST_HUMAN	zw53d02.11 Scores_total_fetus_Nb2HF8_9w Homo sapiens cDNA clone IMAGE:773763 5' similar to contains THR_13 THR repetitive element ;
2290	15899	28327	0.95	1.0E-44	AA398096.1	EST_HUMAN	z889g11.1 Scores_testis_NHT Homo sapiens cDNA clone IMAGE:728476 5'
2770	15762	28763	2.5	1.0E-44	AF186779.1	NT	Homo sapiens transcription factor IGHM enhancer 3, JM11 protein, JM5 protein, T54 protein, JM10 protein, A4 differentiation-dependent protein, triple LIM domain protein 6, and synaptophysin genes, complete cds ; and L-type calcium channel a-
3738	16780		3.01	1.0E-44	AA455899.1	EST_HUMAN	aa01c08.s1 Scores_NHHPu_S1 Homo sapiens cDNA clone IMAGE:811984 3'
8155	18185	31043	0.64	1.0E-44	AJ130755.1	NT	Homo sapiens alpha satellite DNA, M1 monomer type
8155	18185	31044	0.64	1.0E-44	AJ130755.1	NT	Homo sapiens alpha satellite DNA, M1 monomer type

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8608	21576	34991	1.17	1.0E-44	AW967073.1	EST_HUMAN	EST379147 IMAGE: ressequences, MAGJ Homo sapiens cDNA
8608	21576	34992	1.17	1.0E-44	AW967073.1	EST_HUMAN	EST379147 IMAGE: ressequences, MAGJ Homo sapiens cDNA
8993	21959	35385	1.23	1.0E-44	AL163209.2	NT	Homo sapiens chromosome 21 segment HS21C009
9381	22346	35778	0.59	1.0E-44	AI337183.1	EST_HUMAN	q88907.x1 NCI_CGAP_G06 Homo sapiens cDNA clone IMAGE:2009628.3
11354	24304		12.74	1.0E-44	AV714608.1	EST_HUMAN	AV714608 DGB Homo sapiens cDNA clone DOBBYE03.5
11858	24740	38325	3.23	1.0E-44	10082864	NT	Homo sapiens Sushi domain (SCR repeat) containing (BK65A6.2), mRNA
11917	24798	38388	2.7	1.0E-44	AW846967.1	EST_HUMAN	RC1-CT0198-150999-011-C08 CT0198 Homo sapiens cDNA
11917	24798	38389	2.7	1.0E-44	AW846967.1	EST_HUMAN	RC1-CT0198-150999-011-C08 CT0198 Homo sapiens cDNA
4609	17630	30522	1.16	9.0E-45	8922391	NT	Homo sapiens hypothetical protein FLJ10378 (FLJ10378), mRNA
4609	17630	30523	1.16	9.0E-45	8922391	NT	Homo sapiens hypothetical protein FLJ10378 (FLJ10378), mRNA
6806	19890	33147	1.52	9.0E-45	AB023212.1	NT	Homo sapiens mRNA for KIAA0995 protein, partial cds
2529	15532	28553	1.57	8.0E-45	5174718	NT	Homo sapiens TRK-fused gene (NOTE: non-standard symbol and name) (TFG) mRNA
5119	18129	31005	8.66	8.0E-45	5174718	NT	Homo sapiens TRK-fused gene (NOTE: non-standard symbol and name) (TFG) mRNA
8444	21413	34827	0.85	8.0E-45	AA377985.1	EST_HUMAN	EST90893 Synovial sarcoma Homo sapiens cDNA 5' end
2969	15027		0.96	7.0E-45	AL160131.1	NT	Novel human gene mapping to chromosome 22
1556	14588		1	6.0E-45	AB175425.1	EST_HUMAN	w898c06.x1 NCI_CGAP_P28 Homo sapiens cDNA clone IMAGE:2313802.3 similar to contains L1.1 L1 repetitive element:
4003	17042		3.48	6.0E-45	AW157570.1	EST_HUMAN	au83h07.x1 Schneider fetal brain 00004 Homo sapiens cDNA clone IMAGE:2782909.3 similar to SW:R13A_HUMAN P40429 60S RIBOSOMAL PROTEIN L13A:
12836	25948		1.53	6.0E-45	11418213	NT	Homo sapiens ADP-ribosylation factor GTPase activating protein 1 (ARFGAP1), mRNA
893	13948		1.56	5.0E-45	AL163203.2	NT	Homo sapiens chromosome 21 segment HS21C003
2018	15039	28050	4.99	5.0E-45	BF333627.1	EST_HUMAN	CM4-CN0044-180200-515-01 CN0044 Homo sapiens cDNA
3223	16278	29203	1.49	5.0E-45	AI523766.1	EST_HUMAN	ig94f07.x1 NCI_CGAP_CLL1 Homo sapiens cDNA clone IMAGE:2116453.3 similar to SW:PAX1_MOUSE P09084 PAIRED BOX PROTEIN PAX-1;
5590	18686	31654	8.41	5.0E-45	AA397781.1	EST_HUMAN	z72803.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:727877.3 similar to contains element TAR1 repetitive element:
6135	19212	32439	1.48	5.0E-45	Y18933.1	NT	Homo sapiens MCP-1 gene and enhancer region
6135	19212	32440	1.48	5.0E-45	Y18933.1	NT	Homo sapiens MCP-1 gene and enhancer region
6183	19258	32491	0.84	5.0E-45	AB022318.1	NT	Homo sapiens mRNA for inducible nitric oxide synthase, complete cds
6183	19258	32492	0.84	5.0E-45	AB022318.1	NT	Homo sapiens mRNA for inducible nitric oxide synthase, complete cds
6313	19384	32625	1.07	5.0E-45	11496268	NT	Homo sapiens zinc finger protein 277 (ZNF277), mRNA
6313	19384	32626	1.07	5.0E-45	11496268	NT	Homo sapiens zinc finger protein 277 (ZNF277), mRNA
8619	21587	35003	0.66	5.0E-45	11415704	NT	Homo sapiens bone morphogenetic protein 5 (BMP5), mRNA
9396	22361	35792	1.29	5.0E-45	4759223	NT	Homo sapiens programmed cell death 5 (PDCD5), mRNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
12003	24880	38476	2.3	5.0E-45	8923698	NT	Homo sapiens gadin-like protein (GLP), mRNA
1148	14188	27139	10.78	4.0E-45	X95926.1	NT	H. sapiens ART4 gene
2289	15311	28331	1.91	4.0E-45	BE266622.1	EST_HUMAN	601194440F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3638425 5'
4535	17558	30446	0.72	4.0E-45	4759249	NT	Homo sapiens TRAF family member-associated NFKB activator (TANK) mRNA
8308	22273		0.99	4.0E-45	AA226220.1	EST_HUMAN	nc28607.s1 NCL_CGAP_P1 Homo sapiens cDNA clone IMAGE:1009284 similar to contains element L1 repetitive element;
12167	25894	31418	1.4	4.0E-45	11435947	NT	Homo sapiens chromosome 12 open reading frame 3 (C12ORF3), mRNA
4115	16393		0.99	3.0E-45	T71480.1	EST_HUMAN	Y33507.11 Soares fetal liver spleen INFLS Homo sapiens cDNA clone IMAGE:110245 5'
6384	19433	32876	1.13	3.0E-45	6753651	NT	Mus musculus dynein, axon, heavy chain 11 (Dnahc11), mRNA
6384	19433	32877	1.13	3.0E-45	6753651	NT	Mus musculus dynein, axon, heavy chain 11 (Dnahc11), mRNA
8704	21751		1.53	3.0E-45	AV723976.1	EST_HUMAN	AV723976 HTB Homo sapiens cDNA clone HTBAAAG01 5'
9143	22109	35535	3.82	3.0E-45	4758451	NT	Homo sapiens golgi autoantigen, golgin subfamily a, 2 (GOLGA2) mRNA
10670	23592	37087	10.98	3.0E-45	AL163227.2	NT	Homo sapiens chromosome 21 segment HS21C027
10670	23592	37088	10.98	3.0E-45	AL163227.2	NT	Homo sapiens chromosome 21 segment HS21C027
12964	25898		4.13	3.0E-45	X89211.1	NT	H. sapiens DNA for endogenous retroviral like element
2511	15514		1.96	2.0E-45	AL163218.2	NT	Homo sapiens chromosome 21 segment HS21C018
3045	16102	29016	1.6	2.0E-45	AL243213.1	NT	Homo sapiens partial 5-HT4 receptor gene, exons 2 to 5
6671	19728	33004	5.17	2.0E-45	L01665.1	NT	Human eosinophil Charcot-Leyden crystal (CLC) protein (lysophospholipase) gene, promoter and exon 1
7868	20812	34189	1.25	2.0E-45	BE782184.1	EST_HUMAN	601467783F1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:3870838 5'
8768	21725	35148	1.08	2.0E-45	AW834834.1	EST_HUMAN	RCO-LT0001-150200-032-d11 LT0001 Homo sapiens cDNA
11154	25704	37539	25.96	2.0E-45	BE834350.1	EST_HUMAN	MR0-HT0923-190800-201-402 HT0923 Homo sapiens cDNA
11511	24452	38002	3.5	2.0E-45	AA458770.1	EST_HUMAN	aa87112.11 Stralagene fetal retina 837202 Homo sapiens cDNA clone IMAGE:838319 5' similar to
11832	24715	38298	1.67	2.0E-45	AW270280.1	EST_HUMAN	TR:G1144569 G1144569 R-SLY1.
11832	24715	38300	1.67	2.0E-45	AW270280.1	EST_HUMAN	xp72a03.x1 NCL_CGAP_Ow40 Homo sapiens cDNA clone IMAGE:2745868 3'
12999	25556		3.46	2.0E-45	11418157	NT	xp72a03.x1 NCL_CGAP_Ow40 Homo sapiens cDNA clone IMAGE:2745868 3'
124	13482		1.84	1.0E-45	BE389855.1	EST_HUMAN	Homo sapiens calcium channel, voltage-dependent, alpha 11 subunit (CACNA11), mRNA
409	13482		2.09	1.0E-45	BE389855.1	EST_HUMAN	601284360F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3606183 5'
473	13545	26474	1.93	1.0E-45	4506412	NT	601284360F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3606183 5'
1178	14219	27175	1.94	1.0E-45	7657290	NT	Homo sapiens RAP1A, member of RAS oncogene family (RAP1A), mRNA
3120	16177	29088	7.12	1.0E-45	U32169.1	NT	Homo sapiens Langerhans cell specific alpha-type lectin (LANGRIN), mRNA
3503	16560	29477	0.84	1.0E-45	8659558	NT	Human pro-a2 chain of collagen type XI (COL11A2) gene, complete cds
4603	17628	30413	4.06	1.0E-45	BE396833.1	EST_HUMAN	Homo sapiens chromosome 21 open reading frame 1 (C21orf4), mRNA
							601289116F1 NIH_MGC_8 Homo sapiens cDNA clone IMAGE:3618803 5'

Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4757	17777		1.01	1.0E-45	H57443.1	EST_HUMAN	y05b02.r1 Soares fetal liver spleen 1NLS Homo sapiens cDNA clone IMAGE:204363 5'
8355	21334	34745	0.57	1.0E-45	11422236	NT	Homo sapiens peroxisomal biogenesis factor 14 (PEX14), mRNA
8355	21334	34746	0.57	1.0E-45	11422236	NT	Homo sapiens peroxisomal biogenesis factor 14 (PEX14), mRNA
8954	21920	35346	0.85	1.0E-45	D87675.1	NT	Homo sapiens DNA for amyloid precursor protein, complete cds
9476	22440	35880	4.82	1.0E-45	BE887843.1	EST_HUMAN	601511226F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3912535 5'
9880	22833	36287	1.03	1.0E-45	AB002297.1	NT	Human mRNA for KIAA0299 gene, partial cds
12369	25155	31856	9.31	1.0E-45	11418099	NT	Homo sapiens protein kinase C, alpha binding protein (PRKCABF), mRNA
12551	25274		9.31	1.0E-45	11526291	NT	Homo sapiens hypothetical protein FLJ20454 (FLJ20454), mRNA
12556	25277		6.48	1.0E-45	11418177	NT	Homo sapiens Ran GTPase activating protein 1 (RANGAP1), mRNA
12962	25532	31715	3.98	1.0E-45	11418157	NT	Homo sapiens calcium channel, voltage-dependent, alpha 1I subunit (CACNA1I), mRNA
8570	21538	34859	1.68	9.0E-46	9910283	NT	Mus musculus keratin complex 2, gene 6q (Krt2-6q), mRNA
8981	21947		7.02	9.0E-46	AL163209.2	NT	Homo sapiens chromosome 21 segment HS21C009
10845	23765	37264	9.09	9.0E-46	AW246984.1	EST_HUMAN	2822449.5prime NIH_MGC_7 Homo sapiens cDNA clone IMAGE:2822449 5'
2448	15453	28474	11.23	8.0E-46	AI433261.1	EST_HUMAN	t32108.x1 NCI_CGAP_Gas4 Homo sapiens cDNA clone IMAGE:2132199 3' similar to gb:J00314_jma2
2448	15453	28475	11.23	8.0E-46	AI433261.1	EST_HUMAN	TUBULIN BETA-1 CHAIN (HUMAN);
8389	21358		6.79	8.0E-46	BE167244.1	EST_HUMAN	TUBULIN BETA-1 CHAIN (HUMAN);
2248	15262	28289	1.17	7.0E-46	U46007.1	NT	RC5-HT0506-280200-072-C12 HT0506 Homo sapiens cDNA
4611	17832		3.58	7.0E-46	BE386165.1	EST_HUMAN	Rattus norvegicus espin mRNA, complete cds
4845	17862		1.14	7.0E-46	BE064386.1	EST_HUMAN	601277292F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3618119 5'
8160	19235	32466	3.92	7.0E-46	8522708	NT	RC4-BT0310-110300-015-f10 BT0310 Homo sapiens cDNA
8642	19700	32976	1.85	7.0E-46	BF105845.1	EST_HUMAN	Homo sapiens hypothetical protein FLJ10847 (FLJ10847), mRNA
2765	15757	28778	5.63	6.0E-46	AI884381.1	EST_HUMAN	601822835F1 NIH_MGC_77 Homo sapiens cDNA clone IMAGE:4042738 5'
2765	15757	28779	5.63	6.0E-46	AI884381.1	EST_HUMAN	Ymn31f08.x1 NCI_CGAP_U14 Homo sapiens cDNA clone IMAGE:2437575 3' similar to contains MER19.12
6252	19325	32556	10.15	6.0E-46	AI635448.1	EST_HUMAN	MER19 repetitive element;
7426	20393	33743	0.76	6.0E-46	AW513244.1	EST_HUMAN	Ymn31f08.x1 NCI_CGAP_U14 Homo sapiens cDNA clone IMAGE:2437575 3' similar to contains MER19.12
7609	20570	33933	0.51	6.0E-46	BF509740.1	EST_HUMAN	PROTEIN HOMOLOG 2 (HUMAN);
205	13306		6.47	5.0E-46	AL163210.2	NT	U1-H-Bla-agg-b-06-0.U1.e1 NCI_CGAP_Sub8 Homo sapiens cDNA clone IMAGE:3087298 3'
3539	16585	29508	1.01	5.0E-46	BE677194.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C010
							7d81g01.x1 Lupski_doreal_root_ganglion Homo sapiens cDNA clone IMAGE:3279408 3'

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Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3539	16585	29509	1.01	5.0E-46	BE677194.1	EST_HUMAN	7d81g01.x1 Lupsiki_dorsal_root_ganglion Homo sapiens cDNA clone IMAGE:3279408 3'
6899	19951	33248	1.84	5.0E-46	BF590442.1	EST_HUMAN	nas38f07.x1 NCL_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:3258757 3' similar to TR:O75202
7128	20104	33415	3.97	5.0E-46	BF347229.1	EST_HUMAN	O75202 HOMOLOG OF RAT KIDNEY-SPECIFIC;
7302	20273	33609	0.87	5.0E-46	AW582553.1	EST_HUMAN	602021164F1 NCL_CGAP_Bm67 Homo sapiens cDNA clone IMAGE:4156670 5'
7614	20574	33938	0.55	5.0E-46	BE549744.1	EST_HUMAN	QV4-ST0212-120100-075-09 ST0212 Homo sapiens cDNA
642	13708		2.88	4.0E-46	AA601143.1	EST_HUMAN	7b38b05.x1 NCL_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3230481 3'
							no54608.s1 NCL_CGAP_SS1 Homo sapiens cDNA clone IMAGE:1104520 3' similar to gb:X53741_rna1 FIBULIN-1, ISOFORM A PRECURSOR (HUMAN);
1715	14745	27729	7.91	4.0E-46	AW770544.1	EST_HUMAN	h186c03.x1 NCL_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3008836 3' similar to gb:X14008_rna1 LYSOZYME C PRECURSOR (HUMAN); contains element MER37 repetitive element;
1715	14745	27730	7.91	4.0E-46	AW770544.1	EST_HUMAN	h186c03.x1 NCL_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3008836 3' similar to gb:X14008_rna1 LYSOZYME C PRECURSOR (HUMAN); contains element MER37 repetitive element;
2749	15742	28759	3.26	4.0E-46	M18048.1	NT	Human endogenous retrovirus RTVL-H2
4447	17473	30361	0.95	4.0E-46	AB014522.1	NT	Homo sapiens mRNA for KIAA0622 protein, partial cds
4447	17473	30362	0.95	4.0E-46	AB014522.1	NT	Homo sapiens mRNA for KIAA0622 protein, partial cds
5194	18203	31076	0.78	4.0E-46	BE044260.1	EST_HUMAN	h042a07.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:3040020 3'
5194	18203	31077	0.78	4.0E-46	BE044260.1	EST_HUMAN	h042a07.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:3040020 3'
5511	18611	31542	2.11	4.0E-46	M36852.1	NT	Human Ig germline gamma-3 heavy-chain gene V region, partial cds
5511	18611	31543	2.11	4.0E-46	M36852.1	NT	Human Ig germline gamma-3 heavy-chain gene V region, partial cds
12792	25422	31737	2.51	4.0E-46	AB002059.1	NT	Homo sapiens DNA for Human P2XM, complete cds
4421	17448	30339	1.21	3.0E-46	4506376	NT	Homo sapiens mitogen-activated protein kinase kinase kinase 3 (MAP4K3), mRNA
4809	17826	30722	2.84	3.0E-46	Z73660.1	NT	H. sapiens Ig lambda light chain variable region gene (7c.11.2) germline; Ig-Lambda; VLambda
4809	17826	30723	2.84	3.0E-46	Z73660.1	NT	H. sapiens Ig lambda light chain variable region gene (7c.11.2) germline; Ig-Lambda; VLambda
9102	22068	35494	10	3.0E-46	AI831462.1	EST_HUMAN	wj49c04.x1 NCL_CGAP_Lu19 Homo sapiens cDNA clone IMAGE:2406150 3' similar to contains THR.b2 THR repetitive element;
9358	22323	35750	0.59	3.0E-46	LO8850.1	NT	Human AD amyloid mRNA, complete cds
9358	22323	35751	0.59	3.0E-46	LO8850.1	NT	Human AD amyloid mRNA, complete cds
11898	24778	38365	2.01	3.0E-46	D31765.1	NT	Human mRNA for KIAA0061 gene, partial cds
838	13895	26850	10.84	2.0E-46	AA46846.1	EST_HUMAN	ne06a09.s1 NCL_CGAP_Co8 Homo sapiens cDNA clone IMAGE:880408 3' similar to contains THR.b2 THR repetitive element;

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Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1564	14597		2.13	2.0E-46	AA678246.1	EST_HUMAN	z127a11.s1 Soares fetal_liver_spleen_NFLS_ST Homo sapiens cDNA clone IMAGE:431898 3'
1647	14679	27662	4.43	2.0E-46	U78027.1	NT	Homo sapiens Bruton's tyrosine kinase (BTK), alpha-D-galactosidase A (GLA), L44-like ribosomal protein (L44L) and FTP3 (FTP3) genes, complete cds
5010	18024	30910	1.06	2.0E-46	AA339286.1	EST_HUMAN	z159a02.11 Soares testis_NHT Homo sapiens cDNA clone IMAGE:726650 5' similar to SW:RSP1_MOUSE Q01730 RSP-1 PROTEIN.
7726	20682	34046	7.69	2.0E-46	9910569	NT	Mus musculus sperm tail associated protein (Slap), mRNA
8404	21373		1.18	2.0E-46	BE869151.1	EST_HUMAN	601445137F1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3849237 5'
11576	24514		1.82	2.0E-46	7657233	NT	Homo sapiens small acidic protein (IMAGE145052), mRNA
12857	25741	31619	3.22	2.0E-46	AW27214.1	EST_HUMAN	xq78h03.x1 NCL_CGAP_Lu34 Homo sapiens cDNA clone IMAGE:2756789 3'
1237	14273	27233	6.68	1.0E-46	4602694	NT	Homo sapiens cell division cycle 10 (homologous to CDC10 of S. cerevisiae) (CDC10) mRNA
2289	15302	28326	3.28	1.0E-46	AW978516.1	EST_HUMAN	EST390625 IMAGE resequences, MAGP Homo sapiens cDNA
2409	15416	28440	2.9	1.0E-46	H97330.1	EST_HUMAN	EST486095 WATM1 Homo sapiens cDNA clone 486095
3262	16316	29236	1.32	1.0E-46	AA631912.1	EST_HUMAN	np78b02.s1 NCL_CGAP_P22 Homo sapiens cDNA clone IMAGE:1132395 similar to gb:X76717 H.sapiens MT-11 mRNA, (HUMAN);
4908	17925		2.93	1.0E-46	AB023197.1	NT	Homo sapiens mRNA for KIAA0980 protein, partial cds
5784	18876	32058	7.06	1.0E-46	BF194707.1	EST_HUMAN	7692b01.x1 NCL_CGAP_Ov18 Homo sapiens cDNA clone IMAGE:3643705 3'
6089	25653	32382	5.57	1.0E-46	8923762	NT	Homo sapiens centaurin-alpha 2 protein (HSA272195), mRNA
6089	25653	32383	5.57	1.0E-46	8923762	NT	Homo sapiens centaurin-alpha 2 protein (HSA272195), mRNA
6766	19920	33102	0.65	1.0E-46	BF196247.1	EST_HUMAN	7n48e07.x1 NCL_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3567852 3' similar to contains element MER22 repetitive element;
11211	18876	32058	3.61	1.0E-46	BF194707.1	EST_HUMAN	7692b01.x1 NCL_CGAP_Ov18 Homo sapiens cDNA clone IMAGE:3643705 3'
12322	25124	31845	1.52	1.0E-46	BF531102.1	EST_HUMAN	602072284F1 NCL_CGAP_Bm67 Homo sapiens cDNA clone IMAGE:4215398 5'
12322	25124	31846	1.52	1.0E-46	BF531102.1	EST_HUMAN	602072284F1 NCL_CGAP_Bm67 Homo sapiens cDNA clone IMAGE:4215398 5'
13066	25600		4.54	1.0E-46	AV715377.1	EST_HUMAN	AV715377 DCB Homo sapiens cDNA clone DCBAIE03 5'
767	13826		3.24	9.0E-47	AJ271735.1	NT	Homo sapiens Xq pseudautosomal region; segment 1/2
4968	17983	30873	3.91	9.0E-47	AW770928.1	EST_HUMAN	h93e04.x1 NCL_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3009634 3' similar to TR:O75703 O75703 HYPOTHETICAL 12.4 KD PROTEIN.;
6513	19577	32832	1.58	9.0E-47	11425439	NT	Homo sapiens zinc finger protein ZNF286 (ZNF286), mRNA
12816	25843	31432	2.25	9.0E-47	11417968	NT	Homo sapiens SEC14 (S. cerevisiae)-like 2 (SEC14L2), mRNA
1825	14852	27846	47.72	8.0E-47	Y18536.1	NT	Homo sapiens HLA-C gene, exon 5, individual 19323
1825	14852	27847	47.72	8.0E-47	Y18536.1	NT	Homo sapiens HLA-C gene, exon 5, individual 19323
2728	15722	28739	1.77	8.0E-47	5453955	NT	Homo sapiens protein phosphatase 2, regulatory subunit B (B56), epsilon isoform (PPP2R5E) mRNA
3036	16094	29012	2.12	8.0E-47	AJ229043.1	NT	Homo sapiens 959 kb contig between AML1 and CBR1 on chromosome 21q22, segment 3/3

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Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3640	16683	29598	0.78	8.0E-47	AB041926.1	NT	Homo sapiens mRNA for GCK family kinase MINK-2, complete cds
3640	16683	29599	0.78	8.0E-47	AB041926.1	NT	Homo sapiens mRNA for GCK family kinase MINK-2, complete cds
5254	18282	31131	0.65	8.0E-47	7662421	NT	Homo sapiens KIAA0971 protein (KIAA0971), mRNA
2555	15557	28575	2.2	6.0E-47	AL163246.2	NT	Homo sapiens chromosome 21 segment HS21C046
9040	22006	35427	0.49	6.0E-47	U77054.1	EST_HUMAN	HSU77054 Human Homo sapiens cDNA clone N7
9031	22575	36025	6.5	6.0E-47	AI695189.1	EST_HUMAN	U89802.x1 NCI CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2266659 3'
10070	22997	36465	0.86	6.0E-47	AB042824.1	NT	Homo sapiens RECQL5 beta mRNA for DNA helicase recQ5 beta, complete cds
10070	22997	36466	0.86	6.0E-47	AB042824.1	NT	Homo sapiens RECQL5 beta mRNA for DNA helicase recQ5 beta, complete cds
6729	19785	33084	6.56	5.0E-47	11423972	NT	Homo sapiens CDC37 (cell division cycle 37, S. cerevisiae, homolog) (CDC37), mRNA
11147	24107		4.6	5.0E-47	M78590.1	EST_HUMAN	EST00738 Faecal brain, Stratiogene (cat#936206) Homo sapiens cDNA clone HFBCF07
1400	14433	27403	4.48	4.0E-47	4557556	NT	Homo sapiens E1A binding protein p300 (EP300) mRNA
7006	20132	33447	0.98	4.0E-47	BE938896.1	EST_HUMAN	MF4-TN0108-280800-201-404 TN0108 Homo sapiens cDNA
8825	21792	35214	2.45	4.0E-47	BE816483.1	EST_HUMAN	601280486F1 NIH_MGC_39 Homo sapiens cDNA clone IMAGE:3622437 5'
8825	21792	35215	2.45	4.0E-47	BE816483.1	EST_HUMAN	601280486F1 NIH_MGC_39 Homo sapiens cDNA clone IMAGE:3622437 5'
8865	21931	35356	0.81	4.0E-47	AW993777.1	EST_HUMAN	RC3-BN0034-220300-015-f05 BN0034 Homo sapiens cDNA
11954	24833		5.51	4.0E-47	AW515509.1	EST_HUMAN	x66607.x1 NCI CGAP_Lym12 Homo sapiens cDNA clone IMAGE:2848597 3' similar to SW:INT6_MOUSE
546	13617	26538	1.73	3.0E-47	BE007634.1	EST_HUMAN	Q64252 VIRAL INTEGRATION SITE PROTEIN INT-6, [1].
546	13617	26539	1.73	3.0E-47	BE007634.1	EST_HUMAN	601497639F1 NIH_MGC_70 Homo sapiens cDNA clone IMAGE:3889721 5'
819	13877	26826	6.7	3.0E-47	N57483.1	EST_HUMAN	601497639F1 NIH_MGC_70 Homo sapiens cDNA clone IMAGE:3889721 5'
944	13997	26949	7.96	3.0E-47	AL163284.2	NT	y64b04.s1 Scores_multiple_sclerosis_2NBHMSIP Homo sapiens cDNA clone IMAGE:277327 3'
3315	15388	29288	0.7	3.0E-47	4504116	NT	Homo sapiens chromosome 21 segment HS21C084
3990	17030		6.21	3.0E-47	U83181.1	NT	Homo sapiens glutamate receptor, ionotropic, kainate 1 (GRIK1) mRNA
4389	17417	30301	0.98	3.0E-47	M12959.1	NT	Homo sapiens nuclear dual-specificity phosphatase (SBF1) mRNA, partial cds
6128	19206	32429	4.76	3.0E-47	AW408800.1	EST_HUMAN	Human T-cell receptor active alpha-chain mRNA from JM cell line, complete cds
6128	19206	32430	4.76	3.0E-47	AW408800.1	EST_HUMAN	UI-HF-BM0-adv-d-07-0-UI.r1 NIH_MGC_38 Homo sapiens cDNA clone IMAGE:3063205 5'
6128	19206	32430	4.76	3.0E-47	AW408800.1	EST_HUMAN	UI-HF-BM0-adv-d-07-0-UI.r1 NIH_MGC_38 Homo sapiens cDNA clone IMAGE:3063205 5'
6128	19206	32430	4.76	3.0E-47	AW408800.1	EST_HUMAN	UI-HF-BM0-adv-d-07-0-UI.r1 NIH_MGC_38 Homo sapiens cDNA clone IMAGE:3063205 5'
7608	20569	33931	0.59	3.0E-47	AI222413.1	EST_HUMAN	qh04e07.x1 Scores_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1843716 3'
7608	20569	33932	0.59	3.0E-47	AI819755.1	EST_HUMAN	wf11h08.x1 NCI CGAP_Kid12 Homo sapiens cDNA clone IMAGE:2402559 3'
9185	22151	35579	0.59	3.0E-47	AW963796.1	EST_HUMAN	wf11h08.x1 NCI CGAP_Kid12 Homo sapiens cDNA clone IMAGE:2402559 3'
9185	22151	35580	0.59	3.0E-47	AW963796.1	EST_HUMAN	EST375869 IMAGE:3063205 5'
149	13252	26181	1.57	2.0E-47	4505318	NT	EST375869 IMAGE:3063205 5'
969	14021	26973	2.24	2.0E-47	AL163209.2	NT	Homo sapiens myosin phosphatase, target subunit 2 (MYPT2), mRNA
969	14021	26974	2.24	2.0E-47	AL163209.2	NT	Homo sapiens chromosome 21 segment HS21C009

Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1570	14603		1.08	2.0E-47	AI969279.1	EST_HUMAN	wg96b02.x1 NCI_CGAP_GC6 Homo sapiens cDNA clone IMAGE:2479881 3'
1597	14629	27604	2.2	2.0E-47	7682109	NT	Homo sapiens KIA0426 gene product (KIA0426), mRNA
1687	14718	27698	3.87	2.0E-47	AA524514.1	EST_HUMAN	hg43h12.s1 NCI_CGAP_C03 Homo sapiens cDNA clone IMAGE:937607 3'
4374	17402	30282	1.82	2.0E-47	4804868	NT	Homo sapiens ring finger protein (C3HC4 type) 8 (RNF8), mRNA
4411	17439	30327	1.48	2.0E-47	AA569592.1	EST_HUMAN	nt23g07.s1 NCI_CGAP_P1 Homo sapiens cDNA clone IMAGE:914652
4411	17439	30328	1.48	2.0E-47	AA569592.1	EST_HUMAN	nt23g07.s1 NCI_CGAP_P1 Homo sapiens cDNA clone IMAGE:914652
4534	17557	30445	1.68	2.0E-47	5174648	NT	Homo sapiens Rev/Rex activation domain binding protein-related (RAB-R) mRNA
4850	17867	30760	1.22	2.0E-47	AW965166.1	EST_HUMAN	EST377239 IMAGE resequences, MAGI Homo sapiens cDNA
5187	18196		0.7	2.0E-47	AI041128.1	EST_HUMAN	ov61h03.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1641845 3'
5890	18969	32160	1.22	2.0E-47	AF073921.1	NT	Homo sapiens regulator of G-protein signaling 6 variant form (RGSG) mRNA, complete cds
6088	19168	32880	1.29	2.0E-47	BE778475.1	EST_HUMAN	601463932F1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:3867487 5'
6088	19168	32881	1.29	2.0E-47	BE778475.1	EST_HUMAN	601463932F1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:3867487 5'
7964	25892		1.43	2.0E-47	L09731.1	NT	Homo sapiens 5-hydroxytryptamine 1D receptor pseudogene with an Alu repeat insertion
8297	21266	34677	1.76	2.0E-47	D87675.1	NT	Homo sapiens DNA for amyloid precursor protein, complete cds
8297	21266	34678	1.76	2.0E-47	D87675.1	NT	Homo sapiens DNA for amyloid precursor protein, complete cds
9088	22034	35457	1.75	2.0E-47	AF071771.1	NT	Homo sapiens SPH-binding factor mRNA, partial cds
9845	22781	36235	0.76	2.0E-47	11528136	NT	Homo sapiens BTG family, member 3 (BTG3), mRNA
11800	23955	37478	2.31	2.0E-47	M76125.1	NT	Human tyrosine kinase receptor (axl) mRNA, complete cds
12358	25886	31415	2.12	2.0E-47	R42423.1	EST_HUMAN	Hy92e08.s1 Soares infant brain 1NIB Homo sapiens cDNA clone IMAGE:29966 3' similar to contains OFR repetitive element;
1404	14437	27405	6.91	1.0E-47	AI333429.1	EST_HUMAN	qp99h03.x1 Soares_fetal_lung_NbHL18W Homo sapiens cDNA clone IMAGE:1931189 3'
3835	16876	29776	1.18	1.0E-47	BE280477.1	EST_HUMAN	601155321F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3138893 5'
3835	16875	29777	1.18	1.0E-47	BE280477.1	EST_HUMAN	601155321F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3138893 5'
5112	18122	30997	2.55	1.0E-47	AW813906.1	EST_HUMAN	RC3-ST0197-130400-017-002 ST0197 Homo sapiens cDNA
7244	19979	33276	6.6	1.0E-47	AI880886.1	EST_HUMAN	at19e06.x1 Barslead aorta HPLR86 Homo sapiens cDNA clone IMAGE:2355586 3' similar to gb:M22995
9220	22186		0.77	1.0E-47	AW064648.1	EST_HUMAN	RAS-RELATED PROTEIN RAP-1A (HUMAN);
10721	23643	37136	2.41	1.0E-47	L30115.1	NT	h184a11.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2978972 3' similar to gb:M26328 KERATIN, TYPE I CYTOSKELETAL 18 (HUMAN);
1616	14648	27623	3.85	9.0E-48	AF223391.1	NT	Papio hamadryas alcohol dehydrogenase class I (ADH) gene, 5' region
3569	16614	29536	0.7	9.0E-48	BF359947.1	EST_HUMAN	Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced
5763	18855	32035	0.84	9.0E-48	BE888196.1	EST_HUMAN	CM2-MT0100-310700-280-f05 MT0100 Homo sapiens cDNA
5763	18855	32036	0.84	9.0E-48	BE888196.1	EST_HUMAN	601511714F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3913106 5'
						EST_HUMAN	601511714F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3913106 5'

Table 4

Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6220	19294	32528	0.6	9.0E-48	AI833168.1	EST_HUMAN	at75h09.x1 Barstead colon HPLRB7 Homo sapiens cDNA clone IMAGE:2377889 3' similar to TR:O60844
6351	19420	32661	0.73	9.0E-48	AU123240.1	EST_HUMAN	O60844 HOMOLOG OF RAT ZYMOGEN GRANULE MEMBRANE PROTEIN. ;
11452	24395	37940	2.49	9.0E-48	BE338313.1	EST_HUMAN	AU123240 NT2RM1 Homo sapiens cDNA clone NT2RM1000978 5'
1255	14291		1.5	8.0E-48	4501900	NT	601310479F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3632083 5'
1256	14291		1.54	8.0E-48	4501900	NT	Homo sapiens aminocyclase 1 (ACY1), mRNA
3152	16209	29123	3.31	8.0E-48	AW768477.1	EST_HUMAN	Hk61b03.x1 NCI CGAP_Lym12 Homo sapiens cDNA clone IMAGE:3001133 3' similar to gb:X64707
3152	16209	29124	3.31	8.0E-48	AW768477.1	EST_HUMAN	BREAST BASIC CONSERVED PROTEIN 1 (HUMAN);
491	13564		1.64	7.0E-48	AB033036.1	NT	Hk61b03.x1 NCI CGAP_Lym12 Homo sapiens cDNA clone IMAGE:3001133 3' similar to gb:X64707
492	13564		22.81	7.0E-48	AB033035.1	NT	BREAST BASIC CONSERVED PROTEIN 1 (HUMAN);
1496	14529	27501	1.04	7.0E-48	6912719	NT	Homo sapiens mRNA for KIAA1209 protein, partial cds
1943	14875	27648	4.5	7.0E-48	5730038	NT	Homo sapiens SET domain and matrin transposase fusion gene (SETMAR) mRNA
6707	19763	33042	24.74	7.0E-48	1141683.1	EST_HUMAN	Homo sapiens SET domain and matrin transposase fusion gene (SETMAR) mRNA
3612	16657	29575	1.2	6.0E-48	AI761111.1	EST_HUMAN	Homo sapiens histidyl-RNA synthetase (HARS), mRNA
6176	19251	32484	1.12	6.0E-48	AB006955.1	NT	wf69h03.x1 NCI CGAP_Kid12 Homo sapiens cDNA clone IMAGE:2398613 3'
6953	20177	33502	0.89	6.0E-48	11420995	NT	Homo sapiens mRNA for AIE-75, complete cds
7702	25687	34022	0.56	6.0E-48	AB046844.1	NT	Homo sapiens BMX non-receptor tyrosine kinase (BMX), mRNA
7702	25687	34023	0.56	6.0E-48	AB046844.1	NT	Homo sapiens mRNA for KIAA1624 protein, partial cds
9479	22443	35885	1.94	6.0E-48	AF026816.1	NT	Homo sapiens mRNA for KIAA1624 protein, partial cds
9899	22852	36311	1.78	6.0E-48	11427428	NT	Homo sapiens putative oncogene protein mRNA, partial cds
10047	22974	36441	3.3	6.0E-48	AA189080.1	EST_HUMAN	Homo sapiens hypothetical protein FLJ11006 (FLJ11006), mRNA
3320	18313	29292	1.58	5.0E-48	4826897	NT	z45b06.s1 Stragene hNT neuron (#837233) Homo sapiens cDNA clone IMAGE:632627 3' similar to contains Alu repetitive element;
8921	21887	35314	1.11	5.0E-48	BE064410.1	EST_HUMAN	Homo sapiens phosphodiesterase 1A, calmodulin-dependent (PDE1A) mRNA
11305	24255	37782	2.83	4.0E-48	AI620420.1	EST_HUMAN	RC4-BT0311-141195-011-h06 BT0311 Homo sapiens cDNA
1385	14419	27388	1.33	3.0E-48	AV690964.1	EST_HUMAN	tu47a02.x1 NCI CGAP_P728 Homo sapiens cDNA clone IMAGE:2254154 3'
1993	15014	28020	16.21	3.0E-48	4885170	NT	AV690964 GKC Homo sapiens cDNA clone GKCDRE12 5'
1993	15014	28021	16.21	3.0E-48	4885170	NT	Homo sapiens chromosome X open reading frame 6 (CXORF6) mRNA
3429	16477	29396	0.93	3.0E-48	AF172453.1	NT	Homo sapiens chromosome X open reading frame 6 (CXORF6) mRNA
3647	16690	29606	0.75	3.0E-48	AW664531.1	EST_HUMAN	Homo sapiens opid growth factor receptor mRNA, complete cds
4275	17304		0.9	3.0E-48	AA009541.1	EST_HUMAN	hi14b12.x1 NCI CGAP_GU1 Homo sapiens cDNA clone IMAGE:2872255 3' similar to SW:DCRB_HUMAN
							P66555 DOWN SYNDROME CRITICAL REGION PROTEIN B. ;
							204g03.1 Soares fetal_liver脾脏_1NFLS_S1 Homo sapiens cDNA clone IMAGE:429844 5'

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5997	19081	32278	2.41	3.0E-48	BE084571.1	EST_HUMAN	MR4-BT0657-060400-201-e10 BT0657 Homo sapiens cDNA
7215	20237	33571	1.06	3.0E-48	AF087913.1	NT	Human endogenous retrovirus HERV-P-147D
8734	21702		4.11	3.0E-48	AA659930.1	EST_HUMAN	PTR5 repetitive element;
11221	24174	37700	6.89	3.0E-48	BF614170.1	EST_HUMAN	UHL-BW1-enl-a-10-Q-U1.s1 NCL CGAP_Sub7 Homo sapiens cDNA clone IMAGE:3082267 3'
5	13126	26025	2.4	2.0E-48	AA465007.1	EST_HUMAN	zx80c03.r1 Soares ovary tumor NHOT Homo sapiens cDNA clone IMAGE:810052 5'
47	13167	26072	1.23	2.0E-48	AA631940.1	EST_HUMAN	fmo7 Regional genomic DNA specific cDNA library Homo sapiens cDNA clone CR17-26
1223	14261		0.65	2.0E-48	H24278.1	EST_HUMAN	ym55e10.r1 Soares infant brain INIS Homo sapiens cDNA clone IMAGE:52182 5' similar to SP:M6B_MOUSE P35803 MEMBRANE GLYCOPROTEIN ;
4562	17585	30477	0.92	2.0E-48	BE246065.1	EST_HUMAN	TCBAP1D3842 Pediatric pre-B cell acute lymphoblastic leukemia Baylor-HGSC project=TCBA Homo sapiens cDNA clone TCBAP3842
5912	18998	32188	0.63	2.0E-48	AA613171.1	EST_HUMAN	no18g01.s1 NCL CGAP_Phe1 Homo sapiens cDNA clone IMAGE:1101072 3'
5912	18998	32189	0.63	2.0E-48	AA613171.1	EST_HUMAN	no18g01.s1 NCL CGAP_Phe1 Homo sapiens cDNA clone IMAGE:1101072 3'
7762	20715	34086	3.9	2.0E-48	AB040834.1	NT	Homo sapiens mRNA for KIAA1501 protein, partial cds
7762	20715	34087	3.9	2.0E-48	AB040834.1	NT	Homo sapiens mRNA for KIAA1501 protein, partial cds
7777	20730	34103	3.52	2.0E-48	11496238	NT	Homo sapiens v-rel avian reticulendotheliosis viral oncogene homolog A (nuclear factor of kappa light polypeptide gene enhancer in B-cells 3 (p65)) (RELA), mRNA
8698	21666	35089	1.37	2.0E-48	AV743451.1	EST_HUMAN	AV743451 CB Homo sapiens cDNA clone CBCGG10 5'
12318	13126	26025	3.8	2.0E-48	AA465007.1	EST_HUMAN	zx80c03.r1 Soares ovary tumor NHOT Homo sapiens cDNA clone IMAGE:810052 5'
58	13177	28089	3.37	1.0E-48	7706534	NT	Homo sapiens cisplatin resistance-associated overexpressed protein (LOC51747), mRNA
874	13930	26888	1.61	1.0E-48	4502166	NT	Homo sapiens amyloid beta (A4) precursor protein (protease nexin-II, Alzheimer disease) (APP), mRNA
1077	14122	27073	1.8	1.0E-48	7657430	NT	Homo sapiens EBNA-2 co-activator (100kD) (p100), mRNA
1077	14122	27074	1.8	1.0E-48	7657430	NT	Homo sapiens EBNA-2 co-activator (100kD) (p100), mRNA
1299	14335	27298	5.06	1.0E-48	5032032	NT	Homo sapiens RNA binding motif protein 8 (RBM8) mRNA
1933	14957	27954	14.5	1.0E-48	AL163302.2	NT	Homo sapiens chromosome 21 segment HS21C102
3500	16547	29473	0.83	1.0E-48	AL163246.2	NT	Homo sapiens chromosome 21 segment HS21C046
6420	19487	32736	1.17	1.0E-48	AB89077.1	EST_HUMAN	td17c01.x1 NCL CGAP_Co16 Homo sapiens cDNA clone IMAGE:2075904 3' similar to TR:O14588 O14588 SIMILARITY TO U73941 ;
6420	19487	32737	1.17	1.0E-48	AB89077.1	EST_HUMAN	td17c01.x1 NCL CGAP_Co16 Homo sapiens cDNA clone IMAGE:2075904 3' similar to TR:O14588 O14588 SIMILARITY TO U73941 ;
6648	19706		1.03	1.0E-48	Y18000.1	NT	Homo sapiens NF2 gene
6748	19802	33082	0.7	1.0E-48	AB028994.1	NT	Homo sapiens mRNA for KIAA1071 protein, partial cds
6748	19802	33083	0.7	1.0E-48	AB028994.1	NT	Homo sapiens mRNA for KIAA1071 protein, partial cds

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Table 4
Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7471	20437	33794	3.15	1.0E-48	4755137	NT	Homo sapiens huntingtin (Huntington disease) (HD) mRNA
9183	22149	35576	0.49	1.0E-48	4758895	NT	Homo sapiens mitogen-activated protein kinase kinase 13 (MAP3K13), mRNA
9183	22149	35577	0.49	1.0E-48	4758895	NT	Homo sapiens mitogen-activated protein kinase kinase 13 (MAP3K13), mRNA
9568	22530	35980	1.19	1.0E-48	4502838	NT	Homo sapiens Chediak-Higashi syndrome 1 (CHS1) mRNA
9623	22567	36017	7.13	1.0E-48	AB033071.1	NT	Homo sapiens mRNA for KIAA1245 protein, partial cds
9924	22808	36260	0.69	1.0E-48	BE168410.1	EST_HUMAN	QV3-HT0513-060400-147-q01 HT0513 Homo sapiens cDNA
9941	22868	36330	4.48	1.0E-48	BF304683.1	EST_HUMAN	60188809F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4122119 5'
10736	23658	37151	3.85	1.0E-48	11429808	NT	Homo sapiens B cell linker protein (SLP65), mRNA
10736	23658	37152	3.85	1.0E-48	11429808	NT	Homo sapiens B cell linker protein (SLP65), mRNA
12280	25830	32478	1.53	1.0E-48	W26785.1	EST_HUMAN	15d6 Human retina cDNA randomly primed sublibrary Homo sapiens cDNA
6171	19246	32478	3	8.0E-49	10048417	NT	Mus musculus T-box 20 (Tbx20), mRNA
6171	19246	32479	3	8.0E-49	10048417	NT	Mus musculus T-box 20 (Tbx20), mRNA
7017	20143	33460	0.57	8.0E-49	AA642035.1	EST_HUMAN	ns18h03.r1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1184021 5'
8638	21606	35029	3.32	8.0E-49	U23850.1	NT	Human insulin 1,4,5 trisphosphate receptor type 1 mRNA, partial cds
10348	23272	36748	2.1	8.0E-49	AB008881.1	NT	Homo sapiens gene for activin receptor type IIB, complete cds
11204	24158	37688	2.32	8.0E-49	AI623722.1	EST_HUMAN	ts38d12.x1 NCI_CGAP_U14 Homo sapiens cDNA clone IMAGE:2230871 3' similar to contains Alu repetitive element; contains element PTR5 repetitive element;
140	13468	26398	2.24	7.0E-49	5729990	NT	Homo sapiens proteasome (prosome, macropain) 26S subunit, ATPase, 4 (PSMC4) mRNA
140	13468	26399	2.24	7.0E-49	5729990	NT	Homo sapiens proteasome (prosome, macropain) 26S subunit, ATPase, 4 (PSMC4) mRNA
393	13468	26398	1.53	7.0E-49	5729990	NT	Homo sapiens proteasome (prosome, macropain) 26S subunit, ATPase, 4 (PSMC4) mRNA
393	13468	26399	1.53	7.0E-49	5729990	NT	Homo sapiens proteasome (prosome, macropain) 26S subunit, ATPase, 4 (PSMC4) mRNA
394	13468	26398	2.06	7.0E-49	5729990	NT	Homo sapiens proteasome (prosome, macropain) 26S subunit, ATPase, 4 (PSMC4) mRNA
394	13468	26399	2.06	7.0E-49	5729990	NT	Homo sapiens proteasome (prosome, macropain) 26S subunit, ATPase, 4 (PSMC4) mRNA
1225	14263	27220	2.85	7.0E-49	AL163284.2	NT	Homo sapiens chromosome 21 segment HS21C084
5535	18632	31571	1.57	7.0E-49	AI807191.1	EST_HUMAN	wf25h04.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2356663 3' similar to TR:O54923 O54923 RSEC16;
5545	18642	31582	1.33	7.0E-49	AL120837.1	EST_HUMAN	DKFZp762O0333.s1 762 (synonym: hmel2) Homo sapiens cDNA clone DKFZp762O033 3'
5903	18632	31571	0.84	7.0E-49	AI807191.1	EST_HUMAN	wf25h04.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2356663 3' similar to TR:O54923 O54923 RSEC15;
198	13299	26227	86.86	6.0E-49	AW731740.1	EST_HUMAN	bs55g05.x1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:2900504 3' similar to gb:X17208 40S RIBOSOMAL PROTEIN S4 (HUMAN); gb:M20632 Mouse LLRep3 protein mRNA from a repetitive element, complete (MOUSE);
4142	17173	30062	1.14	6.0E-49	AI162091.1	EST_HUMAN	DKFZp761A138.s1 761 (synonym: hamy2) Homo sapiens cDNA clone DKFZp761A138 3'
6562	19642	32909	0.65	6.0E-49	AU140742.1	EST_HUMAN	AU140742 PLAGE4 Homo sapiens cDNA clone PLAGE400148 5'

Table 4

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
11609	24547	38107	2	6.0E-49	AW452218.1	EST_HUMAN	U1-H-B13-alc-a-05-Q-UJ.st NCL CGAP_Sub5 Homo sapiens cDNA clone IMAGE:3068048 3'
11972	24850	38446	4.09	6.0E-49	AA366568.1	EST_HUMAN	EST77525 Pancreas tumor III Homo sapiens cDNA 5' end
11972	24850	38447	4.09	6.0E-49	AA366568.1	EST_HUMAN	EST77525 Pancreas tumor III Homo sapiens cDNA 5' end
12645	25723		1.7	6.0E-49	AA707567.1	EST_HUMAN	z29c08.s1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:451694 3'
713	13775	26708	8.21	5.0E-49	AL163210.2	NT	Homo sapiens chromosome 21 segment HS21C010
713	13775	26709	8.21	5.0E-49	AL163210.2	NT	Homo sapiens chromosome 21 segment HS21C010
1809	14937	27628	3.44	5.0E-49	AA172121.1	EST_HUMAN	z4p29c07.r1 Stratogene neuroepithelium (#937231) Homo sapiens cDNA clone IMAGE:610860 5' similar to TR:G2333226 G2332226 RTVL-H PROTEIN ; contains LTR7 LTR7 LTR7 repetitive element ;
2760	15752	28772	9.75	5.0E-49	U17714.1	NT	Homo sapiens putative tumor suppressor ST13 (ST13) mRNA, complete cds
3286	16340	29259	6.07	5.0E-49	11436355	NT	Homo sapiens similar to ribosomal protein S27 (metallopanstimulin 1) (H. sapiens) (LOC633362), mRNA x08601.x1 NCL CGAP_U4 Homo sapiens cDNA clone IMAGE:2875583 3' similar to W.P.B0350.2B CE06703 ;
526	13597	26514	25.9	4.0E-49	AW189533.1	EST_HUMAN	Homo sapiens mRNA for ankyrin B (440 kDa)
7457	20423	33778	1.08	4.0E-49	Z26634.2	NT	Homo sapiens mRNA for ankyrin B (440 kDa)
7457	20423	33779	1.06	4.0E-49	Z26634.2	NT	Homo sapiens mRNA for ankyrin B (440 kDa)
7487	20452	33811	0.66	4.0E-49	11525737	NT	Homo sapiens UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase 8 (GALNAc-T8) (GALNT8), mRNA
7487	20452	33812	0.66	4.0E-49	11525737	NT	Homo sapiens UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase 8 (GALNAc-T8) (GALNT8), mRNA
8109	21046	34448	0.71	4.0E-49	7862209	NT	Homo sapiens KIA00623 gene product (KIA00623), mRNA
9216	22182	35614	0.53	4.0E-49	11425374	NT	Homo sapiens copine III (CPNE3), mRNA
9216	22182	35615	0.53	4.0E-49	11425374	NT	Homo sapiens copine III (CPNE3), mRNA
12508	25939		8.71	4.0E-49	AA210798.1	EST_HUMAN	z90105.r1 NCL CGAP_G0B1 Homo sapiens cDNA clone IMAGE:682977 5'
12594	25297		3.19	4.0E-49	AF240786.1	NT	Homo sapiens glutathione S-transferase theta 1 (GSTT1) genes, complete cds
562	13632	26549	1.27	3.0E-49	X68968.1	NT	H. sapiens mRNA for acetyl-CoA carboxylase
2656	15653		1.93	3.0E-49	AA016131.1	EST_HUMAN	z631c05.r1 Soares retina N2b4HR Homo sapiens cDNA clone IMAGE:360584 5' similar to contains L1.13 L1 repetitive element ;
5019	18033	30919	2.11	3.0E-49	U46968.1	NT	Human type IV collagen (COL4A4) gene, exon 40
7650	20610	33976	10.82	3.0E-49	H39479.1	EST_HUMAN	EST25612 WATM1 Homo sapiens cDNA clone 25e12
11633	24570	38134	1.54	3.0E-49	AA337581.1	EST_HUMAN	EST42672 Endometrial tumor Homo sapiens cDNA 5' end
662	13728		3.89	2.0E-49	BE165980.1	EST_HUMAN	MR3-HT0487-150200-113-g01 HT0487 Homo sapiens cDNA
3236	16291	29213	1.5	2.0E-49	N26446.1	EST_HUMAN	y23c08.r1 Soares melanocyte 2N6HM Homo sapiens cDNA clone IMAGE:262571 5'

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Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3583	16628	29547	0.78	2.0E-49	AF026564.1	NT	Homo sapiens RNA binding protein II (RBMII) gene, complete cds
6900	19952	33249	1.14	2.0E-49	AV717938.1	EST_HUMAN	AV717938 DCB Homo sapiens cDNA clone DBALB01 5'
8436	21405		1.62	2.0E-49	M86033.1	EST_HUMAN	EST02558 Fetal brain, Stralagene (cat#36206) Homo sapiens cDNA clone HFBCY60
12603	25921		2.57	2.0E-49	AF163864.1	NT	Homo sapiens SNCA isoform (SNCA) gene, complete cds, alternatively spliced
900	13955		9.35	1.0E-49	BF035327.1	EST_HUMAN	601459531F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3662086 5'
1557	14589	27560	1.27	1.0E-49	4557887	NT	Homo sapiens keratin 18 (KRT18) mRNA
1818	14845	27837	3.33	1.0E-49	BE255216.1	EST_HUMAN	601115769F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3356273 5'
5433	18535	31444	5.72	1.0E-49	BF131007.1	EST_HUMAN	6011820053F1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:4052052 5'
6196	19270	32505	0.87	1.0E-49	H18291.1	EST_HUMAN	yr48h04.r1 Soares adult brain N2b5HB55Y Homo sapiens cDNA clone IMAGE:171703 5' similar to SP:GBG1_HUMAN Q08447 GUANINE NUCLEOTIDE-BINDING PROTEIN G(T) GAMMA-1 SUBUNIT ;
6202	19278	32510	1	1.0E-49	AW964640.1	EST_HUMAN	EST376713 MAGE resequences, MAGH Homo sapiens cDNA
7427	20394	33744	0.58	1.0E-49	AV703000.1	EST_HUMAN	AV703000 ADB Homo sapiens cDNA clone ADBCVD11 5'
7427	20394	33745	0.58	1.0E-49	AV703000.1	EST_HUMAN	AV703000 ADB Homo sapiens cDNA clone ADBCVD11 5'
7433	20400	33753	3.3	1.0E-49	BE398110.1	EST_HUMAN	601290330F1 NIH_MGC_8 Homo sapiens cDNA clone IMAGE:3620863 5'
7433	20400	33754	3.3	1.0E-49	BE398110.1	EST_HUMAN	601290330F1 NIH_MGC_8 Homo sapiens cDNA clone IMAGE:3620863 5'
7520	20485	33846	2.2	1.0E-49	N25884.1	EST_HUMAN	yy78g12.s1 Soares placenta_8tc9weeks_2NbhP8tc9W Homo sapiens cDNA clone IMAGE:258406 3' similar to gb:X66873 KINESIN HEAVY CHAIN (HUMAN);
7520	20485	33847	2.2	1.0E-49	N25884.1	EST_HUMAN	yy78g12.s1 Soares placenta_8tc9weeks_2NbhP8tc9W Homo sapiens cDNA clone IMAGE:258406 3' similar to gb:X66873 KINESIN HEAVY CHAIN (HUMAN);
8414	21383	34790	0.69	1.0E-49	11321580	NT	Homo sapiens succinate-CoA ligase, GDP-forming, alpha subunit (SUQLG1), mRNA
8414	21383	34791	0.69	1.0E-49	11321580	NT	Homo sapiens succinate-CoA ligase, GDP-forming, alpha subunit (SUQLG1), mRNA
9023	21989		0.78	1.0E-49	9994184	NT	Homo sapiens RNA binding motif protein 7 (LOC51120), mRNA
9844	22309	35734	1.14	1.0E-49	BE409340.1	EST_HUMAN	601300992F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3635398 5'
10485	23407	36903	1.22	1.0E-49	AL043129.2	EST_HUMAN	DKFZp434D2423_r1 434 (synonym: htes3) Homo sapiens cDNA clone DKFZp434D2423 5'
11399	24344	37877	1.99	1.0E-49	AB020335.1	NT	Homo sapiens Pancreas-specific TSA305 mRNA, complete cds
11640	24577	38143	3.12	1.0E-49	11427366	NT	Homo sapiens brefeldin A-inhibited guanine nucleotide-exchange protein 1 (BIG1), mRNA
12147	25007		1.7	1.0E-49	BE159343.1	EST_HUMAN	MRO-H10407-010200-006-02 HT0407 Homo sapiens cDNA
12502	25241		2.78	1.0E-49	11418322	NT	Homo sapiens cadherin EGF LAG seven-pass G-type receptor 1 (CELSR1), mRNA
6544	26997		1.06	9.0E-50	BE295758.1	EST_HUMAN	601176250F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3631588 5'
171	13273	26198	3.9	8.0E-50	AL163202.2	NT	Homo sapiens chromosome 21 segment HS21C002
720	13782	26716	2.14	8.0E-50	X95097.2	NT	Homo sapiens mRNA for VIP receptor 2
720	13782	26717	2.14	8.0E-50	X95097.2	NT	Homo sapiens mRNA for VIP receptor 2
1778	14807	27793	4	8.0E-50	4501890	NT	Homo sapiens actinin, alpha 1 (ACTN1) mRNA
2710	15704	28720	2.18	8.0E-50	4826658	NT	Homo sapiens capping protein (actin filament) muscle Z-line, beta (CAPZB), mRNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
621	13686	26604	0.68	7.0E-50	BE089591.1	EST_HUMAN	QV0-BT0703-280400-211-e08 BT0703 Homo sapiens cDNA
6952	20176	33500	1.21	7.0E-50	BF091922.1	EST_HUMAN	RC6-TN0073-150900-011-A12 TN0073 Homo sapiens cDNA
6952	20176	33501	1.21	7.0E-50	BF091922.1	EST_HUMAN	RC6-TN0073-150900-011-A12 TN0073 Homo sapiens cDNA
7526	20490	33852	0.62	7.0E-50	AA627822.1	EST_HUMAN	nc99612.s1 NCL_CGAP_C09 Homo sapiens cDNA clone IMAGE:1148206 3' similar to gb:X69391 60S RIBOSOMAL PROTEIN L6 (HUMAN);
11108	24068	37590	28.05	7.0E-50	AI872137.1	EST_HUMAN	wn555g11.x1 NCL_CGAP_U12 Homo sapiens cDNA clone IMAGE:2439908 3'
8556	21524		6.69	6.0E-50	BE044076.1	EST_HUMAN	h36h04.x1 NCL_CGAP_U11 Homo sapiens cDNA clone IMAGE:3039511 3' similar to contains MER29.b3 MER29 repetitive element;
11166	24124	37652	7.96	6.0E-50	AA312079.1	EST_HUMAN	EST182775 Jurkat T-cells V1 Homo sapiens cDNA 5' end
11166	24124	37653	7.96	6.0E-50	AA312079.1	EST_HUMAN	EST182775 Jurkat T-cells V1 Homo sapiens cDNA 5' end
1808	14836	27826	1.18	5.0E-50	BF332938.1	EST_HUMAN	CM0-BT0792-300500-398-b05 BT0792 Homo sapiens cDNA
1808	14836	27827	1.18	5.0E-50	BF332938.1	EST_HUMAN	CM0-BT0792-300500-398-b05 BT0792 Homo sapiens cDNA
9448	22412		5.65	5.0E-50	AA557883.1	EST_HUMAN	nk45h10.s1 NCL_CGAP_P14 Homo sapiens cDNA clone IMAGE:1043683 similar to contains PTR5.13 PTR5 repetitive element;
918	13972		1.45	4.0E-50	AA601143.1	EST_HUMAN	nc54e08.s1 NCL_CGAP_SS1 Homo sapiens cDNA clone IMAGE:1104520 3' similar to gb:X53741_rna1 FIBULIN-1, ISOFORM A PRECURSOR (HUMAN);
6497	19561	32813	0.54	4.0E-50	11440683	NT	Homo sapiens cysteinyl-ferriRNA synthetase (CARS), mRNA
7445	20411	33763	0.93	4.0E-50	BE067538.1	EST_HUMAN	QV1-BT0681-280300-127-f12 BT0681 Homo sapiens cDNA
1955	14978		2.86	3.0E-50	M18048.1	NT	Human endogenous retrovirus RTVL-H2
2525	15528	28549	1.11	3.0E-50	BE259196.1	EST_HUMAN	601109717F1 NIH_JMGC_16 Homo sapiens cDNA clone IMAGE:3350309 5'
3310	16363	29283	0.88	3.0E-50	AA746142.1	EST_HUMAN	db0306.s1 NCL_CGAP_K63 Homo sapiens cDNA clone IMAGE:1322627 3'
6834	19887	33180	0.6	3.0E-50	11419317	NT	Homo sapiens protein tyrosine phosphatase, non-receptor type 12 (PTPN12), mRNA
6834	19887	33181	0.6	3.0E-50	11419317	NT	Homo sapiens protein tyrosine phosphatase, non-receptor type 12 (PTPN12), mRNA
6929	20153	33472	1.56	3.0E-50	11421514	NT	Homo sapiens similar to sema domain, immunoglobulin domain (Ig), short basic domain, secreted, (semaphorin) 3A (H. sapiens) (LOC83292), mRNA
7906	20849	34234	4.3	3.0E-50	AF233436.2	NT	Homo sapiens FYVE domain-containing dual specificity protein phosphatase FYVE-DSP1a mRNA, complete cds
7906	20849	34235	4.3	3.0E-50	AF233436.2	NT	Homo sapiens FYVE domain-containing dual specificity protein phosphatase FYVE-DSP1a mRNA, complete cds
8929	21895	35323	0.61	3.0E-50	6601589	NT	Homo sapiens ankyrin-like with transmembrane domains 1 (ANKTM1), mRNA
10177	23102	36582	1.1	3.0E-50	AB046818.1	NT	Homo sapiens mRNA for KIAA1598 protein, partial cds
10186	23111	36595	0.96	3.0E-50	11418514	NT	Homo sapiens t-complex 10 (a murine top homolog) (TCP10), mRNA
10885	23805	37309	0.74	3.0E-50	AB002297.1	NT	Human mRNA for KIAA0299 gene, partial cds
11438	24381	37920	1.99	3.0E-50	11436955	NT	Homo sapiens Grb2-associated binder 2 (KIAA0571), mRNA

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11792	23947	37468	8.4	3.0E-50	AJ245621.1	NT	Homo sapiens CTL2 gene
778	13837		6.8	2.0E-50	AF050066.1	NT	Homo sapiens MHC class 1 region
1081	14125	27078	6.73	2.0E-50	4557762	NT	Homo sapiens midline 1 (Opitz/BBB syndrome) (MID1) mRNA
1437	14470	27448	0.95	2.0E-50	AF138303.1	NT	Homo sapiens dectin D mRNA, complete cds, alternatively spliced
3300	16353	29272	0.83	2.0E-50	AF111168.2	NT	Homo sapiens serine palmitoyl transferase, subunit II gene, complete cds; and unknown genes
4289	17318	30197	0.75	2.0E-50	D86424.1	NT	Mus musculus mRNA for high-sulfur keratin protein, partial cds
7051	20073	33380	0.51	2.0E-50	AU124065.1	EST_HUMAN	AU124065 NT2RM2 Homo sapiens cDNA clone NT2RM2001609 5'
8659	21627	35047	1.09	2.0E-50	AB038162.1	NT	Homo sapiens TFF gene cluster for trefoil factor, complete cds
8659	21627	35048	1.09	2.0E-50	AB038162.1	NT	Homo sapiens TFF gene cluster for trefoil factor, complete cds
8789	21766	35189	6.78	2.0E-50	X06956.1	NT	Human HALPHA44 gene for alpha-tubulin, exons 1-3
8789	21768	35190	6.78	2.0E-50	X06956.1	NT	Human HALPHA44 gene for alpha-tubulin, exons 1-3
10244	23169	36657	1.43	2.0E-50	9910293	NT	Mus musculus keratin complex 2, gene 6g (Kt2-6g), mRNA
10244	23169	36658	1.43	2.0E-50	9910293	NT	Mus musculus keratin complex 2, gene 6g (Kt2-6g), mRNA
11971	24849		1.52	2.0E-50	AF023861.1	NT	Macaca mulatta cyclophilin A mRNA, complete cds
462	13535	28461	2.26	1.0E-50	AL163209.2	NT	Homo sapiens chromosome 21 segment HS21C009
2373	15381		9.27	1.0E-50	AJ271735.1	NT	Homo sapiens Xq pseudautosomal region; segment 1/2
7970	20909		0.55	1.0E-50	AJ271735.1	NT	Homo sapiens Xq pseudautosomal region; segment 1/2
10553	23475	36870	0.97	1.0E-50	D11078.1	NT	Homo sapiens RGH2 gene, retrovirus-like element
6095	19174	32390	1.01	9.0E-51	AW511225.1	EST_HUMAN	h444e02.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2912378 3' similar to TR:O95636
6350	19419	32660	0.71	9.0E-51	AA744837.1	EST_HUMAN	O95636 CAMP-REGULATED GUANINE NUCLEOTIDE EXCHANGE FACTOR II ;
9020	21986	35407	0.55	9.0E-51	AJ791154.1	EST_HUMAN	ny67h03.s1 NCL_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1283381 3'
9678	22632	36088	1.2	9.0E-51	AA043738.1	EST_HUMAN	ab23g04.x5 Stratagene lung (#937210) Homo sapiens cDNA clone IMAGE:841686 3' similar to
9658	22794	36245	0.52	9.0E-51	AJ791154.1	EST_HUMAN	SW:PSM_HUMAN Q04609 PROSTATE-SPECIFIC MEMBRANE ANTIGEN ;
9658	22794	36246	0.52	9.0E-51	AJ791154.1	EST_HUMAN	ab23g04.x5 Stratagene lung (#937210) Homo sapiens cDNA clone IMAGE:486352 5'
11804	23959	37483	1.5	9.0E-51	H89078.1	EST_HUMAN	SW:PSM_HUMAN Q04609 PROSTATE-SPECIFIC MEMBRANE ANTIGEN ;
11804	23959	37484	1.5	9.0E-51	H89078.1	EST_HUMAN	ab23g04.x5 Stratagene lung (#937210) Homo sapiens cDNA clone IMAGE:841686 3' similar to
4599	17620	30513	6.51	8.0E-51	AA610842.1	EST_HUMAN	SW:PSM_HUMAN Q04609 PROSTATE-SPECIFIC MEMBRANE ANTIGEN ;
7914	20857	34245	2.04	8.0E-51	11439587	NT	ab23g04.x5 Stratagene lung (#937210) Homo sapiens cDNA clone IMAGE:253210 5'
9819	22668		0.96	8.0E-51	AU138590.1	EST_HUMAN	SW:PSM_HUMAN Q04609 PROSTATE-SPECIFIC MEMBRANE ANTIGEN ;
							ny24g06.r1 Morton Fetal Cochlea Homo sapiens cDNA clone IMAGE:253210 5'
							ny24g06.r1 Morton Fetal Cochlea Homo sapiens cDNA clone IMAGE:253210 5'
							np98e09.s1 NCL_CGAP_Lu1 Homo sapiens cDNA clone IMAGE:1142440 3' similar to gb:U12671_mat
							HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN A1 (HUMAN);
							Homo sapiens PDZ-73 protein (PDZ-73/NY-CO-38), mRNA
							AU138590 PLACE1 Homo sapiens cDNA clone PLACE1008887 5'

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3295	16348	29268	1.68	7.0E-51	AW89219.1	EST_HUMAN	QV4NT0028-200400-180-d05 NT0028 Homo sapiens cDNA
3374	16424	29349	0.72	7.0E-51	AW274720.1	EST_HUMAN	xr34a03.x1 NC1_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2695564 3' similar to TR:Q92340
4196	17227	30116	1.4	7.0E-51	AL079928.1	EST_HUMAN	Q92340 A TYPICAL PKC SPECIFIC BINDING PROTEIN. ;
4196	17227	30117	1.4	7.0E-51	AL079928.1	EST_HUMAN	DKFZp434B2229_r1 434 (synonym: hies3) Homo sapiens cDNA clone DKFZp434B2229 5'
4378	17406	30286	1.54	7.0E-51	AW295603.1	EST_HUMAN	DKFZp434B2229_r1 434 (synonym: hies3) Homo sapiens cDNA clone DKFZp434B2229 5'
11993	24870	38466	2.13	7.0E-51	AF161449.1	NT	U1H-BW0-alp-b-05-o-U1.st NC1_CGAP_Sub6 Homo sapiens cDNA clone IMAGE:2729817 3'
1530	14563	27534	0.91	6.0E-51	6678763	NT	Homo sapiens HSPC331 mRNA, partial cds
							Homo sapiens putative DNA binding protein (M96), mRNA
1996	15017	28024	5.54	6.0E-51	7657266	NT	Homo sapiens KIAA0929 protein Mx2 interacting nuclear target (MINT) homolog (KIAA0929), mRNA
3487	16533	29458	17.23	6.0E-51	7657266	NT	Homo sapiens KIAA0929 protein Mx2 interacting nuclear target (MINT) homolog (KIAA0929), mRNA
4338	17365	30247	0.69	6.0E-51	9910553	NT	Homo sapiens solute carrier family 2 (facilitated glucose transporter), member 9 (SLC2A9), mRNA
4338	17365	30248	0.69	6.0E-51	9910553	NT	Homo sapiens solute carrier family 2 (facilitated glucose transporter), member 9 (SLC2A9), mRNA
6105	19184	32403	2.8	6.0E-51	X01788.1	NT	Human haptoglobin related (Hpr) gene exon 3
6116	19194	32417	8.29	6.0E-51	AF070083.1	NT	Homo sapiens mitogen-activated protein kinase kinase 1 (MKK4) gene, exon 4
6116	19194	32418	8.29	6.0E-51	AF070083.1	NT	Homo sapiens mitogen-activated protein kinase kinase 1 (MKK4) gene, exon 4
6925	20149	33469	1.13	6.0E-51	4806736	NT	Homo sapiens ribosomal protein S6 kinase, 70kD, polypeptide 1 (RPS6KB1) mRNA
7076	20098	33408	1.03	6.0E-51	11416751	NT	Homo sapiens non-kinase Cdc42 effector protein SPEC2 (LOC66990), mRNA
7157	18389	31233	2.29	6.0E-51	11428665	NT	Homo sapiens cerebral cell adhesion molecule (LOC61148), mRNA
9492	22456	35895	0.62	6.0E-51	11428525	NT	Homo sapiens hypothetical protein FLJ11042 (FLJ11042), mRNA
9492	22456	35896	0.62	6.0E-51	11428525	NT	Homo sapiens hypothetical protein FLJ11042 (FLJ11042), mRNA
10042	22669	36436	2.04	6.0E-51	7661535	NT	Homo sapiens B9 protein (B9), mRNA
10120	23046	36525	1.14	6.0E-51	U50093.1	NT	Human ankyrin (ANK1) gene, exon 2
11585	24523	38078	1.56	6.0E-51	11526289	NT	Homo sapiens Interleukin 17 receptor (IL17R), mRNA
792	13851	26798	8.57	6.0E-51	AL163203.2	NT	Homo sapiens chromosome 21 segment HS21C003
804	13882	26812	1.9	5.0E-51	4507500	NT	Homo sapiens T-cell lymphoma invasion and metastasis 1 (TTAM1) mRNA
993	15866	26998	1.23	5.0E-51	AL133204.1	NT	Novel human gene mapping to chromosome X
1612	14844	27620	1.02	5.0E-51	5031980	NT	Homo sapiens 26S proteasome-associated pad1 homolog (POH1) mRNA
2599	15900	28619	7.72	5.0E-51	AJ007558.1	NT	Homo sapiens mRNA for nucleoporin 155
3965	17005	29919	1.85	5.0E-51	M30938.1	NT	Human Ku (p70/p80) subunit mRNA, complete cds
3965	17005	29920	1.85	5.0E-51	M30938.1	NT	Human Ku (p70/p80) subunit mRNA, complete cds
11610	24548	38108	4.07	5.0E-51	5803136	NT	Homo sapiens RNA binding motif protein 3 (RBM3), mRNA

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135	13240	26171	1.53	3.0E-51	AI587348.1	EST_HUMAN	tr81c09.x1 NCL CGAP_Pan1 Homo sapiens cDNA clone IMAGE:2224720 3' similar to gb:M26326
1180	14221	27177	3.31	3.0E-51	AI587348.1	EST_HUMAN	KERATIN, TYPE I CYTOSKELETAL 18 (HUMAN);
1940	14964	27961	1.09	3.0E-51	AA211296.1	EST_HUMAN	tr81c09.x1 NCL CGAP_Pan1 Homo sapiens cDNA clone IMAGE:2224720 3' similar to gb:M26326
4354	17381	30263	2.23	3.0E-51	AL159142.1	NT	KERATIN, TYPE I CYTOSKELETAL 18 (HUMAN);
							zc087001.s1 Stratagene hNT neuron (#937233) Homo sapiens cDNA clone IMAGE:649008 3'
							Novel human gene mapping to chromosome 22
7831	20779	34157	1.2	3.0E-51	R15914.1	EST_HUMAN	ye47c08.r1 Soares infant brain 1NIB Homo sapiens cDNA clone IMAGE:53233 5' similar to gb:M14123_cds4
9191	22157		4.32	3.0E-51	M29063.1	NT	RETROVIRUS-RELATED POLYPROTEIN (HUMAN); contains LTR5 repetitive element ;
9423	28008		0.46	3.0E-51	AW583777.1	EST_HUMAN	Human htrRNP C2 protein mRNA
12810	25435		1.36	3.0E-51	AF003528.1	NT	la04d06.y1 Human Pancreatic islets Homo sapiens cDNA 5'
							Homo sapiens X-linked anhidrotic ectodermal dysplasia protein gene (EDA), exon 2 and flanking repeat regions
366	13452	26380	1.19	2.0E-51	4507798	NT	Homo sapiens ubiquitin protein ligase E3A (human papilloma virus E6-associated protein, Angelman syndrome) (UBE3A) mRNA
689	13752	26678	0.66	2.0E-51	BE391063.1	EST_HUMAN	601285694F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3607463 5'
689	13752	26679	0.68	2.0E-51	BE391063.1	EST_HUMAN	601285694F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3607463 5'
1697	14727	27710	4.99	2.0E-51	AA233352.1	EST_HUMAN	z30a05.r1 Striatagene NT2 neuronal precursor 937230 Homo sapiens cDNA clone IMAGE:664890 5' similar to TR:G233226 G233226 RTVL-H PROTEIN, contains LTR7.3 LTR7 repetitive element ;
3745	16787	28699	2.46	2.0E-51	AI492415.1	EST_HUMAN	tr27g03.x1 NCL CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2131732 3'
4521	17546	30433	0.69	2.0E-51	AW137826.1	EST_HUMAN	UI-H-B1-adj-d-02-0-J1.s1 NCL CGAP_Sub3 Homo sapiens cDNA clone IMAGE:2716851 3'
5513	18613	31545	0.57	2.0E-51	AI732851.1	EST_HUMAN	ob34f09.x5 NCL CGAP_Kh5 Homo sapiens cDNA clone IMAGE:1325609 3' similar to SW:NME1_MOUSE
							P35436 GLUTAMATE [NM2A] RECEPTOR SUBUNIT EPSILON 1 PRECURSOR ;
5513	18613	31546	0.57	2.0E-51	AI732851.1	EST_HUMAN	ob34f09.x5 NCL CGAP_Kh5 Homo sapiens cDNA clone IMAGE:1325609 3' similar to SW:NME1_MOUSE
6131	19208	32433	4.17	2.0E-51	BE782015.1	EST_HUMAN	P35436 GLUTAMATE [NM2A] RECEPTOR SUBUNIT EPSILON 1 PRECURSOR ;
7531	20494		0.68	2.0E-51	AF218927.1	NT	601470446F1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:3873563 5'
7690	20848	34012	0.91	2.0E-51	7682349	NT	Homo sapiens diacylglycerol kinase Iota (DGK) gene, exon 23
9046	22012	35434	1.54	2.0E-51	BE901994.1	EST_HUMAN	Homo sapiens cell recognition molecule Caspr2 (KIA00888), mRNA
9046	22012	35435	1.54	2.0E-51	BE901994.1	EST_HUMAN	601676787F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3959613 5'
9389	22354	35785	0.97	2.0E-51	11037064	NT	601676787F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3959613 5'
							Homo sapiens disrupted in schizophrenia 1 (DISC1), mRNA
9870	22823	36276	1.35	2.0E-51	AI917078.1	EST_HUMAN	tr74e07.x1 NCL CGAP_G06 Homo sapiens cDNA clone IMAGE:2236980 3' similar to SW:TRKC_HUMAN
9902	22889	36350	5.78	2.0E-51	BE165980.1	EST_HUMAN	Q16288 NT-3 GROWTH FACTOR RECEPTOR PRECURSOR ;
							MR3-HT0487-150200-113-g01 HT0487 Homo sapiens cDNA

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Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9977	22904	36368	0.53	2.0E-51	AB007926.1	NT	Homo sapiens mRNA for KIAA0457 protein, partial cds
10799	23720	37223	1.54	2.0E-51	AV682474.1	EST_HUMAN	AV682474 GKB Homo sapiens cDNA clone GRBAGF05 5'
10838	23758	37258	1.14	2.0E-51	AA378559.1	EST_HUMAN	EST191296 Synovial sarcoma Homo sapiens cDNA 5' end
11655	18613	31545	7.03	2.0E-51	A1732851.1	EST_HUMAN	ab3409.x5 NCI_CGAP_Kid5 Homo sapiens cDNA clone IMAGE:1325609 3' similar to SW:NM1_MOUSE P35436 GLUTAMATE [NMMA] RECEPTOR SUBUNIT EPSILON 1 PRECURSOR ;
11655	18613	31546	7.03	2.0E-51	A1732851.1	EST_HUMAN	ab3409.x5 NCI_CGAP_Kid5 Homo sapiens cDNA clone IMAGE:1325609 3' similar to SW:NM1_MOUSE P35436 GLUTAMATE [NMMA] RECEPTOR SUBUNIT EPSILON 1 PRECURSOR ;
12122	24991	38592	2.3	2.0E-51	AA011698.1	EST_HUMAN	z103a01.11 Soares_fetal_liver_spleen_INFLS_S1 Homo sapiens cDNA clone IMAGE:429672 5'
12803	25430	31740	2	2.0E-51	11419159	NT	Homo sapiens myeloid/lymphoid or mixed-lineage leukemia (t(11q24) translocation) (MLL4), mRNA
114	13225	26149	8.48	1.0E-51	4503528	NT	Homo sapiens eukaryotic translation initiation factor 4A, isoform 1 (EIF4A1) mRNA
1491	14524		33.7	1.0E-51	AV742248.1	EST_HUMAN	AV742248 CB Homo sapiens cDNA clone CBFBCT12 5'
4437	17463	30352	0.99	1.0E-51	4759071	NT	Homo sapiens small inducible cytokine subfamily A (Cys-Cys), member 15 (SCYA15) mRNA
4437	17463	30353	0.99	1.0E-51	4759071	NT	Homo sapiens small inducible cytokine subfamily A (Cys-Cys), member 15 (SCYA15) mRNA
5463	18565	31476	3.94	1.0E-51	T18862.1	EST_HUMAN	b12056t Testis 1 Homo sapiens cDNA clone b12056
7911	20854	34242	0.98	1.0E-51	AI572532.1	EST_HUMAN	le39g02.x1 Soares_Nhi-MIPu_S1 Homo sapiens cDNA clone IMAGE:2089106 3'
8235	21204	34609	0.79	1.0E-51	BF434359.1	EST_HUMAN	7c98b02.x1 NCI_CGAP_Ov18 Homo sapiens cDNA clone IMAGE:3644091 3' similar to TR:P87892 P87892 PROTEASE ;
12073	28012		1.67	1.0E-51	AV760590.1	EST_HUMAN	AV760590 MDS Homo sapiens cDNA clone MDSB02 5'
12589	25283		5.29	9.0E-52	AA777621.1	EST_HUMAN	z196a07.s1 Soares_fetal_liver_spleen_INFLS_S1 Homo sapiens cDNA clone IMAGE:448500 3' similar to contains THR.B3 THR repetitive element ;
153	13266	26184	9.3	8.0E-52	AA720574.1	EST_HUMAN	rw21g02.s1 NCI_CGAP_GCB0 Homo sapiens cDNA clone IMAGE:1241138 3' similar to contains THR.B3 THR repetitive element ;
1495	14528	27500	1.77	8.0E-52	X84900.1	NT	H.sapiens mRNA for laminin-5, alpha3b chain
1662	14694	27669	2.98	8.0E-52	11968028	NT	Homo sapiens hypothetical protein FLJ13556 similar to N-myc downstream regulated 3 (FLJ13556), mRNA
1662	14694	27670	2.98	8.0E-52	11968028	NT	Homo sapiens hypothetical protein FLJ13556 similar to N-myc downstream regulated 3 (FLJ13556), mRNA
4019	14694	27669	6.44	8.0E-52	11968028	NT	Homo sapiens hypothetical protein FLJ13556 similar to N-myc downstream regulated 3 (FLJ13556), mRNA
4019	14694	27670	6.44	8.0E-52	11968028	NT	Homo sapiens hypothetical protein FLJ13556 similar to N-myc downstream regulated 3 (FLJ13556), mRNA
7760	20713	34082	0.69	8.0E-52	11416585	NT	Homo sapiens transforming growth factor, beta-induced, 68kD (TGFB1), mRNA
7760	20713	34083	0.69	8.0E-52	11416585	NT	Homo sapiens transforming growth factor, beta-induced, 68kD (TGFB1), mRNA

Table 4

Single Exon Probes Expressed In Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9367	22332	35762	1.55	7.0E-52	W56471.1	EST_HUMAN	zc59a06.r1 Scores_parathyroid_tumor_NHHPA Homo sapiens cDNA clone IMAGE:326678 5' similar to contains Alu repetitive element;
1191	14231		0.65	6.0E-52	BE072409.1	EST_HUMAN	QV3-BT0537-271299-049-407 BT0537 Homo sapiens cDNA
1703	14733	27715	3.37	6.0E-52	AF108907.1	NT	Homo sapiens S184 gene, partial cds; PS1 and hypothetical protein genes, complete cds; and S171 gene, partial cds
5816	18906	32089	1.06	6.0E-52	AI208784.1	EST_HUMAN	q044f04.x1 Scores_basile_NHT Homo sapiens cDNA clone IMAGE:1838047 3'
11643	24484	38037	1.63	6.0E-52	BE048172.1	EST_HUMAN	tz46h04.y1 NCL_CGAP_Brn52 Homo sapiens cDNA clone IMAGE:2291671 5' similar to SW:PGBM_MOUSE Q05793 BASEMENT MEMBRANE-SPECIFIC HEPARAN SULFATE PROTEOGLYCAN CORE PROTEIN PRECURSOR;
4488	17495	30383	1.8	5.0E-52	Z78898.1	NT	H. sapiens flow-sorted chromosome 6 HindIII fragment, SC6pA18H7
9747	22888	36144	0.47	5.0E-52	11437365	NT	Homo sapiens FSHD region gene 1 (FRG1), mRNA
1870	14702	27677	1.25	4.0E-52	AF257318.1	NT	Homo sapiens SH3-containing protein SH3GLB1 mRNA, complete cds
1803	14831	27818	1.15	4.0E-52	4758843	NT	Homo sapiens nucleoporin 155kD (NUP155) mRNA
4768	17789	30682	1	4.0E-52	AI768814.1	EST_HUMAN	w189b02.x1 NCL_CGAP_K112 Homo sapiens cDNA clone IMAGE:2400459 3'
5359	18464	31334	1.41	4.0E-52	4506132	NT	Homo sapiens phosphoribosyl pyrophosphate synthetase-associated protein 2 (PRPSAP2) mRNA
5359	18464	31335	1.41	4.0E-52	4506132	NT	Homo sapiens phosphoribosyl pyrophosphate synthetase-associated protein 2 (PRPSAP2) mRNA
7043	20885	34276	0.56	4.0E-52	11525731	NT	Homo sapiens RAD51-interacting protein (PIR51), mRNA
8373	21342	34753	2.33	4.0E-52	BE622032.1	EST_HUMAN	601440687F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3915836 5'
8879	21848	35268	6.18	4.0E-52	11417035	NT	Homo sapiens hydroxysteroid (17-beta) dehydrogenase 4 (HSD17B4), mRNA
12426	25194		3.05	4.0E-52	11418177	NT	Homo sapiens Ran GTPase activating protein 1 (RANGAP1), mRNA
12906	25488		4.73	4.0E-52	AB02059.1	NT	Homo sapiens DNA for Human P2X ₆ , complete cds
4119	17152		11.15	3.0E-52	11437042	NT	Homo sapiens hypothetical protein FLJ10675 (FLJ10675), mRNA
564	13634	26550	1.97	2.0E-52	M10976.1	NT	Human endogenous retroviral DNA (4-1), complete retroviral segment
564	13634	26551	1.97	2.0E-52	M10976.1	NT	Human endogenous retroviral DNA (4-1), complete retroviral segment
2030	15049	28064	1.43	2.0E-52	AB033075.1	NT	Homo sapiens mRNA for KIAA1249 protein, partial cds
2507	15510	28537	1.95	2.0E-52	BE207575.1	EST_HUMAN	bb66b07.y1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3030421 5' similar to gb:X16493 M.musculus mRNA for Zfp-1 zinc finger protein (MOUSE);
2746	15739		10.45	2.0E-52	BF677892.1	EST_HUMAN	602084710F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4248891 5'
5013	18027	30912	3.26	2.0E-52	AL137188.3	NT	Novel human gene mapping to chromosome 20, similar to membrane transporters
5049	18061	30939	0.98	2.0E-52	AI141802.1	EST_HUMAN	qa56a05.s1 Scores_NHMPu_S1 Homo sapiens cDNA clone IMAGE:1630784 3'
5049	18061	30940	0.98	2.0E-52	AI141802.1	EST_HUMAN	qa56a05.s1 Scores_NHMPu_S1 Homo sapiens cDNA clone IMAGE:1630784 3'
5788	18880	32062	3.71	2.0E-52	AW848041.1	EST_HUMAN	IL3-CT0214-231299-053-E12 CT0214 Homo sapiens cDNA
6503	19567	32819	1.7	2.0E-52	11141868	NT	Homo sapiens Interleukin 21 receptor (IL21R), mRNA
6872	18925	33221	1.04	2.0E-52	AB028004.1	NT	Homo sapiens mRNA for KIAA1081 protein, partial cds

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7129	20105	33416	0.73	2.0E-52	AI792146.1	EST_HUMAN	os45d12.y6 NCI_CGAP_Br2 Homo sapiens cDNA clone IMAGE:1608311 5'
8121	21058	34455	0.52	2.0E-52	5032158	NT	Homo sapiens transducin (beta)-like 1 (TBL1) mRNA
8121	21058	34456	0.52	2.0E-52	5032158	NT	Homo sapiens transducin (beta)-like 1 (TBL1) mRNA
9000	21966		11.69	2.0E-52	AF147880.1	NT	Macaca mulatta beta-tubulin mRNA, complete cds
9288	22254	35684	0.87	2.0E-52	AA778795.1	EST_HUMAN	zj45g05.s1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:453272 3'
9834	22883		1.05	2.0E-52		NT	Homo sapiens NADH dehydrogenase (ubiquinone) Fe-S protein 5 (15kD) (NADH-coenzyme Q reductase) (NDUFS5) mRNA
10474	23396	36893	6.19	2.0E-52	5730038	NT	Homo sapiens SET domain and mariner transposase fusion gene (SETMAR) mRNA
10474	23396	36894	6.19	2.0E-52	5730038	NT	Homo sapiens SET domain and mariner transposase fusion gene (SETMAR) mRNA
11538	24479	38029	3.09	2.0E-52	AI831462.1	EST_HUMAN	wj49c04.x1 NCI_CGAP_Lu19 Homo sapiens cDNA clone IMAGE:2406150 3' similar to contains THR.b2 THR repetitive element;
11538	24479	38030	3.09	2.0E-52	AI831462.1	EST_HUMAN	wj49c04.x1 NCI_CGAP_Lu19 Homo sapiens cDNA clone IMAGE:2406150 3' similar to contains THR.b2 THR repetitive element;
11551	24492	38048	2.73	2.0E-52	AV716377.1	EST_HUMAN	AV716377 DCB Homo sapiens cDNA clone DCBAIE03 5'
11690	24846		12.53	2.0E-52	W70280.1	EST_HUMAN	zj49g12.1 Soares_fetal_heart_NbHH19W Homo sapiens cDNA clone IMAGE:344038 5'
11839	24819		2.73	2.0E-52	11417990	NT	Homo sapiens LIM domain kinase 2 (LIMK2), mRNA
12231	25982	31300	18.5	2.0E-52	AW236297.1	EST_HUMAN	xt72e07.x1 NCI_CGAP_CML1 Homo sapiens cDNA clone IMAGE:2700036 3' similar to contains Alu repetitive element; contains element LTR2 repetitive element;
12633	25319		7.5	2.0E-52	AI808985.1	EST_HUMAN	wf67d05.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2360849 3' similar to TR:Q16859 Q16859 CARBOXYLESTERASE;
534	13605	26524	1.45	1.0E-52	AA634445.1	EST_HUMAN	zu75h12.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:743879 3'
1373	14407	27377	9.6	1.0E-52	4504026	NT	Homo sapiens glutamate-aminoligase (glutamine synthase) (GLUL) mRNA
2542	15544		2.17	1.0E-52	4502238	NT	Homo sapiens arylsulfatase D (ARSD), transcript variant 1, mRNA
3072	16129	29041	1.99	1.0E-52	S61070.1	NT	pol-reverse transcriptase homolog (retroviral element) [human, endogenous retroviral element RTVL-Hp1, Genomic, 660 nt]
5406	18509	31386	4.22	1.0E-52	M29426.1	NT	Human P-glycoprotein (MDR1) gene, exon 4
6533	19596	32859	2.4	1.0E-52	U38964.1	NT	Human PMS2 related (hPMSR2) gene, complete cds
7664	20623	33987	2.35	1.0E-52	X07282.1	NT	Human aldolase C gene for fructose-1,6-bisphosphate aldolase
8150	21087	34486	0.55	1.0E-52	U60017.1	NT	Homo sapiens basic transcription factor 2 p44 (btf2p44) gene, partial cds, neuronal apoptosis inhibitory protein (nailp) and survival motor neuron protein (smn) genes, complete cds
8808	21775		1.13	1.0E-52	AL163227.2	NT	Homo sapiens chromosome 21 segment HS21C027
9543	22506	35955	0.7	1.0E-52	AF078779.1	NT	Rattus norvegicus putative four repeat ion channel mRNA, complete cds
10947	23861		1.21	1.0E-52	AW020370.1	EST_HUMAN	df08g05.y1 Morton Fetal Cochlea Homo sapiens cDNA clone IMAGE:2483145 5'
10951	23871		1.14	1.0E-52	AL163202.2	NT	Homo sapiens chromosome 21 segment HS21C002

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Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
11117	24077	37601	1.84	1.0E-52	U48296.1	NT	Homo sapiens protein tyrosine phosphatase PTPCAAX1 (hPTPCAAX1) mRNA, complete cds
13114	25633	31608	1.3	1.0E-52	AB011399.1	NT	Homo sapiens gene for AF-6, complete cds
3805	16945	29752	0.9	9.0E-53	4506064	NT	Homo sapiens protein kinase, cAMP-dependent, regulatory, type II, beta (PRKAR2B) mRNA
4418	17445	30336	0.91	9.0E-53	AF001446.1	NT	Homo sapiens core binding factor alpha1 subunit (CBFA1) gene, exon 3
12477	25225		2.56	7.0E-53	BF238465.1	EST_HUMAN	601904771F1 NIH_MGC_54 Homo sapiens cDNA clone IMAGE:4132783 5'
12881	25868		6.21	7.0E-53	AI421782.1	EST_HUMAN	W4407.x1 NCL_CGAP_Brn23 Homo sapiens cDNA clone IMAGE:2099077 3' similar to contains THR.t1
5215	18224	31088	0.89	6.0E-53	BE295719.1	EST_HUMAN	THR repetitive element;
4126	17159	30047	3	5.0E-53	4758543	NT	60117576F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3530948 5'
12110	24980	38580	1.54	5.0E-53	BE729270.1	EST_HUMAN	Homo sapiens heterogeneous nuclear ribonucleoprotein C (C1/C2) (HNRPC) mRNA
12522	25253		1.67	5.0E-53	AW813563.1	EST_HUMAN	601561627F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3831175 5'
51	13171	26079	2.37	4.0E-53	AL163285.2	NT	RC3-ST0197-151099-011-g10 ST0197 Homo sapiens cDNA
51	13171	26080	2.37	4.0E-53	AL163285.2	NT	Homo sapiens chromosome 21 segment HS21C085
4859	17876	30764	1.11	4.0E-53	7705414	NT	Homo sapiens chromosome 21 segment HS21C085
9771	22712		0.62	4.0E-53	AI613037.1	EST_HUMAN	Homo sapiens hook1 protein (HOOK1), mRNA
10114	23040		0.71	4.0E-53	F13080.1	EST_HUMAN	U06H04.x1 NCL_CGAP_U18 Homo sapiens cDNA clone IMAGE:2278327 3'
11648	24489	38044	2.93	4.0E-53	BF128701.1	EST_HUMAN	HSC3ID041 normalized infant brain cDNA Homo sapiens cDNA clone c-3ld04
11548	24489	38045	2.93	4.0E-53	BF128701.1	EST_HUMAN	60181089F1 NIH_MGC_48 Homo sapiens cDNA clone IMAGE:4053977 5'
							60181096F1 NIH_MGC_48 Homo sapiens cDNA clone IMAGE:4053977 5'
							Homo sapiens DNA, DLEC1 to ORCTL4 gene region, section 1/2 (DLEC1, ORCTL3, ORCTL4 genes, complete cds)
2669	15666	28685	2.64	3.0E-53	AB026998.1	NT	
3744	16786	29698	1.01	3.0E-53	AW050836.1	EST_HUMAN	wz22c07.x1 Soares Dieckgraebe colon_NHCD Homo sapiens cDNA clone IMAGE:2555796 3'
5499	18599	31511	0.92	3.0E-53	AF001212.1	NT	Homo sapiens 26S proteasome subunit 9 mRNA, complete cds
6707	18802	31979	1.09	3.0E-53	11526297	NT	Homo sapiens MIL 1 protein (MIL1), mRNA
6318	19389	32629	0.95	3.0E-53	BE160025.1	EST_HUMAN	QV1-HT0412-280300-123-c04 HT0412 Homo sapiens cDNA
7305	20276	33613	0.98	3.0E-53	Y10388.3	NT	H. sapiens gtf gene
7305	20276	33614	0.98	3.0E-53	Y10388.3	NT	H. sapiens gtf gene
8647	21615	35037	12.56	3.0E-53	S72043.1	NT	GIF-growth inhibitory factor [human, brain, Genomic, 2015 nt]
9211	22177	35607	0.69	3.0E-53	10835090	NT	Homo sapiens bone morphogenetic protein 5 (BMP5), mRNA
9412	22377		9.53	3.0E-53	5801953	NT	Homo sapiens FGF1 oncogene partner (FOP), mRNA
458	13531		2.53	2.0E-53	AA366556.1	EST_HUMAN	EST177525 Pancreas tumor III Homo sapiens cDNA 5' end
2335	15346	28367	6.08	2.0E-53	U78027.1	NT	Homo sapiens Bruton's tyrosine kinase (BTK), alpha-D-galactosidase A (GLA), L44-like ribosomal protein (L44L) and FTP3 (FTP3) genes, complete cds
2543	15545		11.44	2.0E-53		NT	Homo sapiens ATPase, H+ transporting, lysosomal (vacuolar proton pump) 31kD; Vacuolar proton-ATPase, subunit E; V-ATPase, subunit E (ATP6E), mRNA

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Table 4
Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2736	15730	28744	1.17	2.0E-53	4757915	NT	Homo sapiens core-binding factor, runt domain, alpha subunit 2; translocated to, 1; cyclin D-related (CBFA2T1) mRNA
2736	15730	28745	1.17	2.0E-53	4757915	NT	Homo sapiens core-binding factor, runt domain, alpha subunit 2; translocated to, 1; cyclin D-related (CBFA2T1) mRNA
3232	16287	29209	1.46	2.0E-53	7705687	NT	Homo sapiens leucine aminopeptidase (LOC51056), mRNA
3259	16313	29234	0.8	2.0E-53	AF083622.1	NT	Homo sapiens dihydropyridine receptor alpha 2 subunit (CACNA2D1) gene, exon 6
4088	17122	30016	2.78	2.0E-53	M61873.1	NT	Human Kruppel-related DNA-binding protein (TF34) gene, partial cds
4520	17545	30432	1.23	2.0E-53	4508962	NT	Homo sapiens SKAP55 homologue (SKAP-HOM) mRNA
5193	18202	31074	0.96	2.0E-53	AL163281.2	NT	Homo sapiens chromosome 21 segment HS21C081
5193	18202	31075	0.96	2.0E-53	AL163281.2	NT	Homo sapiens chromosome 21 segment HS21C081
5500	18600	31512	3.33	2.0E-53	BF334740.1	EST_HUMAN	PM1-CT0396-170800-001-g03 CT0396 Homo sapiens cDNA
5500	18600	31513	3.33	2.0E-53	BF334740.1	EST_HUMAN	PM1-CT0396-170800-001-g03 CT0396 Homo sapiens cDNA
8203	21173	34583	1.13	2.0E-53	AW975598.1	EST_HUMAN	EST387707 MAGe resequences, MAGN Homo sapiens cDNA
8340	21309		0.61	2.0E-53	AA095652.1	EST_HUMAN	IS429 seq.F Human fetal heart, Lambda ZAP Express Homo sapiens cDNA 5'
9763	22704		15.48	2.0E-53	AW246676.1	EST_HUMAN	2822665.5prime NIH_MGC_7 Homo sapiens cDNA clone IMAGE:2822665 5'
1440	14473	27450	2	1.0E-53	AJ271736.1	NT	Homo sapiens Xq pseudautosomal region; segment 2/2
3421	16469	29389	1.29	1.0E-53	AB026988.1	NT	Homo sapiens DNA, DLEC1 to ORCTL4 gene region, section 1/2 (DLEC1, ORCTL3, ORCTL4 genes, complete cds)
5001	18015	30902	1.32	1.0E-53	BE296386.1	EST_HUMAN	601176726F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3531919 5'
6850	19903	33198	1.43	1.0E-53	BF364201.1	EST_HUMAN	GM4-NN1029-160800-543-e02 NN1029 Homo sapiens cDNA
7459	20425	33781	0.84	1.0E-53	BE012071.1	EST_HUMAN	RCS-BN1058-270400-031-D01 BN1058 Homo sapiens cDNA
8267	21236	34647	0.55	1.0E-53	AA249072.1	EST_HUMAN	I9571 seq.F Human fetal heart, Lambda ZAP Express Homo sapiens cDNA 5'
9444	22408	35945	13.12	1.0E-53	X79536.1	NT	H sapiens mRNA for hnRNP core protein A1
12105	24976	38574	3.08	1.0E-53	X98411.1	NT	H sapiens mRNA for myosin-IE
12105	24976	38575	3.08	1.0E-53	X98411.1	NT	H sapiens mRNA for myosin-IE
5375	25636	31353	5.13	9.0E-54	4508786	NT	Homo sapiens IQ motif containing GTPase activating protein 1 (IQGAP1) mRNA
208	13309	26236	1.73	8.0E-54	BE366785.1	EST_HUMAN	601272863F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3614031 5'
1852	14878	27874	2.4	8.0E-54	4504610	NT	Homo sapiens insulin-like growth factor 2 receptor (IGF2R) mRNA
6045	19127	32333	23.25	8.0E-54	6005700	NT	Homo sapiens ATP-binding cassette, sub-family A (ABC1), member 8 (ABCA8), mRNA
11962	24841	38434	1.67	8.0E-54	AW592568.1	EST_HUMAN	h44e05.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2934752 3'
11962	24841	38435	1.67	8.0E-54	AW592568.1	EST_HUMAN	h44e05.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2934752 3'
384	13497	26429	1.85	7.0E-54	AA812637.1	EST_HUMAN	at79c12.s1 Soares_testis_NHT Homo sapiens cDNA clone 1377046 3' similar to contains MER30.13 MER30 repetitive element;
1847	14873	27869	1.51	7.0E-54	Y16645.1	NT	Homo sapiens mRNA for monocyte chemotactic protein-2

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Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2215	15229	28252	4.54	7.0E-54	N27177.1	EST_HUMAN	yw68d12.s1 Soares_placenta_8to9weeks_2NbHP8tc9W Homo sapiens cDNA clone IMAGE:257399 3' similar to contains LTR7.L3 LTR7 repetitive element ;
10487	23409	36906	1.91	7.0E-54	11417222	NT	Homo sapiens similar to nuclear factor related to kappa B binding protein (H. sapiens) (LOC63182), mRNA qb67g03.x1 Soares_fetal_heart_NbHH19W Homo sapiens cDNA clone IMAGE:1705204 3' similar to contains ORF.11 ORF repetitive element ;
11623	24561		3.26	7.0E-54	AI160189.1	EST_HUMAN	Homo sapiens DNA for MICB, exon 4, 5 and partial cds
25	13145	26045	2.05	6.0E-54	AB003618.1	NT	Homo sapiens hypothetical protein DKFZp434M035 (DKFZp434M035), mRNA
385	13498	26430	0.67	6.0E-54	8922148	NT	Homo sapiens hypothetical protein DKFZp434M035 (DKFZp434M035), mRNA
385	13498	26431	0.67	6.0E-54	8922148	NT	Homo sapiens hypothetical protein DKFZp434M035 (DKFZp434M035), mRNA
3296	16349	29269	0.99	6.0E-54	8922148	NT	Homo sapiens hypothetical protein DKFZp434M035 (DKFZp434M035), mRNA
3546	16592	29517	0.96	6.0E-54	AL163247.2	NT	Homo sapiens chromosome 21 segment HS21C047
4030	17068	29969	1.48	6.0E-54	4802872	NT	Homo sapiens chloride channel 6 (CLCN6) mRNA
4489	17314	30402	0.78	6.0E-54	AV754746.1	EST_HUMAN	AV754746 TP Homo sapiens cDNA clone TPGAAC10 5'
4819	17836	30734	0.94	6.0E-54	AV724885.1	EST_HUMAN	AV724885 HTB Homo sapiens cDNA clone HTBACE02 5'
4880	17897	30786	1.95	6.0E-54	4805806	NT	Homo sapiens phosphatidylinositol 4-kinase, catalytic, alpha polypeptide (PIK4CA) mRNA
4909	17926		1.23	6.0E-54	Y09846.1	NT	H. sapiens shc pseudogene, p66 isoform
5035	17926		1.27	6.0E-54	Y09846.1	NT	H. sapiens shc pseudogene, p66 isoform
11771	23926	37446	1.6	6.0E-54	11433623	NT	Homo sapiens KIAA0071 protein (KIAA0071), mRNA
11771	23926	37447	1.6	6.0E-54	11433623	NT	Homo sapiens KIAA0071 protein (KIAA0071), mRNA
2160	15176	28197	3.75	5.0E-54	P51523	SWISSPROT	ZINC FINGER PROTEIN 84 (ZINC FINGER PROTEIN HPF2)
184	13284		319.6	4.0E-54	AF110103.1	NT	Tupala belangeri beta-actin mRNA, partial cds
957	14010	26963	29.88	4.0E-54	AA306764.1	EST_HUMAN	EST177696 Jurkat T-cells VI Homo sapiens cDNA 5' end similar to glyceraldehyde-3-phosphate dehydrogenase
1822	14849	27842	2.91	4.0E-54	D38521.1	NT	Human mRNA for KIAA0077 gene, partial cds
1822	14849	27843	2.91	4.0E-54	D38521.1	NT	Human mRNA for KIAA0077 gene, partial cds
3217	16272		1.03	4.0E-54	AI83086.1	EST_HUMAN	wid26d11.x1 Soares_NFL_T_GBC S1 Homo sapiens cDNA clone IMAGE:2329289 3' similar to TR:002711
7524	20488		0.68	4.0E-54	BE544889.1	EST_HUMAN	O02711 PRO-POL-DUTPASE POLYPROTEIN ;
83	13209	26133	13.65	3.0E-54	AA313487.1	EST_HUMAN	601075004F1 NIH_MGC_12 Homo sapiens cDNA clone IMAGE:3461017 5'
2632	15631		1.1	3.0E-54	AI908757.1	EST_HUMAN	EST185371 Colon carcinoma (HCC) cell line Homo sapiens cDNA 5' end
6007	19090	32290	1.52	3.0E-54	4502434	NT	IL-BT189-180399-007 BT189 Homo sapiens cDNA
7618	20579	33942	1.49	3.0E-54	AA844061.1	EST_HUMAN	Homo sapiens BMX non-receptor tyrosine kinase (BMX) mRNA
7619	20579	33943	1.49	3.0E-54	AA844061.1	EST_HUMAN	ai92c08.s1 Soares_parathyroid_tumor_NbHPA Homo sapiens cDNA clone IMAGE:1388270 3'
8081	21018	34418	0.51	3.0E-54	AI742622.1	EST_HUMAN	ai92c08.s1 Soares_NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:1388270 3'

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
11363	24312		4.82	3.0E-54	11434806	NT	Homo sapiens golgi autoantigen, golgin subfamily a, 5 (GOLGA5), mRNA
11423	24367	37902	3.55	3.0E-54	BF345600.1	EST_HUMAN	602018408F1 NCL_CGAP_Brn67 Homo sapiens cDNA clone IMAGE:4155121 5'
11696	24661	38239	2.11	3.0E-54	AA393382.1	EST_HUMAN	z707f12.1 Soares testis NHT Homo sapiens cDNA clone IMAGE:727727 5' similar to TR:G191315
12334	25134	31850	4.08	3.0E-54	AW654559.1	EST_HUMAN	G191315 ANDROGEN-DEPENDENT EXPRESSED PROTEIN.;
12380	25942		1.67	3.0E-54	AW748965.1	EST_HUMAN	EST356629 IMAGE resequences, MAGC Homo sapiens cDNA
643	13709	26629	6.22	2.0E-54	5031900	NT	RC1-BT0313-131199-011-b09 BT0313 Homo sapiens cDNA
1367	14401	27371	1.48	2.0E-54	4507164	NT	Homo sapiens killer cell lectin-like receptor subfamily G, member 1 (KLRG1), mRNA
1550	14583	27554	1.32	2.0E-54	AA655008.1	EST_HUMAN	Homo sapiens nuclear antigen Sp100 (SP100) mRNA
2546	15547	28570	1.04	2.0E-54	AW163175.1	EST_HUMAN	nt78a08.s1 NCL_CGAP_P3 Homo sapiens cDNA clone IMAGE:1204600 similar to contains element L1 repetitive element;
2608	16607	28631	1.45	2.0E-54	AL163210.2	NT	au2g03.y1 Schneider fetal brain 00004 Homo sapiens cDNA clone IMAGE:2783764 5' similar to SW:CUL1 HUMAN Q13616 CULLIN HOMOLOG 1;
2805	15964	28887	1.4	2.0E-54	AW057524.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C010 wy60b12.x1 Soares NSF_F8_gw_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:2552927 3' similar to TR:Q62084 Q62084 PHOSPHOLIPASE C NEIGHBORING;
3559	16605		5.43	2.0E-54	AA532925.1	EST_HUMAN	nj45g08.s1 NCL_CGAP_P18 Homo sapiens cDNA clone IMAGE:995488 similar to gb:X53777 60S RIBOSOMAL PROTEIN L23 (HUMAN);
4232	17261		1.73	2.0E-54	4502642	NT	Homo sapiens chaperonin containing T-complex subunit 6 (CCT6) mRNA
4470	17496		1.18	2.0E-54	AF208161.1	NT	Homo sapiens syncytin precursor, mRNA, complete cds
4914	17931	30822	0.99	2.0E-54	7706446	NT	Homo sapiens peptidylarginine deiminase type III (LOC51702), mRNA
5278	18284	31147	1.07	2.0E-54	4506962	NT	Homo sapiens SKAP55 homologue (SKAP-HOM) mRNA
5551	18648	31591	1.8	2.0E-54	4759069	NT	Homo sapiens small inducible cytokine subfamily A (Cys-Cys), member 14 (SCYA14) mRNA
5684	18779	31952	1.25	2.0E-54	BE047864.1	EST_HUMAN	tx3ct11.y1 NCL_CGAP_Brn52 Homo sapiens cDNA clone IMAGE:2291348 5'
5856	18946	32131	3.9	2.0E-54	11426657	NT	Homo sapiens KIAA0100 gene product (KIAA0100), mRNA
5961	19046	32245	10.03	2.0E-54	AB046811.1	NT	Homo sapiens mRNA for KIAA1591 protein, partial cds
5961	19046	32246	10.03	2.0E-54	AB046811.1	NT	Homo sapiens mRNA for KIAA1591 protein, partial cds
6814	19968	33157	0.77	2.0E-54	AF008915.1	NT	Homo sapiens EVI5 homolog mRNA, complete cds
6983	20206	33535	0.73	2.0E-54	AB023212.1	NT	Homo sapiens mRNA for KIAA0995 protein, partial cds
6983	20206	33536	0.73	2.0E-54	AB023212.1	NT	Homo sapiens mRNA for KIAA0995 protein, partial cds
7330	20301	33645	7.68	2.0E-54	11426544	NT	Homo sapiens neurofibromin 1 (neurofibromatosis, von Recklinghausen disease, Watson disease) (NF1), mRNA
9967	22914	36379	4.03	2.0E-54	AB001025.1	NT	Homo sapiens mRNA for brain tyrosine receptor, complete cds
10369	23292	36768	1.61	2.0E-54	11429127	NT	Homo sapiens Janus kinase 2 (a protein tyrosine kinase) (JAK2), mRNA
10480	23402	36899	0.88	2.0E-54	11416762	NT	Homo sapiens serologically defined colon cancer antigen 10 (SDCCAG10), mRNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10480	23402	36900	0.88	2.0E-54	11416762	NT	Homo sapiens serologically defined colon cancer antigen 10 (SDCCAG10), mRNA
12034	24910		4.31	2.0E-54	7557454	NT	Homo sapiens pascadillo (zebrafish) homolog 1, containing BRCT domain (PEST), mRNA
4492	17517		1.6	1.0E-54	BF316418.1	EST_HUMAN	801899230F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4128535 5'
9081	22047	35470					Homo sapiens similar to nuclear factor related to kappa B binding protein (H. sapiens) (LOC63182), mRNA
10815	23537	37035	0.51	1.0E-54	AA412409.1	EST_HUMAN	zu10a09.t1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:731464 5'
10815	23537	37036	0.51	1.0E-54	AA412409.1	EST_HUMAN	zu10a09.t1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:731464 5'
12998	25554		4.2	1.0E-54	ALU077341.1	EST_HUMAN	AU077341 Sugano cDNA library Homo sapiens cDNA clone Zr6C980 similar to 5'-end region of Human gamma-glutamyl transpeptidase mRNA, 5 end
10724	23648	37139	0.95	9.0E-55	BE081469.1	EST_HUMAN	QV2-BT0635-160400-143-112 BT0635 Homo sapiens cDNA
1318	14353		0.98	8.0E-55	Y07829.2	NT	Homo sapiens RFB30 gene for RING finger protein
1321	14356		2.63	8.0E-55	Y07829.2	NT	Homo sapiens RFB30 gene for RING finger protein
11528	24469		1.73	8.0E-55	AW409714.1	EST_HUMAN	fn02a02.x1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:2960907 5'
12390	25167		1.3	8.0E-55	BE327189.1	EST_HUMAN	hw08d06.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3182315 3' similar to TR:Q9Z1J8
1083	14127	27081	1.52	7.0E-55	R08346.1	EST_HUMAN	Q9Z1J8 45 KDA SECRETORY PROTEIN ; SP:C581_BOVIN P10897 CYTOCHROME ; yf26e04.t1 Soares_fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:127998 5' similar to xd76c02.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2603522 3' similar to TR:O60365
9156	22122		1.54	7.0E-55	AW103839.1	EST_HUMAN	Q60365 FOS3554.1 ;
9336	22499	35947	1.22	7.0E-55	AA889581.1	EST_HUMAN	ak28a11.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1407260 3'
9370	22532	35982	2.15	7.0E-55	AU139909.1	EST_HUMAN	AU139909 PLACE1 Homo sapiens cDNA clone PLACE1011576 5'
11544	24485	38038	8.31	7.0E-55	AI561056.1	EST_HUMAN	iq28f09.x1 NCI_CGAP_U11 Homo sapiens cDNA clone IMAGE:2210249 3'
11544	24485	38039	8.31	7.0E-55	AI561056.1	EST_HUMAN	iq28f09.x1 NCI_CGAP_U11 Homo sapiens cDNA clone IMAGE:2210249 3'
12135	25004		1.8	7.0E-55	H48714.1	EST_HUMAN	yq78d03.t1 Soares_fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:201893 5'
12966	25876		1.78	7.0E-55	H23396.1	EST_HUMAN	yml57g07.t1 Soares_fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:32444 5'
11843	24726	35313	1.85	6.0E-55	AB040934.1	NT	Homo sapiens mRNA for KIAA1501 protein, partial cds
1785	14814	27798	1.3	5.0E-55	AA704971.1	EST_HUMAN	zj95b09.s1 Soares_fetal liver spleen 1NFLS_S1 Homo sapiens cDNA clone IMAGE:462617 3'
1785	14814	27799	1.3	5.0E-55	AA704971.1	EST_HUMAN	zj95b09.s1 Soares_fetal liver spleen 1NFLS_S1 Homo sapiens cDNA clone IMAGE:462617 3'
6990	19747	33023	1.65	5.0E-55	4502240	NT	Homo sapiens arylsulfatase E (chondrodysplasia punctata 1) (ARSE), mRNA
6990	19747	33024	1.65	5.0E-55	4502240	NT	Homo sapiens arylsulfatase E (chondrodysplasia punctata 1) (ARSE), mRNA
7237	20268	33592	0.69	5.0E-55	7382477	NT	Homo sapiens Rho GTPase activating protein 6 (RHGAP6), transcript variant 5, mRNA
7513	20478	33839	0.68	5.0E-55	11434422	NT	Homo sapiens speckle-type POZ protein (SPOP), mRNA
8327	21296	34711	0.74	5.0E-55	11526491	NT	Homo sapiens BCL2-associated alphanogene (BAG1), mRNA
9399	22364	35796	2.57	5.0E-55	4506302	NT	Homo sapiens protein tyrosine phosphatase, receptor type, alpha polypeptide (PTPRA) mRNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9674	22627		1.9	5.0E-55	BE064386.1	EST_HUMAN	RC4-BT0310-110300-016-110 BT0310 Homo sapiens cDNA
10397	23319	36801	1.31	5.0E-55	AB014511.1	NT	Homo sapiens mRNA for KIA00611 protein, partial cds
10397	23319	36802	1.31	5.0E-55	AB014511.1	NT	Homo sapiens mRNA for KIA00611 protein, partial cds
10582	23504	36997	1.2	5.0E-55	5453765	NT	Homo sapiens tel (chicken)-like 2 (NELL2), mRNA
12419	25189		3.4	5.0E-55	11417972	NT	Homo sapiens pascadillo (zabrafish) homolog 1, containing BRCT domain (PES1), mRNA
57	15831	26088	1.49	4.0E-55	AW957984.1	EST_HUMAN	EST370064 MAGE resequences, MAGE Homo sapiens cDNA
673	13737	26664	31.1	4.0E-55	4826973	NT	Homo sapiens RNA binding motif protein, Y chromosome, family 1, member A1 (RBM1A1) mRNA
1517	14549		1.97	4.0E-55	BF061411.1	EST_HUMAN	715210.X1 Soares_NSF_F9_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:3390043 3' similar to contains L1 L3 L1 repetitive element
2040	15059	28078	1.04	4.0E-55	4506180	NT	Homo sapiens proteasome (prosome, macropain) subunit, alpha type, 2 (PSMA2) mRNA
2040	15059	28079	1.04	4.0E-55	4506180	NT	Homo sapiens proteasome (prosome, macropain) subunit, alpha type, 2 (PSMA2) mRNA
2097	15114	28134	8.73	4.0E-55	4503314	NT	Homo sapiens diacylglycerol kinase, gamma (90kD) (DGKG) mRNA
2097	15114	28135	8.73	4.0E-55	4503314	NT	Homo sapiens diacylglycerol kinase, gamma (90kD) (DGKG) mRNA
2319	15330	28354	2.05	4.0E-55	4507794	NT	Homo sapiens ubiquitin-conjugating enzyme E2 variant 1 (UBE2V1) mRNA
8887	21655		11	4.0E-55	AL163210.2	NT	Homo sapiens chromosome 21 segment HS21C010
11563	24503		2.89	4.0E-55	W28189.1	EST_HUMAN	43c5 Human retina cDNA randomly primed sublibrary Homo sapiens cDNA
12335	25135		3.84	4.0E-55	BF303941.1	EST_HUMAN	601886575F2 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4120338 5'
6751	19805	33086	0.78	3.0E-55	AA077158.1	EST_HUMAN	7803A09 Chromosome 7 Fetal Brain cDNA Library Homo sapiens cDNA clone 7B09A09
12271	25093		1.91	3.0E-55	BE178619.1	EST_HUMAN	PM1-HT0603-090300-001-g08 HT0603 Homo sapiens cDNA
13007	25560		1.9	3.0E-55	AL163284.2	NT	Homo sapiens chromosome 21 segment HS21C084
377	13461	26391	2.24	2.0E-55	X57147.1	NT	Human endogenous retrovirus pHE.1 (ERV9)
553	13623		1.59	2.0E-55	M10976.1	NT	Human endogenous retroviral DNA (4-1), complete retroviral segment
650	13716	26638	3.26	2.0E-55	4507296	NT	Homo sapiens syntaxin-binding protein 1 (STXB1) mRNA, and translated products
2970	16028	28951	1.02	2.0E-55	4507798	NT	Homo sapiens ubiquitin protein ligase E3a (human papilloma virus E6-associated protein, Angelman syndrome) (UBE3A) mRNA
4808	17825	30721	2.19	2.0E-55	BE719986.1	EST_HUMAN	GM1-HT0876-150800-357-g03 HT0876 Homo sapiens cDNA
7747	25689	34067	0.69	2.0E-55	AW501988.1	EST_HUMAN	U1-HF-BNO-aks-F06-Q-J1r1 NIH_MGC_50 Homo sapiens cDNA clone IMAGE:3078275 5'
9420	22385	35823	0.51	2.0E-55	BF224452.1	EST_HUMAN	h76h08.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:3134463 3'
9420	22385	35824	0.51	2.0E-55	BF224452.1	EST_HUMAN	h76h08.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:3134463 3'
9515	22478		6.16	2.0E-55	A1002836.1	EST_HUMAN	ans8h05.s1 Stratagene schizo brain S11 Homo sapiens cDNA clone IMAGE:1884185 3' similar to contains THR b2 THR repetitive element
9596	22558		0.78	2.0E-55	BE007959.1	EST_HUMAN	QV0-BN0147-280400-213-g08 BN0147 Homo sapiens cDNA
10607	23529	37024	0.43	2.0E-55	AI439401.1	EST_HUMAN	h03h08.x1 NCI_CGAP_Gaa4 Homo sapiens cDNA clone IMAGE:2140479 3'
11296	24246	37773	1.84	2.0E-55	AU119344.1	EST_HUMAN	AU119344 HEMBA1 Homo sapiens cDNA clone HEMBA1005683 5'

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF-SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
12113	24983	38584	1.51	2.0E-55	BE886059.1	EST_HUMAN	601507718F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3908076 5'
98	13212	26136	2.4	1.0E-55	4503060	NT	Homo sapiens mannose-6-phosphate receptor (cation dependent) (M6PR) mRNA
191	13282	26218	93.01	1.0E-55	U09823.1	NT	Oryctolagus cuniculus New Zealand white elongation factor 1 alpha (Rabelfa2) mRNA, complete cds
576	13645	26558	0.75	1.0E-55	A028718.1	EST_HUMAN	016509.X1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1644160 3'
1152	14194	27146	4.22	1.0E-55	AB020710.1	NT	Homo sapiens mRNA for KIAA0903 protein, partial cds
1967	14988	27990	1.65	1.0E-55	BE277861.1	EST_HUMAN	601120116F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:2967027 5'
1967	14988	27991	1.65	1.0E-55	BE277861.1	EST_HUMAN	601120116F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:2967027 5'
2333	15344		3.95	1.0E-55	8803174	NT	Homo sapiens SMA3 (SMA3), mRNA
2345	15824	28376	1.31	1.0E-55	AF000990.1	NT	Homo sapiens testis-specific Testis Transcript Y 1 (TTY1) mRNA, partial cds
2624	15527	28548	52.04	1.0E-55	X13111.1	NT	Human mRNA for HLA-A11E, a MHC class I molecule (major histocompatibility complex)
2561	15562	28580	4.62	1.0E-55	AB007868.2	NT	Homo sapiens mRNA for KIAA0406 protein, partial cds
2561	15562	28581	4.62	1.0E-55	AB007866.2	NT	Homo sapiens mRNA for KIAA0406 protein, partial cds
2619	15617	28641	4.76	1.0E-55	L54057.1	NT	Homo sapiens CLP mRNA, partial cds
2801	15793	28811	0.98	1.0E-55	AB033046.1	NT	Homo sapiens mRNA for KIAA1219 protein, partial cds
3420	16468	29388	0.96	1.0E-55	W28189.1	EST_HUMAN	43c5 Human retina cDNA randomly primed sublibrary Homo sapiens cDNA
4015	17054	29655	4.23	1.0E-55	AL163267.2	NT	Homo sapiens chromosome 21 segment HS21C067
4323	17352	30238	1.08	1.0E-55	AL163210.2	NT	Homo sapiens chromosome 21 segment HS21C010
4762	17782		1.21	1.0E-55	N77261.1	EST_HUMAN	y44g03.1T Soares fetal liver spleen cDNA clone IMAGE:245620 5'
4865	17882	30769	1.79	1.0E-55	AB037163.1	NT	Homo sapiens DSCR5b mRNA, complete cds
4865	17882	30770	1.79	1.0E-55	AB037163.1	NT	Homo sapiens DSCR5b mRNA, complete cds
5177	18186	31063	1.3	1.0E-55	8923126	NT	Homo sapiens hypothetical protein FLJ20126 (FLJ20126), mRNA
5575	18671	31634	0.56	1.0E-55	AF119856.1	NT	Homo sapiens PRO1851 mRNA, complete cds
6402	19470	32718	7	1.0E-55	11433048	NT	Homo sapiens hct domain and RLD 2 (HERC2), mRNA
6402	19470	32719	7	1.0E-55	11433048	NT	Homo sapiens hct domain and RLD 2 (HERC2), mRNA
7282	20015		0.66	1.0E-55	AF189420.1	NT	Homo sapiens F-box protein FBL4 (FBL4) mRNA, complete cds
8321	21290	34704	1.25	1.0E-55	11432994	NT	Homo sapiens discs, large (Drosophila) homolog 2 (chapsyn-110) (DLG2), mRNA
8321	21290	34705	1.25	1.0E-55	11432994	NT	Homo sapiens discs, large (Drosophila) homolog 2 (chapsyn-110) (DLG2), mRNA
8410	21379	34785	0.49	1.0E-55	11421649	NT	Homo sapiens SKAP65 homologue (SKAP-HOM), mRNA
8418	21387	34796	1.27	1.0E-55	AF224492.1	NT	Homo sapiens phospholipid scramblase 1 gene, complete cds
8418	21387	34797	1.27	1.0E-55	AF224492.1	NT	Homo sapiens phospholipid scramblase 1 gene, complete cds
11776	23931	37452	1.65	1.0E-55	U50950.1	NT	Human infant brain unknown product mRNA, complete cds
11795	23950	37471	1.58	1.0E-55	T10045.1	EST_HUMAN	seq1575 b4HB3MA Cdx8-HAP-F1 Homo sapiens cDNA clone b4HB3MA-COT8-HAP-F161 5' similar to similar to Chinese Hamster DHFR c-amplified protein mRNA

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Table 4
Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
11902	24783	38371	1.74	1.0E-55	10587821	NT	Homo sapiens DNA-binding protein (LOC56242), mRNA
7860	20551	33912	1.89	9.0E-56	BE379074.1	EST_HUMAN	60123702F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3609552 5'
2743	15737	28753	6.5	7.0E-56	H19834.1	EST_HUMAN	yt62g03.r1 Soares adult brain N265HB55Y Homo sapiens cDNA clone IMAGE:173044 5' similar to contains THR repetitive element ;
7902	20845	34229	2.13	7.0E-56	AW361213.1	EST_HUMAN	RC1-CT0252-231099-013-b07 CT0252 Homo sapiens cDNA
7902	20845	34230	2.13	7.0E-56	AW361213.1	EST_HUMAN	RC1-CT0252-231099-013-b07 CT0252 Homo sapiens cDNA
1701	14731	27713	1.99	5.0E-56	AW997712.1	EST_HUMAN	RC3-BN0053-170200-011-h01 BN0053 Homo sapiens cDNA
9516	22479	35923	0.61	5.0E-56	AW015507.1	EST_HUMAN	UIH-B10p-eau-a-05-o-UJ.st1 NCI CGAP Sub2 Homo sapiens cDNA
10754	23676	31309	1.7	5.0E-56	W28189.1	EST_HUMAN	43c5 Human retina cDNA randomly primed sublibrary Homo sapiens cDNA
12507	25930	31309	5.41	5.0E-56	H55099.1	EST_HUMAN	CHR220038 Chromosome 22 exon Homo sapiens cDNA clone C22_55 5'
30	13150	28049	12.5	4.0E-56	AF141349.1	NT	Homo sapiens beta-tubulin mRNA, complete cds
30	13150	28050	12.5	4.0E-56	AF141349.1	NT	Homo sapiens beta-tubulin mRNA, complete cds
2719	15713	28730	4.9	4.0E-56	4507728	NT	Homo sapiens tubulin, beta polypeptide (TUBB) mRNA
2719	15713	28731	4.9	4.0E-56	4507728	NT	Homo sapiens tubulin, beta polypeptide (TUBB) mRNA
2823	13598	26516	3.69	4.0E-56	AF003528.1	NT	Homo sapiens X-linked anhidrotic ectodermal dysplasia protein gene (EDA), exon 2 and flanking repeat regions
2843	15620	28644	1.16	4.0E-56	A1632488.1	EST_HUMAN	wb09f08.x1 NCI CGAP_G06 Homo sapiens cDNA clone IMAGE:2305191 3' similar to SW:DCOR_MUSPA P27119 ORNITHINE DECARBOXYLASE ;
2843	15620	28644	1.16	4.0E-56	A1632488.1	EST_HUMAN	wb09f08.x1 NCI CGAP_G06 Homo sapiens cDNA clone IMAGE:2305191 3' similar to SW:DCOR_MUSPA P27119 ORNITHINE DECARBOXYLASE ;
6387	19455	32700	5.85	4.0E-56	AF217508.1	NT	Homo sapiens uncharacterized bone marrow protein BM031 mRNA, complete cds
6387	19455	32701	5.85	4.0E-56	AF217508.1	NT	Homo sapiens uncharacterized bone marrow protein BM031 mRNA, complete cds
10872	23792	37293	3.94	4.0E-56	AF043349.1	NT	Homo sapiens lymphocyte-specific protein 1 (LSP1) gene, LSP1.7 allele, partial cds
11268	24220	37743	7.82	4.0E-56	A1498066.1	EST_HUMAN	tm65g12.x1 NCI CGAP_Bm25 Homo sapiens cDNA clone IMAGE:2163046 3'
11268	24220	37744	7.82	4.0E-56	A1498066.1	EST_HUMAN	tm65g12.x1 NCI CGAP_Bm25 Homo sapiens cDNA clone IMAGE:2163046 3'
1345	14380	27349	1.74	3.0E-56	8924029	NT	Homo sapiens hypothetical protein PRO1304 (PRO1304), mRNA
1779	14808	27794	0.99	3.0E-56	6912743	NT	Homo sapiens 5'-3' exoribonuclease 2 (XRN2), mRNA
3142	16199	29109	1.83	3.0E-56	AA325826.1	EST_HUMAN	EST28889 Cerebellum II Homo sapiens cDNA 5' end
3142	16199	29110	1.83	3.0E-56	AA325826.1	EST_HUMAN	EST28889 Cerebellum II Homo sapiens cDNA 5' end
3847	16887	29110	1.73	3.0E-56	AF055066.1	NT	Homo sapiens MHC class I region
3938	16878	29893	1.1	3.0E-56	BE393512.1	EST_HUMAN	601310203F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3631848 5'
4454	17480	30366	4.84	3.0E-56	AL163268.2	NT	Homo sapiens chromosome 21 segment HS21C068
4603	17624	30517	2.34	3.0E-56	5902085	NT	Homo sapiens superkiller viral-like activity 2 (S. cerevisiae homolog)-like (SKV2L), mRNA
4841	17858		1.81	3.0E-56	BE803572.1	EST_HUMAN	601438154F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:39223100 5'

Table 4

Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5787	18859	32038	1.64	3.0E-56	4759163	NT	Homo sapiens sparco/osteoneclin, cwov and kazal-like domains proteoglycan (testican) (SPOCK) mRNA
5787	18859	32039	1.64	3.0E-56	4759163	NT	Homo sapiens sparco/osteoneclin, cwov and kazal-like domains proteoglycan (testican) (SPOCK) mRNA
7058	20080	33389	5.05	3.0E-56	11421124	NT	Homo sapiens lysosomal-associated membrane protein 2 (LAMP2), mRNA
9168	22134	35560	5	3.0E-56	11418704	NT	Homo sapiens bone morphogenetic protein 5 (BMP5), mRNA
10172	23097	36577	1.12	3.0E-56	D83478.2	NT	Homo sapiens mRNA for KIAA0145 protein, partial cds
10849	23786	37265	1.63	3.0E-56	11434056	NT	Homo sapiens KIAA0317 gene product (KIAA0317), mRNA
11643	24580	38147	4.97	3.0E-56	5902013	NT	Homo sapiens nuclear pore complex interacting protein (NPIP), mRNA
11983	24960	38455	7.15	3.0E-56	U46900.1	NT	Homo sapiens NACP/alpha-synuclein gene, exon 5
11983	24960	38456	7.15	3.0E-56	U46900.1	NT	Homo sapiens NACP/alpha-synuclein gene, exon 5
12378	25160	31812	2.99	3.0E-56	11434876	NT	Homo sapiens caveolin 3 (CAV3), mRNA
12378	25160	31813	2.99	3.0E-56	11434876	NT	Homo sapiens caveolin 3 (CAV3), mRNA
525	13596		1.82	2.0E-56	AA199818.1	EST_HUMAN	zq52a08.st Stratagene neuroepithelium (#837231) Homo sapiens cDNA clone IMAGE:846206 3'
734	15849	26732	2.02	2.0E-56	BE084386.1	EST_HUMAN	RC4-BT0310-110300-015-f10 BT0310 Homo sapiens cDNA
734	15849	26733	2.02	2.0E-56	BE084386.1	EST_HUMAN	RC4-BT0310-110300-015-f10 BT0310 Homo sapiens cDNA
2392	15400	28425	1.22	2.0E-56	M26081.1	NT	Human cGMP phosphodiesterase alpha subunit (CGPR-A) mRNA, complete cds
2392	15400	28426	1.22	2.0E-56	M26081.1	NT	Human cGMP phosphodiesterase alpha subunit (CGPR-A) mRNA, complete cds
3001	16059	28978	1.52	2.0E-56	AB037835.1	NT	Homo sapiens mRNA for KIAA1414 protein, partial cds
3327	16378		1.71	2.0E-56	AB088881.1	NT	Homo sapiens gene for activin receptor type IIB, complete cds
3544	16590	29515	1.18	2.0E-56	AV703184.1	EST_HUMAN	AV703184 ADB Homo sapiens cDNA clone ADBCF10 5'
7297	20269	33604	1.24	2.0E-56	5730038	NT	Homo sapiens SET domain and mariner transposase fusion gene (SETMAR) mRNA
981	14032		1.28	1.0E-56	AF190930.1	NT	Macaca fascicularis protein tyrosine phosphatase (PRL-1) mRNA, complete cds
3698	16731	29842	2.08	1.0E-56	AW589833.1	EST_HUMAN	hg23c11.x1 NCI CGAP CG6 Homo sapiens cDNA clone IMAGE:2946452 3'
3698	16731	29843	2.08	1.0E-56	AW589833.1	EST_HUMAN	hg23c11.x1 NCI CGAP CG6 Homo sapiens cDNA clone IMAGE:2946452 3'
5071	18081	30962	1.22	1.0E-56	AI905162.1	EST_HUMAN	QV-BT077-130189-079 BT077 Homo sapiens cDNA
6995	20121	33435	0.56	1.0E-56	AW609820.1	EST_HUMAN	MR3-ST0203-180100-208-h02 ST0203 Homo sapiens cDNA
10315	23239		0.61	1.0E-56	AL163203.2	NT	Homo sapiens chromosome 21 segment HS21C003
10408	23330	36816	1.82	1.0E-56	AW845987.1	EST_HUMAN	RC2-CT0163-220989-001-E02 CT0163 Homo sapiens cDNA
626	13891		2.17	9.0E-57	AW860885.1	EST_HUMAN	QV-O-T00033-070300-162-h03 OT0033 Homo sapiens cDNA
11554	24494	38050	1.51	9.0E-57	AF228497.1	NT	Homo sapiens serine protease 17 (KLK4) gene, complete cds
11554	24494	38051	1.51	9.0E-57	AF228497.1	NT	Homo sapiens serine protease 17 (KLK4) gene, complete cds
11850	24733	38320	2.23	9.0E-57	AB020881.1	NT	Homo sapiens mRNA for cyclin B2, complete cds

Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
14	13134	26032	1.11	8.0E-57	8823349	NT	Homo sapiens hypothetical protein FLJ20371 (FLJ20371), mRNA
297	13391	26319	3.14	8.0E-57	AW816405.1	EST_HUMAN	QV4-ST0234-181199-037-005 ST0234 Homo sapiens cDNA
885	13940	26898	9.74	8.0E-57	AW264599.1	EST_HUMAN	xd05d10.x1 NCI_CGAP_Bm53 Homo sapiens cDNA clone IMAGE:2759251 3' similar to gb:U05875
1833	14860	27858	2.19	8.0E-57	AA496109.1	EST_HUMAN	INTERFERON-GAMMA RECEPTOR BETA CHAIN PRECURSOR (HUMAN);
4946	17862	30852	1.11	8.0E-57	4557630	NT	z51b12.1 Soares testis_NHT Homo sapiens cDNA clone IMAGE:757151 5'
5073	18083	30865	1.32	8.0E-57	BE299916.1	EST_HUMAN	Homo sapiens glutamate receptor, ionotropic, AMPA 4 (GRIA4) mRNA
5312	25849	31435	1.69	8.0E-57	11418185	NT	Homo sapiens aconitase 2, mitochondrial (ACO2), mRNA
6539	19601	32863	0.54	8.0E-57	AB020705.1	NT	Homo sapiens mRNA for KIAA0898 protein, partial cds
6808	19866	32841	12.66	8.0E-57	AB023177.1	NT	Homo sapiens mRNA for KIAA0960 protein, partial cds
6808	19866	32842	12.66	8.0E-57	AB023177.1	NT	Homo sapiens mRNA for KIAA0960 protein, partial cds
7682	20840	34003	0.71	8.0E-57	7662263	NT	Homo sapiens KIAA0716 gene product (KIAA0716), mRNA
8024	20961	34357	2.69	8.0E-57	AB020644.1	NT	Homo sapiens mRNA for KIAA0837 protein, partial cds
8024	20961	34358	2.69	8.0E-57	AB020644.1	NT	Homo sapiens mRNA for KIAA0837 protein, partial cds
10848	23768	37267	0.44	8.0E-57	11428710	NT	Homo sapiens paired box gene 5 (B-cell lineage specific activator protein) (PAX5), mRNA
11807	13134	26032	2.8	8.0E-57	8823349	NT	Homo sapiens hypothetical protein FLJ20371 (FLJ20371), mRNA
12088	24960	38557	1.67	8.0E-57	11431260	NT	Homo sapiens Ras suppressor protein 1 (RSU1), mRNA
12733	25386	31751	3.29	8.0E-57	11545732	NT	Homo sapiens SH3-domain binding protein 1 (SH3BP1), mRNA
12749	25386	31751	1.39	8.0E-57	11545732	NT	Homo sapiens SH3-domain binding protein 1 (SH3BP1), mRNA
3263	16317	29237	1.09	7.0E-57	7242168	NT	Homo sapiens NME7 (NME7), mRNA
3263	16317	29238	1.09	7.0E-57	7242168	NT	Homo sapiens NME7 (NME7), mRNA
3284	16338	29258	0.65	7.0E-57	6005979	NT	Homo sapiens Kruppel-like factor 8 (KLF8), mRNA
3891	16931	29840	2.63	7.0E-57	AF012872.1	NT	Homo sapiens phosphatidylinositol 4-kinase 230 (p4K230) mRNA, complete cds
3891	16931	29841	2.63	7.0E-57	AF012872.1	NT	Homo sapiens phosphatidylinositol 4-kinase 230 (p4K230) mRNA, complete cds
4816	17833	30731	1.03	7.0E-57	U11058.2	NT	Homo sapiens large conductance calcium- and voltage-dependent potassium channel alpha subunit (MaxK) mRNA, complete cds
13075	25884		3.96	5.0E-57	AJ217135.1	NT	Homo sapiens Xq pseudautosomal region; segment 1/2
3766	16908	29718	2.12	4.0E-57	AB026998.1	NT	Homo sapiens DNA, DLEC1 to ORCTL4 gene region, section 1/2 (DLEC1, ORCTL3, ORCTL4 genes, complete cds)
805	13863	26813	0.93	3.0E-57	4507798	NT	Homo sapiens ubiquitin protein ligase E3A (human papilloma virus E6-associated protein, Angelman syndrome) (UBE3A) mRNA
1334	14368		58.49	3.0E-57	AA230279.1	EST_HUMAN	nc13107.s1 NCI_CGAP_Prl Homo sapiens cDNA clone IMAGE:1008037 similar to SW:RS10_HUMAN
2400	15407	28431	0.95	3.0E-57	AA348335.1	EST_HUMAN	P46783 40S RIBOSOMAL PROTEIN S10.; EST164770 Hippocampus II Homo sapiens cDNA 5' end

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Table 4

Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2714	15708	28724	1.19	3.0E-57	BE676622.1	EST_HUMAN	753b10.x1 NCI_CGAP_CELL1 Homo sapiens cDNA clone IMAGE:3296443 3' similar to WP:Y47H8C.2 OE20263 ;
2714	15708	28725	1.19	3.0E-57	BE676622.1	EST_HUMAN	753b10.x1 NCI_CGAP_CELL1 Homo sapiens cDNA clone IMAGE:3296443 3' similar to WP:Y47H8C.2 OE20263 ;
3711	18754	28725	28.47	3.0E-57	AW853964.1	EST_HUMAN	RC3-CT0254-110300-027-q10 CT0254 Homo sapiens cDNA
6145	19220	32450	1.37	3.0E-57	11225608	NT	Homo sapiens angiotensin converting enzyme (peptidyl-dipeptidase A) 2 (ACE2), mRNA
6246	19319	32549	3.49	3.0E-57	BE796537.1	EST_HUMAN	601589896F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3944302 5'
8484	21462	34870	2.61	3.0E-57	W28130.1	EST_HUMAN	4216 Human retina cDNA randomly primed sublibrary Homo sapiens cDNA
8510	21478	34891	1.9	3.0E-57	11545798	NT	Homo sapiens hypothetical protein FLJ11656 (FLJ11656), mRNA
8510	21478	34892	1.9	3.0E-57	11545798	NT	Homo sapiens hypothetical protein FLJ11656 (FLJ11656), mRNA
8624	21592	35011	0.56	3.0E-57	11427757	NT	Homo sapiens KIAA0649 gene product (KIAA0649), mRNA
8772	21739	35160	0.86	3.0E-57	J05282.1	NT	Human farnesyl pyrophosphate synthetase mRNA, complete cds
9210	22176	35606	4.95	3.0E-57	AU117659.1	EST_HUMAN	AU117659 HEMBA1 Homo sapiens cDNA clone HEMBA1001010 5'
9605	22809	36060	0.7	3.0E-57	11545798	NT	Homo sapiens hypothetical protein FLJ11656 (FLJ11656), mRNA
9605	22809	36061	0.7	3.0E-57	11545798	NT	Homo sapiens hypothetical protein FLJ11656 (FLJ11656), mRNA
11254	24207	37729	2.96	3.0E-57	AW248374.1	EST_HUMAN	2820473.5prime NIH_MGC_7 Homo sapiens cDNA clone IMAGE:2820473 5'
12384	25951	31314	7.53	3.0E-57	W23871.1	EST_HUMAN	zb45d11.11 Soares fetal lung_NbHL10W Homo sapiens cDNA clone IMAGE:306549 5'
1500	14533	27504	1.05	2.0E-57	AF248219.1	NT	Homo sapiens SNARE protein kinase SNAK mRNA, complete cds
1500	14533	27505	1.05	2.0E-57	AF248219.1	NT	Homo sapiens SNARE protein kinase SNAK mRNA, complete cds
3452	16498		2.19	2.0E-57	AL163204.2	NT	Homo sapiens chromosome 21 segment HS21C004
3562	16608	29529	0.85	2.0E-57	R07702.1	EST_HUMAN	ye88h01.11 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:125809 5'
3562	16608	29530	0.85	2.0E-57	R07702.1	EST_HUMAN	ye88h01.11 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:125809 5'
3951	16991	29907	0.86	2.0E-57	BE073284.1	EST_HUMAN	MRO-BT0551-060300-103-503 BT0551 Homo sapiens cDNA
4538	17581	30448	6.88	2.0E-57	AL163283.2	NT	Homo sapiens chromosome 21 segment HS21C083
5139	18148	31027	1.74	2.0E-57	AL163206.2	NT	Homo sapiens chromosome 21 segment HS21C006
5751	18845		1.67	2.0E-57	AA016131.1	EST_HUMAN	ze31c05.11 Soares retina N2b4HR Homo sapiens cDNA clone IMAGE:360584 5' similar to contains L1.13 L1 repetitive element ;
6150	19225		32.23	2.0E-57	BF115266.1	EST_HUMAN	7n80704.x1 NCI_CGAP_OV18 Homo sapiens cDNA clone IMAGE:3570866 3' similar to contains TAR1.11 MER22 repetitive element ;
6283	19355	32551	0.7	2.0E-57	11431281	NT	Homo sapiens small inducible cytokine subfamily A (Cys-Cys), member 22 (SCYA22), mRNA
8978	21944	35368	1.02	2.0E-57	AF045452.1	NT	Homo sapiens cell-line KG1 transcriptional regulatory protein p64 mRNA, complete cds
10205	23130	36617	1.63	2.0E-57	AF057722.1	NT	Homo sapiens 17-beta-hydroxysteroid dehydrogenase IV (HSD17B4) gene, exons 3 and 4
11601	24539	38097	1.88	2.0E-57	11424084	NT	Homo sapiens hypothetical protein FLJ20041 (FLJ20041), mRNA
11601	24539	38098	1.88	2.0E-57	11424084	NT	Homo sapiens hypothetical protein FLJ20041 (FLJ20041), mRNA

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Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
11642	24579	38145	1.74	2.0E-57	AJ245503.1	NT	Homo sapiens partial mRNA for PEX5 related protein
11642	24579	38146	1.74	2.0E-57	AJ245503.1	NT	Homo sapiens partial mRNA for PEX5 related protein
2240	15284	28278	1.49	1.0E-57	AW503208.1	EST_HUMAN	UHF-BNO-akt-g-07-0-U1.1 NIH_MGC_50 Homo sapiens cDNA clone IMAGE:3078348 5'
9041	22007		4.47	1.0E-57	BE043031.1	EST_HUMAN	h32a08.x1 NCL CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3039062 3' similar to TR:O00246 O00246
							HYPOTHETICAL 9.3 KD PROTEIN ;
							h33306.x1 NCL CGAP_Kid12 Homo sapiens cDNA clone IMAGE:2875499 3' similar to contains THR.b3
							THR repetitive element ;
12537	25261		3.65	1.0E-57	AW470791.1	EST_HUMAN	EST11348 Uterus Homo sapiens cDNA 5' end
5760	18853	32033	1.01	9.0E-58	AA297847.1	EST_HUMAN	601309465F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3631000 5'
12785	25424	31738	2.37	9.0E-58	BE395081.1	EST_HUMAN	601445948F1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3850211 5'
591	13658		2.43	8.0E-58	BE868715.1	EST_HUMAN	h34507.x1 NCL CGAP_Ov23 Homo sapiens cDNA clone IMAGE:2220181 3' similar to TR:O15475 O15475
655	13721	26644	2.84	8.0E-58	AI798376.1	EST_HUMAN	UNNAMED HERV-H PROTEIN ;
							h34507.x1 NCL CGAP_Ov23 Homo sapiens cDNA clone IMAGE:2220181 3' similar to TR:O15475 O15475
655	13721	26645	2.84	8.0E-58	AI798376.1	EST_HUMAN	UNNAMED HERV-H PROTEIN ;
1874	14899	27897	1.98	8.0E-58	11434921	NT	Homo sapiens putative protein O-mannosyltransferase (POMT2), mRNA
1874	14899	27898	1.98	8.0E-58	11434921	NT	Homo sapiens putative protein O-mannosyltransferase (POMT2), mRNA
2987	18045		2.65	8.0E-58	7706132	NT	Homo sapiens DHHC1 protein (LOC51304), mRNA
7449	20415	33769	0.95	7.0E-58	BE661971.1	EST_HUMAN	601346704F1 NIH_MGC_8 Homo sapiens cDNA clone IMAGE:3887577 5'
							Homo sapiens MADS box transcription enhancer factor 2, polypeptide B (myocyte enhancer factor 2B)
11203	24157		4.96	7.0E-58	5174542	NT	(MEF2B) mRNA
11275	24227	37753	2.79	7.0E-58	AW504109.1	EST_HUMAN	UHF-BNO-ali-g-10-0-U1.1 NIH_MGC_50 Homo sapiens cDNA clone IMAGE:3079867 5'
11275	24227	37754	2.79	7.0E-58	AW504109.1	EST_HUMAN	UHF-BNO-ali-g-10-0-U1.1 NIH_MGC_50 Homo sapiens cDNA clone IMAGE:3079867 5'
2385	15393	28419	4.05	6.0E-58	AU130689.1	EST_HUMAN	AU130689 NT2RP3 Homo sapiens cDNA clone NT2RP3001263 5'
							TCAAP1E1219 Pediatric acute myelogenous leukemia cell (FAB M1) Baylor-HGSC project TCAA Homo sapiens cDNA clone TCAAP1219
2912	15970	28893	1.62	6.0E-58	BE242150.1	EST_HUMAN	TCAAP1E1219 Pediatric acute myelogenous leukemia cell (FAB M1) Baylor-HGSC project TCAA Homo sapiens cDNA clone TCAAP1219
2912	15970	28894	1.62	6.0E-58	BE242150.1	EST_HUMAN	sapiens cDNA clone TCAAP1219
6294	19368	32605	1.16	6.0E-58	AF106911.1	NT	Homo sapiens chemokine MIP-2 gamma (MIP-2 gamma) mRNA, complete cds
10872	23594	37091	1.02	6.0E-58	11434746	NT	Homo sapiens protein tyrosine phosphatase, non-receptor type 21 (PTPN21), mRNA
12629	25316		1.41	6.0E-58	11526291	NT	Homo sapiens hypothetical protein FLJ20454 (FLJ20454), mRNA
300	13394	26321	4.35	5.0E-58	4507334	NT	Homo sapiens synaptotagmin 1 (SYN1), mRNA
711	13773	26707	7.63	5.0E-58	BE763984.1	EST_HUMAN	RC4-NT0057-160600-016-b05 NT0057 Homo sapiens cDNA
1199	14239	27195	3.77	5.0E-58	AW797948.1	EST_HUMAN	CKX3-UM0043-240300-127-e07 UM0043 Homo sapiens cDNA
1199	14239	27196	3.77	5.0E-58	AW797948.1	EST_HUMAN	CKX3-UM0043-240300-127-e07 UM0043 Homo sapiens cDNA

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1200	14239	27195	3.1	5.0E-58	AW787948.1	EST_HUMAN	CM3-UM0043-240300-127-e07 UM0043 Homo sapiens cDNA
1200	14239	27196	3.1	5.0E-58	AW787948.1	EST_HUMAN	CM3-UM0043-240300-127-e07 UM0043 Homo sapiens cDNA
3334	16385	28306	3.85	5.0E-58	AA988183.1	EST_HUMAN	cr98a07.s1 NCL CGAP_Lu5 Homo sapiens cDNA clone IMAGE:1603908 3'
4287	17316	30195	0.86	5.0E-58	AI638745.1	EST_HUMAN	ts89e07.x1 NCL CGAP_GC6 Homo sapiens cDNA clone IMAGE:2239488 3' similar to SW:PRO2_ACACA P16984 PROFILIN II;
5710	18804		2.2	5.0E-58	11496282	NT	Homo sapiens placenta-specific 1 (PLAC1), mRNA
6302	19373	32812	5.97	5.0E-58	H23072.1	EST_HUMAN	ym51h07.r1 Soares infant brain 1N1B Homo sapiens cDNA clone IMAGE:52071 5'
6534	19597	32860	0.94	5.0E-58	AL163285.2	NT	Homo sapiens chromosome 21 segment HS21C085
6616	19673	32951	1.16	5.0E-58	11421330	NT	Homo sapiens apical protein, Xenopus laevis-like (APXL), mRNA
6945	20169	33492	0.7	5.0E-58	AF051334.1	NT	Homo sapiens ribin (NBS) mRNA, complete cds
6945	20169	33493	0.7	5.0E-58	AF051334.1	NT	Homo sapiens ribin (NBS) mRNA, complete cds
7313	20284	33625	0.8	5.0E-58	4885400	NT	Homo sapiens ribin (NBS) mRNA, complete cds
8302	21271	34683	7.52	5.0E-58	8922693	NT	Homo sapiens holocytochrome c synthase (cytochrome c heme-lyase) (HCCS) mRNA
8696	21664	35088	0.76	5.0E-58	AB046837.1	NT	Homo sapiens mRNA for KIAA1617 protein, partial cds
9695	22648	36103	1.34	5.0E-58	5231227	NT	Homo sapiens ribonuclease 6 precursor (RNASE6P) mRNA
9895	22848	36104	1.34	5.0E-58	5231227	NT	Homo sapiens ribonuclease 6 precursor (RNASE6P) mRNA
10216	23141	36629	1.01	5.0E-58	11430647	NT	Homo sapiens pre-mRNA splicing factor similar to S. cerevisiae Prp18 (PRP18), mRNA
10482	23404	36601	1.68	5.0E-58	AL163218.2	NT	Homo sapiens chromosome 21 segment HS21C018
10766	23687	37183	0.51	5.0E-58	AB014511.1	NT	Homo sapiens mRNA for KIAA0811 protein, partial cds
10766	23687	37184	0.51	5.0E-58	AB014511.1	NT	Homo sapiens mRNA for KIAA0811 protein, partial cds
12352	25878		2.17	5.0E-58	11528293	NT	Homo sapiens cat eye syndrome chromosome region, candidate 1 (CECR1), mRNA
12791	25904		1.48	5.0E-58	11428423	NT	Homo sapiens acetyl-Coenzyme A carboxylase alpha (ACACA), mRNA
13015	25565		2.08	5.0E-58	11418177	NT	Homo sapiens Ran GTPase activating protein 1 (RANGAP1), mRNA
373	13459	26388	1.85	4.0E-58	4502302	NT	Homo sapiens ATP synthase, H ⁺ -transporting, mitochondrial F1 complex, O subunit (oligomycin sensitivity conferring protein) (ATP5O) mRNA
797	13658	26803	1.42	4.0E-58	4504634	NT	Homo sapiens interleukin 10 receptor, beta (IL10RB), mRNA
1464	14497	27471	1.14	4.0E-58	4503648	NT	Homo sapiens coagulation factor IX (plasma thromboplastic component, Christmas disease, hemophilia B) (F9) mRNA
2639	15638	28661	2.02	4.0E-58	U36251.1	NT	Human beta-prime-adaptin (BAM22) gene, exon 3
3336	16387	29308	1.11	4.0E-58	D16470.1	NT	Human mRNA, Xq terminal portion
3753	16795	29706	1.02	4.0E-58	5031660	NT	Homo sapiens EGF-like repeats and discoidin-like domains 3 (EDIL3), mRNA
8120	21057	34454	0.89	4.0E-58	BE463857.1	EST_HUMAN	hy18a02.x1 NCL CGAP_GC6 Homo sapiens cDNA clone IMAGE:3197842 3'
11671	24607	38184	7.52	4.0E-58	11424059	NT	Homo sapiens E1B-55kDa-associated protein 5 (E1B-AP5), mRNA
335	13424		0.84	3.0E-58	R17879.1	EST_HUMAN	yg10e02.r1 Soares infant brain 1N1B Homo sapiens cDNA clone IMAGE:31093 5'

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1380	14424	27393	2.32	3.0E-58	4758081	NT	Homo sapiens peptide YY (PYY) mRNA
3193	16248	29165	2.57	3.0E-58	BF569848.1	EST_HUMAN	602185789F1 NIH_MGC_45 Homo sapiens cDNA clone IMAGE:4309943 5'
3193	16248	29166	2.57	3.0E-58	BF569848.1	EST_HUMAN	602185789F1 NIH_MGC_45 Homo sapiens cDNA clone IMAGE:4309943 5'
6390	19458	32703	0.61	3.0E-58	BE09509.1	EST_HUMAN	QV0-BT0702-170400-194-09 BT0702 Homo sapiens cDNA
6587	19647	32916	0.79	3.0E-58	F07056.1	EST_HUMAN	HSC1T0081 normalized infant brain cDNA Homo sapiens cDNA clone c-1g08
6797	19851	33136	3.92	3.0E-58	AV712977.1	EST_HUMAN	AV712977 DCA Homo sapiens cDNA clone DCAA2G04 5'
939	13992	26944	8.85	2.0E-58	AF068624.1	NT	Homo sapiens 5-aminolevulinic acid synthase 2 (ALAS2) gene, complete cds
							ba08007.v1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:2823733 5' similar to gb:X69391.60S RIBOSOMAL PROTEIN L6 (HUMAN); gb:X81987 M.musculus mRNA for TAX responsive element binding protein (MOUSE);
1294	14329		8.41	2.0E-58	BE208532.1	EST_HUMAN	xa08a09.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2567704 3'
5409	18512	31390	0.75	2.0E-58	AW074931.1	EST_HUMAN	601499961F1 NIH_MGC_70 Homo sapiens cDNA clone IMAGE:3901911 5'
5431	25638	31413	3.25	2.0E-58	BE907186.1	EST_HUMAN	601499961F1 NIH_MGC_70 Homo sapiens cDNA clone IMAGE:3901911 5'
5431	25638	31441	3.25	2.0E-58	BE907186.1	EST_HUMAN	601499961F1 NIH_MGC_70 Homo sapiens cDNA clone IMAGE:3901911 5'
6175	19250	32483	1.09	2.0E-58	BF513488.1	EST_HUMAN	U1-H-BW1-ams-g-11-o-U1.s1 NCI_CGAP_Sub7 Homo sapiens cDNA clone IMAGE:3071060 3'
							am57e02.x1 Johnston frontal cortex Homo sapiens cDNA clone IMAGE:1539674 3' similar to WP:ZK328.1 CE05065 UBIQUITIN CONJUGATING ENZYME; RECOVERIN SUBFAMILY OF EF-HAND CALCIUM BINDING PROTEIN ;
6244	19317	32547	1.85	2.0E-58	A124874.1	EST_HUMAN	Y08H06.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:196379 5'
6278	19350	32584	0.83	2.0E-58	R92567.1	EST_HUMAN	qm84c01.x1 NCI_CGAP_Lu5 Homo sapiens cDNA clone IMAGE:1895424 3'
7112	20046	33348	0.83	2.0E-58	A1291407.1	EST_HUMAN	Homo sapiens endocytic receptor Endo180 (ENDO180) mRNA, complete cds
7364	20334	33683	2.68	2.0E-58	AF134838.1	NT	Homo sapiens endocytic receptor Endo180 (ENDO180) mRNA, complete cds
7364	20334	33684	2.68	2.0E-58	AF134838.1	NT	Homo sapiens endocytic receptor Endo180 (ENDO180) mRNA, complete cds
11093	24053	37576	18.24	2.0E-58	BF307745.1	EST_HUMAN	601890812F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4131891 5'
11312	24262	37788	1.48	2.0E-58	AW672641.1	EST_HUMAN	hm25f08.x1 NCI_CGAP_Thy4 Homo sapiens cDNA clone IMAGE:30719671 3'
723	13785	28719	0.68	1.0E-58	M65134.1	NT	Human complement component C5 mRNA, 3' end
							Homo sapiens NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 9 (22kD, B22) (NDUFB9), mRNA
1089	14114	27084	5.86	1.0E-58	6274549	NT	EST369252 MAGC resequences; MAGD Homo sapiens cDNA
1330	14365	27333	2.03	1.0E-58	AW957182.1	EST_HUMAN	EST369252 MAGC resequences; MAGD Homo sapiens cDNA
1330	14365	27334	2.03	1.0E-58	AW957182.1	EST_HUMAN	EST369252 MAGC resequences; MAGD Homo sapiens cDNA
1397	14431	27400	0.98	1.0E-58	AJ238093.1	NT	Homo sapiens partial AF-4 gene, exons 2 to 7 and Alu repeat elements
1672	14704	27681	0.95	1.0E-58	BE466132.1	EST_HUMAN	hy10f08.x1 NCI_CGAP_GC8 Homo sapiens cDNA clone IMAGE:3166935 3'
2814	15806	28825	1.21	1.0E-58	4758169	NT	Homo sapiens sterol regulatory element binding transcription factor 2 (SREBF2) mRNA
3548	16594	29520	1.19	1.0E-58	4758081	NT	Homo sapiens chondroitin sulfate proteoglycan 2 (versican) (GSPG2) mRNA
3548	16594	29521	1.18	1.0E-58	4758081	NT	[Homo sapiens chondroitin sulfate proteoglycan 2 (versican) (GSPG2) mRNA
3733	16775	29687	0.7	1.0E-58	4807628	NT	Homo sapiens transition protein 1 (during histone to protamine replacement) (TNPI1) mRNA

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Table 4
Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5008	18020	30908	5.17	1.0E-58	AI141063.1	EST_HUMAN	oz43h01.x1 Soares_NHMPu_S1 Homo sapiens cDNA clone IMAGE:1678129 3'
5941	19027	32221	1.18	1.0E-58	BE081880.1	EST_HUMAN	RC1-BT0254-290100-015-e01 BT0254 Homo sapiens cDNA
7046	20068	33374	0.64	1.0E-58	11422031	NT	Homo sapiens hypothetical protein (LOC51260), mRNA
8451	21420	35619	0.5	1.0E-58	AW973537.1	EST_HUMAN	EST385637 MAGE resequences, MAGM Homo sapiens cDNA
9221	22187	35619	0.59	1.0E-58	4505314	NT	Homo sapiens myomesin (M-protein) 2 (165KD) (MYOM2), mRNA
8033	22288	35727	0.94	1.0E-58	AV751001.1	EST_HUMAN	AV751001 NPC Homo sapiens cDNA clone NPCACH09 5'
9436	22400	35837	0.65	1.0E-58	AA412397.1	EST_HUMAN	z89f05.1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:730497 5'
9438	22400	35838	0.56	1.0E-58	AA412397.1	EST_HUMAN	z89f05.1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:730497 5'
10546	23468	36963	0.58	1.0E-58	11432994	NT	Homo sapiens discs, large (Drosophila) homolog 2 (chapsyn-110) (DLG2), mRNA
12059	24942		2.61	1.0E-58	X63392.1	NT	H. sapiens immunoglobulin kappa light chain variable region L14
2238	15262	28276	21.09	8.0E-59	4507378	NT	Homo sapiens TATA box binding protein (TBP), mRNA
7016	20141	33458	0.71	8.0E-59	AA382281.1	EST_HUMAN	EST195683 Testis I Homo sapiens cDNA 5' end
7015	20141	33459	0.71	8.0E-59	AA382291.1	EST_HUMAN	EST195683 Testis I Homo sapiens cDNA 5' end
8521	21489	34904	3.74	8.0E-59	AF161963.1	EST_HUMAN	wh50d06.x1 NCJ CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2384171 3'
179	15834		3.9	6.0E-59	BF035327.1	EST_HUMAN	gm81a04.s1 NCJ CGAP_Kid8 Homo sapiens cDNA clone IMAGE:3862086 5'
8151	21089	34489	1.64	6.0E-59	AA982431.1	EST_HUMAN	SA GENE PRODUCT PRECURSOR, ;
8588	21556	34972	0.56	6.0E-59	AF750970.1	EST_HUMAN	cn06h02.y1 Normal Human Trabecular Bone Cells Homo sapiens cDNA clone NHTBC_cn06h02 random
1768	14797	27782	1.19	5.0E-59	AW187281.1	EST_HUMAN	au63h05.x1 Schneider fetal brain 00004 Homo sapiens cDNA clone IMAGE:2783865 3' similar to
1768	14797	27783	1.19	5.0E-59	AW187281.1	EST_HUMAN	TR:075786 075786 GANGLIOSIDE-INDUCED DIFFERENTIATION ASSOCIATED PROTEIN 1.;
3144	16201	29112	7.03	5.0E-59	AI807484.1	EST_HUMAN	au63h05.x1 Schneider fetal brain 00004 Homo sapiens cDNA clone IMAGE:2783865 3' similar to
4687	17708	30601	7.38	5.0E-59	X83497.1	NT	TR:075786 075786 GANGLIOSIDE-INDUCED DIFFERENTIATION ASSOCIATED PROTEIN 1.;
5796	18888	32070	0.58	5.0E-59	6005698	NT	wf48c11.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2388836 3'
7182	18413	31215	7.91	5.0E-59	AW162304.1	EST_HUMAN	H. sapiens DNA for ZNF80-linked ERV9 long terminal repeat
9158	22124	36563	0.96	5.0E-59	11421778	NT	Homo sapiens ataxin 2 related protein (A2LP), mRNA
10093	22960	36459	1.64	5.0E-59	AV762869.1	EST_HUMAN	au66c07.x1 Schneider fetal brain 00004 Homo sapiens cDNA clone IMAGE:2781228 3' similar to contains element TAR1 repetitive element;
11253	24206	37728	3.1	5.0E-59	11434908	NT	Homo sapiens polymerase (RNA) III (DNA directed) (39KD) (RPC39), mRNA
794	13653	26801	3.22	4.0E-59	D80006.1	NT	AV762869 MDS Homo sapiens cDNA clone MDSEIC12 5'
1242	14278	27239	0.75	4.0E-59	4505818	NT	Homo sapiens hypothetical protein (LOC57143), mRNA
							Human mRNA for KIAA0184 gene, partial cds
							Homo sapiens phosphatidylinositol-4-phosphate 5-kinase, type II, beta (PIP5K2B) mRNA, and translated products

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1242	14278	27240	0.75	4.0E-59	4503818	NT	Homo sapiens phosphatidylinositol-4-phosphate 5-kinase, type II, beta (PIPSK2B) mRNA, and translated products
5615	18711	31869	1.04	4.0E-59	11034810	NT	Homo sapiens catenin (cadherin-associated protein), delta 2 (neural plakophilin-related arm-repeat protein) (CTNND2), mRNA
12107	24977	38578	1.5	4.0E-59	7657426	NT	Homo sapiens origin recognition complex, subunit 6 (yeast homolog)-like (ORC6L), mRNA
12492	25810		2.98	4.0E-59	AF057720.1	NT	Homo sapiens 17-beta-hydroxysteroid dehydrogenase IV (HSD17B4) gene, promoter region and exon 1
10	13130		6.6	3.0E-59	AW966524.1	EST_HUMAN	EST137582 IMAGE resequences, MAGI Homo sapiens cDNA
228	13327	26250	4.47	3.0E-59	7682247	NT	Homo sapiens KIAA0880 gene product (KIAA0880), mRNA
1723	14753	27738	11.42	3.0E-59	4505860	NT	Homo sapiens plasminogen activator, tissue (PLATa) mRNA
1723	14753	27739	11.42	3.0E-59	4605860	NT	Homo sapiens plasminogen activator, tissue (PLATa) mRNA
2139	15156	28171	6.05	3.0E-59	AB028035.1	NT	Homo sapiens mRNA for KIAA1112 protein, partial cds
2139	15156	28172	6.05	3.0E-59	AB028035.1	NT	Homo sapiens mRNA for KIAA1112 protein, partial cds
3146	16203	29116	2.91	3.0E-59	4602014	NT	Homo sapiens A kinase (PRKA) anchor protein 1 (AKAP1), mRNA
3146	16203	29117	2.91	3.0E-59	4602014	NT	Homo sapiens A kinase (PRKA) anchor protein 1 (AKAP1), mRNA
3838	16878	29781	1.26	3.0E-59	4508044	NT	Homo sapiens zona pellucida glycoprotein 2 (sperm receptor) (ZP2) mRNA
4712	17732	30826	1.4	3.0E-59	AL163284.2	NT	Homo sapiens chromosome 21 segment HS21C084
4878	17895	30785	1.66	3.0E-59	7427522	NT	Homo sapiens protein tyrosine phosphatase, receptor type, T (PTPRT), mRNA
5091	18101		1.05	3.0E-59	IG95961.1	NT	Human prothrombin converting enzyme (NEC2) gene, exon 2
6348	19415	32656	1.98	3.0E-59	8924074	NT	Homo sapiens hypothetical protein PRO1741 (PRO1741), mRNA
7584	20545	33906	2.12	3.0E-59	6454137	NT	Homo sapiens nuclear receptor co-repressor 1 (NCO1), mRNA
8263	21232	34842	1.5	3.0E-59	X12556.1	NT	Human mRNA for dbi proto-oncogene
8263	21232	34843	1.5	3.0E-59	X12556.1	NT	Human mRNA for dbi proto-oncogene
10404	23326	36909	0.84	3.0E-59	X70251.1	NT	H. sapiens CKII-alpha gene
10404	23326	36810	0.84	3.0E-59	X70251.1	NT	H. sapiens CKII-alpha gene
12470	25219		1.37	3.0E-59	11417866	NT	Homo sapiens gamma-glutamyltransferase-like activity 1 (GGTLA1), mRNA
12812	25311		7.97	3.0E-59	11417866	NT	Homo sapiens gamma-glutamyltransferase-like activity 1 (GGTLA1), mRNA
5985	19070	32268	0.82	2.0E-59	BF509383.1	EST_HUMAN	U1H-B14-ayb-b-02-Q-U1 st NCI CGAP SubB Homo sapiens cDNA clone IMAGE:3086522 3'
5985	19070	32269	0.82	2.0E-59	BF509383.1	EST_HUMAN	U1H-B14-ayb-b-02-Q-U1 st NCI CGAP SubB Homo sapiens cDNA clone IMAGE:3086522 3'
6979	20202		0.61	2.0E-59	AA470073.1	EST_HUMAN	289405 st Scores_testis NHT Homo sapiens cDNA clone IMAGE:730377 3'
7272	20007	33307	0.57	2.0E-59	AF135187.1	NT	Homo sapiens interferon-induced protein p78 (NX1) gene, complete cds
8082	21019		0.62	2.0E-59	BF373329.1	EST_HUMAN	MIR-F10144-250700-002-at10 F10144 Homo sapiens cDNA
9995	22922		4.9	2.0E-59	AA309774.1	EST_HUMAN	EST180833 Jurkat T-cells V Homo sapiens cDNA 5' end
10893	23813		1.55	2.0E-59	BE365454.1	EST_HUMAN	RCO-NT0036-1007003-032-a07 NT0036 Homo sapiens cDNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
11180	24136	37667	2.34	2.0E-59	AW410698.1	EST_HUMAN	h07h04.x1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:2961854 5'
11180	24136	37668	2.34	2.0E-59	AW410698.1	EST_HUMAN	h07h04.x1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:2961854 5'
12373	25158	31857	6.96	2.0E-59	AI631809.1	EST_HUMAN	wa38612.x1 NCL_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2300182 3' similar to TR:Q86542
12884	25836	31426	4.02	2.0E-59	L11645.1	NT	Q86542 RTVL-H PROTEIN, contains LTR7.b1 LTR7 repetitive element;
184	13267		18.92	1.0E-59	BE296411.1	EST_HUMAN	Homo sapiens alpha-tubulin mRNA, complete cds
2625	15624		3.89	1.0E-59	AA748468.1	EST_HUMAN	ca58h11.s1 NCL_CGAP_G081 Homo sapiens cDNA clone IMAGE:1308029 3' similar to TR:Q13537
7812	20761	34137	1.18	1.0E-59	AJ130894.1	NT	Q13537 MER37 TRANSPOSABLE ELEMENT, COMPLETE CONSENSUS SEQUENCE.;
7986	20925	34319	1.07	1.0E-59	BE266814.1	EST_HUMAN	Homo sapiens mRNA for transcription factor
7986	20925	34320	1.07	1.0E-59	BE266814.1	EST_HUMAN	601111951F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3352692 5'
9740	22768	36222	0.85	1.0E-59	11419630	NT	601111951F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3352692 5'
9993	22890	36351	0.54	1.0E-59	11428849	NT	Homo sapiens zinc finger protein 275 (ZNF275), mRNA
9993	22890	36352	0.54	1.0E-59	11428849	NT	Homo sapiens 3-hydroxybutyryl-Coenzyme A hydrolase (HIBCH), mRNA
11201	20761	34137	9.85	1.0E-59	AJ130894.1	NT	Homo sapiens 3-hydroxybutyryl-Coenzyme A hydrolase (HIBCH), mRNA
764	13824	26768	2.29	8.0E-60	AW977845.1	EST_HUMAN	Homo sapiens mRNA for transcription factor
1487	14500	27474	2.85	8.0E-60	4759159	NT	EST389849 IMAGE resequences, MAGO Homo sapiens cDNA
2182	15197	28217	2.65	8.0E-60	5174656	NT	Homo sapiens small nuclear ribonucleoprotein D3 polypeptide (18kD) (SNRPD3) mRNA
2182	15197	28218	2.65	8.0E-60	5174656	NT	Homo sapiens differentiation-related gene 1 (nickel-specific induction protein) (RTP) mRNA
6094	19173	32389	0.94	8.0E-60	AB029004.1	NT	Homo sapiens differentiation-related gene 1 (nickel-specific induction protein) (RTP) mRNA
6653	19710	32987	1.01	8.0E-60	S83182.1	NT	Homo sapiens mRNA for KIAA1081 protein, partial cds
7992	20903	34295	0.99	8.0E-60	11420841	NT	hyaluronan-binding protein=hepatocyte growth factor activator homolog [human, plasma, mRNA, 2408 nt]
8298	21267	34678	2.37	8.0E-60	X17033.1	NT	Homo sapiens phosphate cycidylyltransferase 1, choline, beta isoform (PCYT1B), mRNA
9291	22257	35687	2.68	8.0E-60	11428949	NT	Human mRNA for integrin alpha-2 subunit
9828	22875	36130	1.2	8.0E-60	11417118	NT	Homo sapiens S-antigen; retina and pineal gland (arrestin) (SAG), mRNA
9828	22875	36131	1.2	8.0E-60	11417118	NT	Homo sapiens KIAA0433 protein (KIAA0433), mRNA
10938	23858	37373	0.68	8.0E-60	5453997	NT	Homo sapiens KIAA0433 protein (KIAA0433), mRNA
11182	24138	37670	4.65	8.0E-60	AL163204.2	NT	Homo sapiens KIAA0433 protein (KIAA0433), mRNA
11182	24138	37671	4.65	8.0E-60	AL163204.2	NT	Homo sapiens RAN binding protein 7 (RANBP7), mRNA
755	13816	26760	30.34	7.0E-60	AF050666.1	NT	Homo sapiens chromosome 21 segment HS21C004
758	13816	26760	69.13	7.0E-60	AF050666.1	NT	Homo sapiens chromosome 21 segment HS21C004
816	13874	26822	1.17	7.0E-60	4504634	NT	Homo sapiens MHC class 1 region
2138	15155	28170	1.04	7.0E-60	AF077183.1	NT	Homo sapiens interleukin 10 receptor, beta (IL10RB), mRNA
							Homo sapiens cullin 4A (CUL4A) mRNA, complete cds

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Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2706	15788	28806	1.18	7.0E-60	AB011153.1	NT	Homo sapiens mRNA for KIAA0591 protein, partial cds
4208	17237	30124	3.1	7.0E-60	4505488	NT	Homo sapiens ornithine decarboxylase 1 (ODC1) mRNA
4606	17627	30519	0.72	7.0E-60	AF284750.1	NT	Homo sapiens ALR-like protein mRNA, partial cds
9762	22703	36161	3.69	7.0E-60	H6804.1	EST_HUMAN	y1204.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:205087 5' similar to contains LTR5 repetitive element;
11692	24657	38235	1.57	7.0E-60	H6804.1	EST_HUMAN	y1204.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:205087 5' similar to contains LTR5 repetitive element;
2189	15204	28224	1.01	6.0E-60	BE984974.2	EST_HUMAN	60165875R1 NIH_MGC_59 Homo sapiens cDNA clone IMAGE:3866069 3'
8156	21094	34493	0.56	6.0E-60	11421735	NT	Homo sapiens cAMP response element-binding protein CRE-BP a (H_GS169L15.1), mRNA
8780	21747		8.33	6.0E-60	H62458.1	EST_HUMAN	y47809.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:201953 5' similar to contains OFR repetitive element;
84	13200	26123	1.13	5.0E-60	A1807917.1	EST_HUMAN	wf52c07.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2359212 3'
84	13200	26124	1.13	5.0E-60	A1807917.1	EST_HUMAN	wf52c07.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2359212 3'
2244	15258	28284	1.25	4.0E-60	AW503208.1	EST_HUMAN	U1-HF-BNO-akt-g-07-0-U1.r1 NIH_MGC_50 Homo sapiens cDNA clone IMAGE:3078348 5'
2244	15258	28285	1.25	4.0E-60	AW503208.1	EST_HUMAN	U1-HF-BNO-akt-g-07-0-U1.r1 NIH_MGC_50 Homo sapiens cDNA clone IMAGE:3078348 5'
2984	16042		1.31	4.0E-60	AA299037.1	EST_HUMAN	EST11498 Uterus Homo sapiens cDNA 5' end similar to similar to retrovirus-related pol
7576	20538	33897	0.91	4.0E-60	BF195098.1	EST_HUMAN	hr81f05.x1 NCL CGAP_Kid11 Homo sapiens cDNA clone IMAGE:3134913 3' similar to SW:RHOP_MOUSE
9482	22446		0.59	4.0E-60	AL163278.2	NT	Homo sapiens chromosome 21 segment HS21C078
11628	24566	38127	1.7	4.0E-60	11433597	NT	Homo sapiens v-raf-1 murine leukemia viral oncogene homolog 1 (RAF1), mRNA
11628	24566	38128	1.7	4.0E-60	11433597	NT	Homo sapiens v-raf-1 murine leukemia viral oncogene homolog 1 (RAF1), mRNA
1876	14901	27900	4.44	3.0E-60	BE562611.1	EST_HUMAN	601336446F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3690395 5'
1876	14901	27901	4.44	3.0E-60	BE562611.1	EST_HUMAN	601336446F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3690395 5'
1885	14910		1.88	3.0E-60	6031190	NT	Homo sapiens prohibitin (PHB) mRNA
4485	17510	30398	2.27	3.0E-60	AJ271735.1	NT	Homo sapiens Xq pseudautosomal region; segment 1/2
5452	18564	31485	2.11	3.0E-60	BF365143.1	EST_HUMAN	QV4-NN1149-250900-423-f01 NN1149 Homo sapiens cDNA
5724	18818	31997	2.11	3.0E-60	AW838198.1	EST_HUMAN	RC3-LT0023-200100-012-a01 LT0023 Homo sapiens cDNA
7143	18375	31253	0.95	3.0E-60	A1792814.1	EST_HUMAN	ol60h11.y5 NCL CGAP_Kid3 Homo sapiens cDNA clone IMAGE:1634063 5' similar to SW:UDP_MOUSE
8745	21713	35135	5.22	3.0E-60	5174644	NT	P52824 URIDINE PHOSPHORYLASE;
8745	21713	35136	5.22	3.0E-60	5174644	NT	Homo sapiens proline dehydrogenase (proline oxidase) (PRODH) mRNA
8930	21896	35324	0.58	3.0E-60	A1040235.1	EST_HUMAN	Homo sapiens proline dehydrogenase (proline oxidase) (PRODH) mRNA
9094	22060	35485	4.2	3.0E-60	5174644	NT	ox66d09.x1 Soares_NHMPu_S1 Homo sapiens cDNA clone IMAGE:1660337 3' similar to SW:FORM_MOUSE Q05860 FORMIN;
							Homo sapiens proline dehydrogenase (proline oxidase) (PRODH) mRNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10017	22944	36411	0.42	3.0E-60	BF102612.1	EST_HUMAN	601646227F1 NIH_MGC_60 Homo sapiens cDNA clone IMAGE:3930980 6'
12970	25871		1.53	3.0E-60	AA485286.1	EST_HUMAN	ab07h04.11 Stragene lung (#37210) Homo sapiens cDNA clone IMAGE:840151 5' similar to contains LTR10.11 LTR10 repetitive element;
33	13153	26054	1.7	2.0E-60	AY008285.1	NT	Homo sapiens solute carrier (SLC25A18) mRNA, complete cds; nuclear gene for mitochondrial product
1421	14454	27428	2.76	2.0E-60	Z11694.1	NT	H. sapiens 41kDa protein kinase related to rat ERK2
1734	14764	27747	1.34	2.0E-60	M24603.1	NT	Human bcr protein mRNA, 5' end
1743	14773	27758	1.01	2.0E-60	AY008285.1	NT	Homo sapiens solute carrier (SLC25A18) mRNA, complete cds; nuclear gene for mitochondrial product
2492	15495	28520	1.76	2.0E-60	AW380450.1	EST_HUMAN	RC1-HT0268-031299-012-02 HT0268 Homo sapiens cDNA
2614	15612	28637	1.38	2.0E-60	7657229	NT	Homo sapiens interleukin 17 receptor (IL17R) mRNA
2721	15715	28733	0.84	2.0E-60	AW978005.1	EST_HUMAN	EST390114 IMAGE resequences; MAGO Homo sapiens cDNA
3592	16637	29557	1.49	2.0E-60	4757867	NT	Homo sapiens v-raf murine sarcoma viral oncogene homolog B1 (BRAF) mRNA
3935	16975	29889	0.83	2.0E-60	AF231919.1	NT	Homo sapiens chromosome 21 unknown mRNA
4151	17182		0.65	2.0E-60	BF513458.1	EST_HUMAN	U1-H-BW1-ams-e-05-0-JL.s1 NCL CGAP_Sub7 Homo sapiens cDNA clone IMAGE:3070952 3'
6433	19499	32752	0.9	2.0E-60	A1791952.1	EST_HUMAN	nm01112.y5 NCL CGAP_Co8 Homo sapiens cDNA clone IMAGE:1076495 5' similar to contains THR.11 THR repetitive element;
6640	19698	32974	1.49	2.0E-60	AF004877.1	NT	Homo sapiens pro-alpha 2(I) collagen (COL1A2) gene, complete cds
6874	19927	33224	0.92	2.0E-60	AF167476.1	NT	Homo sapiens DNA polymerase zeta catalytic subunit (REV3) mRNA, complete cds
7027	18359	31279	2.05	2.0E-60	4503044	NT	Homo sapiens corticotropin releasing hormone receptor 2 (CRHR2) mRNA
7027	18359	31280	2.05	2.0E-60	4503044	NT	Homo sapiens corticotropin releasing hormone receptor 2 (CRHR2) mRNA
7317	20288	33630	6.6	2.0E-60	AA311159.1	EST_HUMAN	EST181949 Jurkat T-cells V Homo sapiens cDNA 5' end similar to similar to prothymosin, alpha
7317	20288	33631	6.6	2.0E-60	AA311159.1	EST_HUMAN	EST181949 Jurkat T-cells V Homo sapiens cDNA 5' end similar to similar to prothymosin, alpha
7434	20401	33755	0.53	2.0E-60	A1308124.1	EST_HUMAN	tb23d09.x1 NCL CGAP_Kk12 Homo sapiens cDNA clone IMAGE:2055185 3' similar to SW:GALR_RAT
7894	20837		1.06	2.0E-60	BF512808.1	EST_HUMAN	Q62805 GALANIN RECEPTOR;
8338	21307	34722	1.09	2.0E-60	X85597.1	EST_HUMAN	U1-H-BW1-ams-c-02-0-JL.s1 NCL CGAP_Sub7 Homo sapiens cDNA clone IMAGE:3071210 3'
9219	22185	35618	4.86	2.0E-60	L36033.1	NT	HS1B8EST human adult testis Homo sapiens cDNA clone CAM_EST15
10337	23261	36740	2.2	2.0E-60	11991659	NT	Human pre-B cell stimulating factor homologue (SDF1b) mRNA, complete cds
10337	23261	36741	2.2	2.0E-60	11991659	NT	Homo sapiens sema domain, transmembrane domain (TM), and cytoplasmic domain, (semaphorin) 8A (SEMA6A) mRNA
12094	24965	38561	1.9	2.0E-60	AW751191.1	EST_HUMAN	Homo sapiens sema domain, transmembrane domain (TM), and cytoplasmic domain, (semaphorin) 8A (SEMA6A) mRNA
12094	24965	38562	1.9	2.0E-60	AW751191.1	EST_HUMAN	CN0-CT0013-290698-017-03 CT0013 Homo sapiens cDNA
							CN0-CT0013-290698-017-03 CT0013 Homo sapiens cDNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
12347	25330		1.38	2.0E-60	11418192	NT	Homo sapiens non-histone chromosome protein 2 (S. cerevisiae)-like 1 (NHP2L1), mRNA
12771	25800		1.82	2.0E-60	AF068757.1	NT	Homo sapiens somatostatin receptor subtype 3 (SSTR3) gene, 5' flanking region and partial cds
12773	25411		5.84	2.0E-60	11418068	NT	Homo sapiens similar to HSPC022 protein (H. sapiens) (LOC63504), mRNA
12789	25421		2.36	2.0E-60	AB011399.1	NT	Homo sapiens gene for AF-6, complete cds
523	13594	26512	0.97	1.0E-60	BE178566.1	EST_HUMAN	PM3-HT0605-270200-001-e06 HT0605 Homo sapiens cDNA
3920	16660	29873	1.46	1.0E-60	AU143389.1	EST_HUMAN	AU143389 Y79AA1 Homo sapiens cDNA clone Y79AA1001854 5'
4993	18008	30896	1.34	1.0E-60	AL163286.2	NT	Homo sapiens chromosome 21 segment HS21C085
8280	21249	34661	0.98	1.0E-60	BE064410.1	EST_HUMAN	RC4-BT0311-141199-011-h06 BT0311 Homo sapiens cDNA
9108	22074		3.08	1.0E-60	AA244041.1	EST_HUMAN	nc04612.1 NCL_CGAP_P1 Homo sapiens cDNA clone IMAGE:1007182 similar to contains L1.11 L1 repetitive element
9134	22100	35626	1.38	1.0E-60	AV754081.1	EST_HUMAN	AV754081 TP Homo sapiens cDNA clone TPGAED05 5'
1101	14145	27095	1.85	8.0E-61	AU119344.1	EST_HUMAN	AU119344 HEMBA1 Homo sapiens cDNA clone HEMBA1005583 5'
9061	22027	35450	0.46	9.0E-61	4885546	NT	Homo sapiens PHD finger protein 2 (PHF2) mRNA
9061	22027	35451	0.46	9.0E-61	4885546	NT	Homo sapiens PHD finger protein 2 (PHF2) mRNA
2678	15674	28694	1.17	8.0E-61	AW006478.1	EST_HUMAN	wf05b10.x1 NCL_CGAP_Co3 Homo sapiens cDNA clone IMAGE:2506555 3'
2678	15674	28695	1.17	8.0E-61	AW006478.1	EST_HUMAN	wf05b10.x1 NCL_CGAP_Co3 Homo sapiens cDNA clone IMAGE:2506555 3'
2962	16020		1.66	8.0E-61	X57147.1	NT	Human endogenous retrovirus pHE.1 (ERV9)
8227	21196	34604	0.73	8.0E-61	AA583968.1	EST_HUMAN	nt59g06.s1 NCL_CGAP_Lar1 Homo sapiens cDNA clone IMAGE:1088218 3'
11926	24807	38400	1.47	8.0E-61	H71225.1	EST_HUMAN	ye12e09.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:214600 5' similar to SP:C40H1.1 CE00109 OVARIAN PROTEIN ;
11926	24807	38401	1.47	8.0E-61	H71225.1	EST_HUMAN	ye12e09.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:214600 5' similar to SP:C40H1.1 CE00109 OVARIAN PROTEIN ;
128	13234	26163	0.67	7.0E-61	7706670	NT	Homo sapiens PXR2b protein (PXR2b), mRNA
128	13234	26164	0.67	7.0E-61	7706670	NT	Homo sapiens PXR2b protein (PXR2b), mRNA
265	13361	26285	2.61	6.0E-61	BE409310.1	EST_HUMAN	601300938F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3635480 5'
812	13870	26819	2.17	6.0E-61	BE409310.1	EST_HUMAN	601300938F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3635480 5'
1324	14359	27326	13.5	6.0E-61	AF119860.1	NT	Homo sapiens PRO2014 mRNA, complete cds
1634	14666	27642	0.9	6.0E-61	BE257400.1	EST_HUMAN	601109238F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3350145 5'
1655	14687	27662	2.32	6.0E-61	AA596033.1	EST_HUMAN	mm66109.s1 NCL_CGAP_Lar1 Homo sapiens cDNA clone IMAGE:1088897 3'
2137	15154	28169	0.91	6.0E-61	AY006285.1	NT	Homo sapiens solute carrier (SLC25A18) mRNA, complete cds; nuclear gene for mitochondrial product
3317	16370	29290	8.07	6.0E-61	AU130689.1	EST_HUMAN	AU130689 NT2RP3 Homo sapiens cDNA clone NT2RP3001263 5'
8147	19222	32452	3.06	6.0E-61	S79249.1	NT	Ig-beta/B29-CD79b (alternatively spliced) [human, B cells, mRNA Partial, 375 nt]
7565	20528	33887	1.53	6.0E-61	U24498.1	NT	Human autosomal dominant polycystic kidney disease protein 1 (PKD1) gene

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Single Exon Probes Expressed In Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7878	20822	34199	1.87	6.0E-61	AF035737.1	NT	Homo sapiens general transcription factor 2-1 (GTF2) mRNA, complete cds
221	13321	26246	1.14	5.0E-61	8922990	NT	Homo sapiens hypothetical protein FLJ11316 (FLJ11316), mRNA
221	13321	26247	1.14	5.0E-61	8922990	NT	Homo sapiens hypothetical protein FLJ11316 (FLJ11316), mRNA
1688	14719	27699	3.18	5.0E-61	4506008	NT	Homo sapiens protein phosphatase 1, regulatory subunit 10 (PPP1R10), mRNA
3048	16106	28020	1.96	5.0E-61	AL163276.2	NT	Homo sapiens chromosome 21 segment HS21C076
4006	17045		1.87	5.0E-61	AJ229041.1	NT	Homo sapiens 959 kb contig between AML1 and CBR1 on chromosome 21q22; segment 1/3
1774	14803	27788	1.17	4.0E-61	AU140307.1	EST_HUMAN	AU140307 PLACE2 Homo sapiens cDNA clone PLACE2000302 5'
5813	18989	32190	0.51	4.0E-61	7681637	NT	Homo sapiens DKFZP566B023 protein (DKFZP566B023), mRNA
12348	25143		2.27	4.0E-61	AV731140.1	EST_HUMAN	AV731140 HTF Homo sapiens cDNA clone HTFARB01 5'
8764	21731	35154	0.65	3.0E-61	AF150190.1	EST_HUMAN	AF150190 Human mRNA from cd34+ stem cells Homo sapiens cDNA clone CBDAGB04
499	13571	26493	1.74	2.0E-61	8922829	NT	Homo sapiens hypothetical protein FLJ11028 (FLJ11028), mRNA
1217	14255	27213	3.4	2.0E-61	BE168410.1	EST_HUMAN	QV3-HT0513-060400-147-d01 HT0513 Homo sapiens cDNA
1217	14255	27214	3.4	2.0E-61	BE168410.1	EST_HUMAN	QV3-HT0513-060400-147-d01 HT0513 Homo sapiens cDNA
1674	14706	27684	1.34	2.0E-61	NS0399.1	EST_HUMAN	y63d11.s1 Soares fetal liver spleen 1N1LS Homo sapiens cDNA clone IMAGE:246483 3' similar to
2649	15646		1.25	2.0E-61	NS9397.1	EST_HUMAN	gb:125444 60S RIBOSOMAL PROTEIN L35A (HUMAN);
6566	19626	32891	0.92	2.0E-61	11426168	NT	y03f11.1r1 Soares melanocyte 2N6HM Homo sapiens cDNA clone IMAGE:270189 5'
9369	22334	35765	1.07	2.0E-61	AV694317.1	EST_HUMAN	Homo sapiens ATPase, H+ transporting, lysosomal (vacuolar proton pump) non-catalytic accessory protein 1A (110/116kD) (ATP6N1A), mRNA
9920	22741		1.27	2.0E-61	AB011108.1	NT	AV694317 GKC Homo sapiens cDNA clone GKEELG06 5'
10282	23207	36692	1.61	2.0E-61	AW500256.1	EST_HUMAN	Homo sapiens mRNA for KIAA0538 protein, partial cds
10612	23534	37031	2.88	2.0E-61	11421778	NT	UI-HF-BN0-akd-f-12-0-UI.1 NIH_MGC_50 Homo sapiens cDNA clone IMAGE:3076774 5'
11230	24183		6.91	2.0E-61	11419729	NT	Homo sapiens polymerase (RNA) III (DNA directed) (39kD) (RPC39), mRNA
13042	25583	31701	1.39	2.0E-61	AW96326.1	EST_HUMAN	Homo sapiens ribosomal protein L44 (RPL44), mRNA
435	13509		1.85	1.0E-61	AL163203.2	NT	QV0-BN0042-170300-162-f10 BN0042 Homo sapiens cDNA
774	13833	26778	0.96	1.0E-61	5453829	NT	Homo sapiens chromosome 21 segment HS21C003
1784	14813		0.95	1.0E-61	U92657.1	NT	Homo sapiens origin recognition complex, subunit 2 (yeast homolog)-like (ORC2L) mRNA
1875	14900	27899	4.69	1.0E-61	6005983	NT	Human polymorphic trinucleotide repeat in X-linked retinitis pigmentosa (RP3) gene region
2206	15221	28241	1.52	1.0E-61	AW627281.1	EST_HUMAN	Homo sapiens zona pellucida glycoprotein 3A (sperm receptor) (ZP3A), mRNA
2846	15906	28831	1.58	1.0E-61	BE396383.1	EST_HUMAN	xs11b09.y1 NCI_CGAP_L15 Homo sapiens cDNA clone IMAGE:2683369 5' similar to contains element
3387	16436	28963	0.87	1.0E-61	7662319	NT	MSR1 repetitive element;
4288	17317	30196	1	1.0E-61	M68840.1	NT	601273513f1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3614667 5'
4488	17494	30381	1.02	1.0E-61	4759249	NT	Homo sapiens KIAA0806 gene product (KIAA0806), mRNA
							Human monamine oxidase A (MAOA) mRNA, complete cds
							Homo sapiens TRAF family member-associated NFKB activator (TANK) mRNA

Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4468	17494	30382	1.02	1.0E-61	4759249	NT	Homo sapiens TRAF family member-associated NFKB activator (TANK) mRNA
4893	17910	30799	9.18	1.0E-61	AW298181.1	EST_HUMAN	U1-H-BW0-aj1-b-08-0-U1.s1 NCI_CGAP_Sub6 Homo sapiens cDNA clone IMAGE:2732871 3'
4893	17910	30800	9.18	1.0E-61	AW298181.1	EST_HUMAN	U1-H-BW0-aj1-b-08-0-U1.s1 NCI_CGAP_Sub6 Homo sapiens cDNA clone IMAGE:2732871 3'
4971	17986	30876	0.94	1.0E-61	7705898	NT	Homo sapiens flavohemoglobin b5-b5R (LOC51167). mRNA
4971	17986	30877	0.94	1.0E-61	7705898	NT	Homo sapiens flavohemoglobin b5-b5R (LOC51167). mRNA
5467	18569	31479	0.68	1.0E-61	M76423.1	NT	H. sapiens carbonic anhydrase VII (CA VII) gene, exons 4,5,6, and 7, and complete cds
5773	18865	32046	0.74	1.0E-61	7662303	NT	Homo sapiens KIA00783 gene product (KIA00783). mRNA
5984	19069	32267	1.02	1.0E-61	11416891	NT	Homo sapiens survival of motor neuron 1, telomeric (SMN1). mRNA
7085	20019	33321	7.63	1.0E-61	M30135.1	NT	Human P40 T-cell and mast cell growth factor (hP40) gene, complete cds
7298	20270	33905	0.95	1.0E-61	4759171	NT	Homo sapiens SC95-interacting protein 1 (SRRP129). mRNA
7397	20365	33717	1.58	1.0E-61	8923130	NT	Homo sapiens hypothetical protein FLJ20128 (FLJ20128). mRNA
7397	20365	33718	1.58	1.0E-61	8923130	NT	Homo sapiens hypothetical protein FLJ20128 (FLJ20128). mRNA
8471	21440	34858	4.19	1.0E-61	11034840	NT	Homo sapiens growth hormone releasing hormone (GHRH). mRNA
8666	21624	35044	3.41	1.0E-61	AF224693.1	NT	Homo sapiens mannosidase, beta A, lysosomal (MANBA) gene, and ubiquitin-conjugating enzyme E2D 3 (UBE2D3) genes, complete cds
9637	22581		2.94	1.0E-61	AW699726.1	EST_HUMAN	MRO-BN0070-040400-010-H01 BN0070 Homo sapiens cDNA
9712	22865	36122	0.99	1.0E-61	11418280	NT	Homo sapiens cadherin 18 (CDH18). mRNA
10389	23311	36790	5.56	1.0E-61	11428892	NT	Homo sapiens KIA00971 protein (KIA00971). mRNA
10998	23964	37488	3.38	1.0E-61	11425578	NT	Homo sapiens actinin, alpha 4 (ACTN4). mRNA
11661	24567		3.58	1.0E-61	BE439409.1	EST_HUMAN	HTM1-025F1 HTM1 Homo sapiens cDNA
12283	25846	31433	4.15	1.0E-61	11430460	NT	Homo sapiens low density lipoprotein-related protein 2 (LRP2). mRNA
12283	25846	31434	4.15	1.0E-61	11430460	NT	Homo sapiens low density lipoprotein-related protein 2 (LRP2). mRNA
12652	25335	31761	23.14	1.0E-61	M20809.1	NT	Human kappa-immunoglobulin germline pseudogene (Chr1) variable region (subgroup V kappa I)
12942	25621	31711	10.09	1.0E-61	11418127	NT	Homo sapiens GTP binding protein 1 (GTPBP1). mRNA
10722	23644	37137	2.13	9.0E-62	BE064386.1	EST_HUMAN	RC4-BT0310-110300-015-110 BT0310 Homo sapiens cDNA
4581	17603	30500	1.04	8.0E-62	AA830420.1	EST_HUMAN	cc66h11.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1354725 3' similar to SW:POL_MLVRK
1109	14153	27103	1.9	7.0E-62	AV714334.1	EST_HUMAN	P31795 POL. POLYPROTEIN ;
3517	16563	29488	0.7	7.0E-62	P17480	SWISSPROT	AV714334 DCB Homo sapiens cDNA clone DCBAMA08 5'
6023	19106	32309	1.13	7.0E-62	11427965	NT	NUCLEAR TRANSCRIPTION FACTOR 1 (UPSTREAM BINDING FACTOR 1) (UBF-1)
11678	24644	38221	9.39	7.0E-62	A1208981.1	EST_HUMAN	Homo sapiens hypothetical protein (FLJ20281). mRNA
3012	16070		1.49	6.0E-62	U09410.1	NT	q956a04.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1839150 3' similar to Trc:O15103 O15103 HYPOTHETICAL 27.3 KD PROTEIN ; Human zinc finger protein ZNF131 mRNA, partial cds

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Table 4
Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3395	16444		4.9	6.0E-62	11418255	NT	Homo sapiens CGI-56 protein (CGI-56), mRNA
7887	20831	34209	3.27	6.0E-62	A1762801.1	EST_HUMAN	w04d02.x1 NCI_CGAP_CLL1 Homo sapiens cDNA clone IMAGE:2388251 3'
7887	20831	34210	3.27	6.0E-62	A1762801.1	EST_HUMAN	w04d02.x1 NCI_CGAP_CLL1 Homo sapiens cDNA clone IMAGE:2388251 3'
8422	21391		0.72	6.0E-62	AW501124.1	EST_HUMAN	UI-HF-BPOp-ait-0-08-0-UI-1 NIH_MGC_51 Homo sapiens cDNA clone IMAGE:3072833 5'
8600	21568	34984	1.4	6.0E-62	11431139	NT	Homo sapiens CGI-18 protein (LOC51008), mRNA
9709	22662	36118	4.02	6.0E-62	AW814393.1	EST_HUMAN	MR3-ST0203-130100-025-a09 ST0203 Homo sapiens cDNA
416	13489	28424	2.28	5.0E-62	A1950528.1	EST_HUMAN	w051e07.x1 NCI_CGAP_Lu28 Homo sapiens cDNA clone IMAGE:2547204 3' similar to SW:GG65_HUMAN
2416	15423	28446	3.61	5.0E-62	AJ271735.1	NT	Q06379 GOLGIN-95, contains element MIER22 repetitive element;
2416	15423	28447	3.61	5.0E-62	AJ271735.1	NT	Homo sapiens Xq pseudautosomal region; segment 1/2
2596	15597	28615	1.43	5.0E-62	U39487.1	NT	Homo sapiens Xq pseudautosomal region; segment 1/2
2596	15597	28616	1.43	5.0E-62	U39487.1	NT	Human xanthine dehydrogenase/oxidase mRNA, complete cds
3430	16478	28697	2.95	5.0E-62	4506758	NT	Human xanthine dehydrogenase/oxidase mRNA, complete cds
4355	17382	30264	1.91	5.0E-62	AA431093.1	EST_HUMAN	Homo sapiens tyrosine receptor 3 (RYR3) mRNA
4589	17611		1.1	5.0E-62	AW805897.1	EST_HUMAN	zw78e09.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:782344 3' similar to SW:NRDC_RAT
8894	21860	35283	0.64	5.0E-62	4506758	NT	P47245 NARDILYSIN
9875	22828	36282	8.13	5.0E-62	AW410687.1	EST_HUMAN	RC5-NN1089-100500-021-H03 NN1089 Homo sapiens cDNA
11596	24534	38090	2.18	5.0E-62	11425574	NT	Homo sapiens tyrosine receptor 3 (RYR3) mRNA
11596	24534	38091	2.18	5.0E-62	11425574	NT	Homo sapiens muscle specific gene (M9), mRNA
841	13898	26853	2.29	4.0E-62	AW161479.1	EST_HUMAN	Homo sapiens muscle specific gene (M9), mRNA
841	13898	26854	2.29	4.0E-62	AW161479.1	EST_HUMAN	au71d03.y1 Schneider fetal brain 00004 Homo sapiens cDNA clone IMAGE:2781701 5' similar to gb:M37104
842	13898	26853	1.27	4.0E-62	AW161479.1	EST_HUMAN	ATP SYNTHASE COUPLING FACTOR 6, MITOCHONDRIAL PRECURSOR (HUMAN);
842	13898	26854	1.27	4.0E-62	AW161479.1	EST_HUMAN	ATP SYNTHASE COUPLING FACTOR 6, MITOCHONDRIAL PRECURSOR (HUMAN);
1458	14491		1	4.0E-62	AA311281.1	EST_HUMAN	au71d03.y1 Schneider fetal brain 00004 Homo sapiens cDNA clone IMAGE:2781701 5' similar to gb:M37104
2484	15468	28491	2.85	4.0E-62	A1827800.1	EST_HUMAN	ATP SYNTHASE COUPLING FACTOR 6, MITOCHONDRIAL PRECURSOR (HUMAN);
2484	15468	28492	2.85	4.0E-62	A1827900.1	EST_HUMAN	ATP SYNTHASE COUPLING FACTOR 6, MITOCHONDRIAL PRECURSOR (HUMAN);
3410	16459		6.48	4.0E-62	4557887	NT	EST182043 Jurkat T-cells V Homo sapiens cDNA 5' and
							wf12b08.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2350359 3' similar to
							gb:X57138_ma1 HISTONE H2B.2 (HUMAN);
							wf12b08.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2350359 3' similar to
							gb:X57138_ma1 HISTONE H2B.2 (HUMAN);
							Homo sapiens keratin 18 (KRT18) mRNA

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Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Description
6032	19115	32318	1.63	4.0E-62	4506978	NT	Homo sapiens solute carrier family 13 (sodium-dependent dicarboxylate transporter), member 2 (SLC13A2) mRNA
6429	19495	32748	2.53	4.0E-62	11420654	NT	Homo sapiens ubiquitin specific protease 9, X chromosome (Drosophila fat facets related) (USP9X), mRNA
7371	20347	33698	2.08	4.0E-62	11421041	NT	Homo sapiens phosphoribosyl pyrophosphate synthetase 2 (PRPS2), mRNA
7896	20839	34219	2.59	4.0E-62	7657057	NT	Homo sapiens eukaryotic translation initiation factor 2B, subunit 2 (beta, 39kD) (EIF2B2), mRNA
7896	20839	34220	2.59	4.0E-62	7657057	NT	Homo sapiens eukaryotic translation initiation factor 2B, subunit 2 (beta, 39kD) (EIF2B2), mRNA
8511	21479	34893	0.93	4.0E-62	11429873	NT	Homo sapiens 26S proteasome-associated pad1 homolog (POH1), mRNA
9198	22164	35594	5.95	4.0E-62	AB033089.1	NT	Homo sapiens mRNA for KIAA1263 protein, partial cds
11353	24303	37830	3.05	4.0E-62	Z78786.1	NT	H. sapiens flow-sorted chromosome 6 HindIII fragment, SC9pA16D3
11353	24303	37831	3.05	4.0E-62	Z78786.1	NT	H. sapiens flow-sorted chromosome 6 HindIII fragment, SC9pA16D3
11598	24536	38093	1.57	4.0E-62	AW023559.1	EST_HUMAN	cd55g04.y1 Morion Fetal Cochlea Homo sapiens cDNA clone IMAGE 2487751.5'
12287	25090	38176	3.39	4.0E-62	11418036	NT	Homo sapiens putative nuclear protein (HRIHFB2122), mRNA
12491	25903		1.3	4.0E-62	11418192	NT	Homo sapiens non-histone chromosome protein 2 (S. cerevisiae)-like 1 (NHP2L1), mRNA
12871	25505	31706	1.96	4.0E-62	11418322	NT	Homo sapiens cadherin EGF LAG seven-pass G-type receptor 1 (KIAA0330), mRNA
12924	25500	31703	19.77	4.0E-62	11417862	NT	Homo sapiens calcineurin binding protein 1 (KIAA0330), mRNA
12924	25500	31704	19.77	4.0E-62	11417862	NT	Homo sapiens calcineurin binding protein 1 (KIAA0330), mRNA
12971	25542	31717	3.07	4.0E-62	11430460	NT	Homo sapiens low density lipoprotein-related protein 2 (LRP2), mRNA
76	13192	26114	0.68	3.0E-62	4557794	NT	Homo sapiens neurofibromin 2 (bilateral acoustic neuroma) (NF2) mRNA
3059	16116	29029	1.02	3.0E-62	AB040909.1	NT	Homo sapiens mRNA for KIAA1476 protein, partial cds
3059	16116	29030	1.02	3.0E-62	AB040909.1	NT	Homo sapiens mRNA for KIAA1476 protein, partial cds
3712	16755	29669	3.52	3.0E-62	X52858.1	NT	Human cyclophilin-related processed pseudogene
8885	21851	35272	4.85	3.0E-62	AI632733.1	EST_HUMAN	wa33f04.x1 NCL CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2298903 3' similar to contains THR12 THR repetitive element;
1235	14272	27232	2.78	2.0E-62	AL163284.2	NT	Homo sapiens chromosome 21 segment HS21C084
8142	21079	34479	0.68	2.0E-62	AA307490.1	EST_HUMAN	EST178374 Colon carcinoma (HCC) cell line Homo sapiens cDNA 5' end
9127	22093	35520	4.47	2.0E-62	BF329811.1	EST_HUMAN	RCO-BN0284-300500-031-e05 BN0284 Homo sapiens cDNA
9127	22093	35521	4.47	2.0E-62	BF329811.1	EST_HUMAN	RCO-BN0284-300500-031-e05 BN0284 Homo sapiens cDNA
10533	23455		4.96	2.0E-62	AF224668.1	NT	Homo sapiens mannosidase, beta A, lysosomal (MANBA) gene, and ubiquitin-conjugating enzyme E2D 3 (UBE2D3) genes, complete cds
11896	24873		20.5	2.0E-62	BF330876.1	EST_HUMAN	QV4-BT0257-081189-017-e03 BT0257 Homo sapiens cDNA
1045	14091	27044	1.88	1.0E-62	AF248540.1	NT	Homo sapiens intersecin 2 (SH3D7B) mRNA, complete cds
1547	14580	27552	12.74	1.0E-62	L78910.1	NT	Homo sapiens ADP/ATP carrier protein (ANT-2) gene, complete cds

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Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1815	14842	27833	1.18	1.0E-62	AA625207.1	EST_HUMAN	at70e11.r1 Soares_NhHMPu_S1 Homo sapiens cDNA clone IMAGE:1047404 5' similar to WP:K01H12.1 CE03453 ;
2925	15983	28606	1.45	1.0E-62	AL099044.1	EST_HUMAN	DKFZp566f104_r1 566 (synonym: htkd2) Homo sapiens cDNA clone DKFZp566f104 5'
3435	16482		1.15	1.0E-62	AB040911.1	NT	Homo sapiens mRNA for KIAA1478 protein, partial cds
4556	17579	30470	1.43	1.0E-62	8923201	NT	Homo sapiens hypothetical protein FLJ20212 (FLJ20212), mRNA
5169	18178	31056	0.88	1.0E-62	AA148922.1	EST_HUMAN	z06b08.r1 Soares_pregnant_uterus_NbHPU Homo sapiens cDNA clone IMAGE:491511 5' similar to SW: C561_BOVIN P10897 CYTOCHROME B561 ;
5198	18205	31078	0.94	1.0E-62	L23503.1	NT	Human glucagon-like peptide-1 receptor (GLP-1) mRNA, complete cds
6421	19488	32738					Homo sapiens X28 region near ALD locus containing dual specificity phosphatase 9 (DUSP9), ribosomal protein L18a (RPL18a), Ca2+/Calmodulin-dependent protein kinase I (CAMKI), creatine transporter (CRT), CDM protein (CDM), adrenoleukodystrophy protein >
7341	20312	33655	2.84	1.0E-62	U52111.2	NT	ab05c02.s1 Stragene fetal retina 937202 Homo sapiens cDNA clone IMAGE:839906 3'
7352	20322	33669	0.91	1.0E-62	AA490060.1	EST_HUMAN	zg89f10.s1 Soares_fetal_heart_NbHH19W Homo sapiens cDNA clone IMAGE:408771 3'
7352	20322	33670	2.48	1.0E-62	AA722878.1	EST_HUMAN	zg89f10.s1 Soares_fetal_heart_NbHH19W Homo sapiens cDNA clone IMAGE:408771 3'
9110	22078	35502	0.68	1.0E-62	AA280050.1	EST_HUMAN	zs93e07.r1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:705080 5'
9413	22378	35816	1.82	1.0E-62	7662289	NT	Homo sapiens KIAA0763 gene product (KIAA0763), mRNA
9413	22378	35817	1.82	1.0E-62	7662289	NT	Homo sapiens KIAA0763 gene product (KIAA0763), mRNA
9457	22421	35858	1.97	1.0E-62	X15633.1	NT	H. sapiens lysosomal acid phosphatase gene (EC 3.1.3.2) Exon 9
9457	22421	35859	1.97	1.0E-62	X15633.1	NT	H. sapiens lysosomal acid phosphatase gene (EC 3.1.3.2) Exon 9
9915	22736	38189	3.42	1.0E-62	AA465170.1	EST_HUMAN	aa33d08.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:815055 3'
11694	24659	38237	2.41	1.0E-62	Z78688.1	NT	H. sapiens flow-sorted chromosome 6 HindIII fragment, SO6pA14D8
12750	25397		2.22	1.0E-62	11418322	NT	Homo sapiens cadherin EGF LAG seven-pass G-type receptor 1 (CELSR1), mRNA
12956	25529	31714	3.25	1.0E-62	11430460	NT	Homo sapiens low density lipoprotein-related protein 2 (LRP2), mRNA
338	13427	26349	2.41	9.0E-63	AW816405.1	EST_HUMAN	QV4-S10234-181199-037-05 ST0234 Homo sapiens cDNA
2353	15962		1.51	9.0E-63	C18159.1	EST_HUMAN	C18159 Human placenta cDNA (TFUJ1wara) Homo sapiens cDNA clone GEN:558C10 5'
4071	17107	30000	8.29	9.0E-63	AB002348.2	NT	Homo sapiens mRNA for KIAA0350 protein, partial cds
4071	17107	30001	9.29	9.0E-63	AB002348.2	NT	Homo sapiens mRNA for KIAA0350 protein, partial cds
5315	18331	38614	2.17	9.0E-63	11418185	NT	Homo sapiens acylase 2, mitochondrial (ACO2), mRNA
5541	18638	31578	1.3	9.0E-63	Y15056.1	NT	Homo sapiens mRNA for PLB kinase
7388	20357	33709	3.41	9.0E-63	11426985	NT	Homo sapiens nucleoporin 88kD (NUP88), mRNA
8138	21075	34475	0.73	9.0E-63	4885644	NT	Homo sapiens pyruvate dehydrogenase kinase, isoenzyme 3 (PDK3) mRNA
8669	21637	35080	1.58	9.0E-63	11421160	NT	Homo sapiens Ras association (RasGDS/AF-6) domain family 2 (RASSF2), mRNA
11246	24199	37719	1.54	9.0E-63	7662289	NT	Homo sapiens KIAA0763 gene product (KIAA0763), mRNA
11246	24199	37720	1.54	9.0E-63	7662289	NT	Homo sapiens KIAA0763 gene product (KIAA0763), mRNA

Table 4

Single Exon Probes Expressed In Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2351	15360	28392	1.1	8.0E-63	4557734	NT	Homo sapiens monoamine oxidase A (MAOA), nuclear gene encoding mitochondrial protein, mRNA
2383	15391	28416	2.49	8.0E-63	5031810	NT	Homo sapiens IL2-inducible T-cell kinase (ITK), mRNA
3475	16521	29443	3.42	8.0E-63	AF198349.1	NT	Gallus gallus Dach2 protein (Dach2) mRNA, complete cds
3475	16521	29444	3.42	8.0E-63	AF198349.1	NT	Gallus gallus Dach2 protein (Dach2) mRNA, complete cds
4294	17323	30203	3.75	8.0E-63	AL163269.2	NT	Homo sapiens chromosome 21 segment HS21C088
929	19882		1.67	7.0E-63	AB72137.1	EST_HUMAN	wn55g11.x1 NCI_CGAP_U12 Homo sapiens cDNA clone IMAGE:2439608 3'
5412	18515		23.22	6.0E-63	AA420803.1	EST_HUMAN	nc6302.r1 NCI_CGAP_P11 Homo sapiens cDNA clone IMAGE:745947 similar to gb:Y00361 60S
9226	22192	35622	0.63	5.0E-63	11528464	NT	RIBOSOMAL PROTEIN (HUMAN);
3332	16383	29305	0.7	4.0E-63	AL163278.2	NT	Homo sapiens G protein-coupled receptor 51 (GPR51), mRNA
3821	16861	29764	1.16	4.0E-63	AB014607.1	NT	Homo sapiens chromosome 21 segment HS21C078
3821	16861	29785	1.16	4.0E-63	AB014607.1	NT	Homo sapiens mRNA for KIAA0707 protein, partial cds
6588	19648	32917	2.92	4.0E-63	AW750372.1	EST_HUMAN	Homo sapiens mRNA for KIAA0707 protein, partial cds
6588	19648	32918	2.92	4.0E-63	AW750372.1	EST_HUMAN	CM3-BT0595-190100-072-409 BT0595 Homo sapiens cDNA
11467	24410	37958	2.12	4.0E-63	AW134709.1	EST_HUMAN	CM3-BT0595-190100-072-409 BT0595 Homo sapiens cDNA
11467	24410	37959	2.12	4.0E-63	AW134709.1	EST_HUMAN	UI-H-B11-abq-a-02-Q-U1.s1 NCI_CGAP_Sub3 Homo sapiens cDNA clone IMAGE:2712482 3'
13023	25571		1.49	4.0E-63	AA629056.1	EST_HUMAN	UI-H-B11-abq-a-02-Q-U1.s1 NCI_CGAP_Sub3 Homo sapiens cDNA clone IMAGE:2712482 3'
1952	14975	27975	2.52	3.0E-63	AB018260.1	NT	z184b01.s1 Scores_testis_NHT Homo sapiens cDNA clone IMAGE:744649 3' similar to contains L1.H L1
2790	15782	28798	1.85	3.0E-63	J00310.1	NT	repetitive element;
2832	14280	27243	15.82	3.0E-63	6005963	NT	Homo sapiens mRNA for KIAA0717 protein, partial cds
6619	19677	32954	32.29	3.0E-63	11545810	NT	Human Met-RNA-I gene 1
10064	22991	36460	0.51	3.0E-63	BE876158.1	EST_HUMAN	Homo sapiens zinc finger protein 144 (ZNF144), mRNA
10064	22991	36461	0.51	3.0E-63	BE876158.1	EST_HUMAN	Homo sapiens hepatocellular carcinoma antigen gene 520 (LOC63928), mRNA
193	13294	28221	1.91	2.0E-63	U07804.1	NT	60148565F1 NIH_MGC_69 Homo sapiens cDNA clone IMAGE:3888253 5'
199	13300	26228	1.91	2.0E-63	4885228	NT	60148565F1 NIH_MGC_69 Homo sapiens cDNA clone IMAGE:3888253 5'
498	13570		3.06	2.0E-63	4557624	NT	Human DNA topoisomerase I mRNA, partial cds
827	13885	26838	1.7	2.0E-63	7657042	NT	Homo sapiens eyes absent (Drosophila) homolog 2 (EYA2), mRNA
1569	14602	27577	4.18	2.0E-63	AB030388.1	NT	Homo sapiens Down syndrome candidate region 1 (DSOR1), mRNA
1569	14602	27578	4.18	2.0E-63	AB030388.1	NT	Homo sapiens RHCE mRNA for Rh blood CE group antigen polypeptide, complete cds
1781	14870	27796	1.33	2.0E-63	BE410799.1	EST_HUMAN	Homo sapiens RHCE mRNA for Rh blood CE group antigen polypeptide, complete cds
3298	16351	29271	2.77	2.0E-63	AF109718.1	NT	601301627F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3636103 5'

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Table 4
Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3925	16955	29878	3.84	2.0E-63	L39891.1	NT	Homo sapiens polycystic kidney disease-associated protein (PKD1) gene, complete cds
4901	17918	30810	0.95	2.0E-63	AF111467.2	NT	Homo sapiens Jun dimerization protein gene, partial cds; cfos gene, complete cds; and unknown gene
5189	18197	31070	1.19	2.0E-63	BE146928.1	EST_HUMAN	QV4-HT0222-011199-018-g01 HT0222 Homo sapiens cDNA
5232	18240	31112	1.69	2.0E-63	6912617	NT	Homo sapiens glutamyl-peptide cyclotransferase (glutaminyl cyclase) (QPCT), mRNA
5334	25635	31192	0.57	2.0E-63	11419429	NT	Homo sapiens similar to ectonucleotide pyrophosphatase/phosphodiesterase 3 (H. sapiens) (LOC63214), mRNA
5986	19071	32270	2.49	2.0E-63	BF373541.1	EST_HUMAN	QV1-FT0170-040700-265-c05 FT0170 Homo sapiens cDNA
5988	19071	32271	2.49	2.0E-63	BF373541.1	EST_HUMAN	QV1-FT0170-040700-265-c05 FT0170 Homo sapiens cDNA
6310	19381	32620	0.83	2.0E-63	11421940	NT	Homo sapiens protein kinase, cAMP-dependent, regulatory, type II, beta (PRKAR2B), mRNA
6310	19381	32621	0.83	2.0E-63	11421940	NT	Homo sapiens protein kinase, cAMP-dependent, regulatory, type II, beta (PRKAR2B), mRNA
							Human gemline T-cell receptor beta chain Dopamine-beta-hydroxylase-like, TRY1, TRY2, TRY3, TORBV2751P, TORBV22S1A2N1T, TORBV8S1A1T, TORBV7S1A1N2T, TORBV6S1A1T, TORBV13S3, TORBV6S7P, TORBV7S3A2T, TORBV13S2A1T, TORBV6S2A2PT, TORBV7S2A1N4T, TORBV13S9/13S>
6960	19913	33209	1.23	2.0E-63	U66059.1	NT	Homo sapiens MIST mRNA, partial cds
6911	19963	33259	0.81	2.0E-63	AB032369.1	NT	Homo sapiens MIST mRNA, partial cds
6911	19963	33260	0.81	2.0E-63	AB032369.1	NT	Homo sapiens MIST mRNA, partial cds
7278	20012	33316	1.46	2.0E-63	9910365	NT	Homo sapiens Carbonic anhydrase-related protein 10 (LOC56634), mRNA
8058	20995	34391	0.82	2.0E-63	AB046844.1	NT	Homo sapiens Carbonic anhydrase-related protein 10 (LOC56634), mRNA
8878	21845	35267	3.8	2.0E-63	AL163210.2	NT	Homo sapiens chromosome 21 segment HS21C010
9409	22374	35810	1.06	2.0E-63	11420949	NT	Homo sapiens kinesin family member 3B (KIF3B), mRNA
10299	23224	36707	0.98	2.0E-63	AL163218.2	NT	Homo sapiens kinesin family member 3B (KIF3B), mRNA
11098	24058	37582	13.74	2.0E-63	N78945.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C018
11127	24087	37814	2.32	2.0E-63	AF098910.1	NT	gb:U17206.40S RIBOSOMAL PROTEIN S4 (HUMAN);
11127	24087	37815	2.32	2.0E-63	AF098910.1	NT	Homo sapiens neuroxin III-alpha gene, partial cds
12381	25747	31515	8.02	2.0E-63	11418185	NT	Homo sapiens neuroxin III-alpha gene, partial cds
1515	14547	27518	0.93	1.0E-63	F08485.1	EST_HUMAN	Homo sapiens aconitase 2, mitochondrial (ACO2), mRNA
1515	14547	27519	0.93	1.0E-63	F08485.1	EST_HUMAN	HSCZVD111 normalized infant brain cDNA Homo sapiens cDNA clone c-zid11
4370	17397	30276	3.4	1.0E-63	F08485.1	EST_HUMAN	HSCZVD111 normalized infant brain cDNA Homo sapiens cDNA clone c-zid11
4370	17397	30277	3.4	1.0E-63	F08485.1	EST_HUMAN	HSCZVD111 normalized infant brain cDNA Homo sapiens cDNA clone c-zid11
5426	18529	31408	1.66	1.0E-63	AJ271736.1	NT	Homo sapiens Xq pseudautosomal region; segment 2/2

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5864	18953	32140	97.84	1.0E-63	AW582266.1	EST_HUMAN	QVQ-ST0215-060700-083-b09 ST0215 Homo sapiens cDNA
5531	19694	32855	0.72	1.0E-63	AW451950.1	EST_HUMAN	U1-H-B18-alt-h-02-Q-U1.s1 NCL_CGAP_Sub5 Homo sapiens cDNA clone IMAGE:3068763 3'
6531	19694	32856	0.72	1.0E-63	AW451950.1	EST_HUMAN	U1-H-B18-alt-h-02-Q-U1.s1 NCL_CGAP_Sub5 Homo sapiens cDNA clone IMAGE:3068763 3'
8816	21783		2.94	1.0E-63	AL163247.2	NT	Homo sapiens chromosome 21 segment HS21C047
13020	25859		5.18	1.0E-63	AL163207.2	NT	Homo sapiens chromosome 21 segment HS21C007
6079	19159	32370	0.98	9.0E-64	AW401433.1	EST_HUMAN	U1-HF-BKO-aad-b-09-Q-U1.r1 NIH_MGC_38 Homo sapiens cDNA clone IMAGE:3053153 5'
8198	21169	34579	4.61	9.0E-64	AI478188.1	EST_HUMAN	Im50b07.x1 NCL_CGAP_Kd11 Homo sapiens cDNA clone IMAGE:2161525 3'
1048	14094		2.71	8.0E-64	BE280796.1	EST_HUMAN	601155232F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3139038 5'
6263	19336	32569	3.25	8.0E-64	BE886755.1	EST_HUMAN	60150896F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3910336 5'
12187	25034		6.22	8.0E-64	11418177	NT	Homo sapiens Ran GTPase activating protein 1 (RANGAP1), mRNA
12239	25070		2.63	8.0E-64	T60651.1	EST_HUMAN	y698b02.r1 Stralagene lung (#637210) Homo sapiens cDNA clone IMAGE:79179 5'
3540	16566		0.8	7.0E-64	BE394321.1	EST_HUMAN	601311455F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3633204 5'
4763	17783	30678	3.2	7.0E-64	4507490	NT	Homo sapiens thimet oligopeptidase 1 (THOP1), mRNA
4763	17783	30679	3.2	7.0E-64	4507490	NT	Homo sapiens thimet oligopeptidase 1 (THOP1), mRNA
8096	21032	34430	0.64	7.0E-64	4508786	NT	Homo sapiens IQ motif containing GTPase activating protein 1 (IQGAP1), mRNA
10393	23315	36794	4.76	7.0E-64	Y07848.1	NT	Homo sapiens EVIS, gar22, rp22 and bam22 genes
1735	14765	27748	3.86	6.0E-64	AI651992.1	EST_HUMAN	w651e07.x1 NCL_CGAP_GC8 Homo sapiens cDNA clone IMAGE:2309220 3' similar to gb:M15182 BETA-GLUCURONIDASE PRECURSOR (HUMAN);
1735	14765	27749	3.86	6.0E-64	AI651992.1	EST_HUMAN	w651e07.x1 NCL_CGAP_GC8 Homo sapiens cDNA clone IMAGE:2309220 3' similar to gb:M15182 BETA-GLUCURONIDASE PRECURSOR (HUMAN);
3139	16196	29105	4.25	6.0E-64	AW026445.1	EST_HUMAN	WY13603.x1 NCL_CGAP_Brn23 Homo sapiens cDNA clone IMAGE:2529436 3'
3139	16196	29106	4.25	6.0E-64	AW026445.1	EST_HUMAN	WY13603.x1 NCL_CGAP_Brn23 Homo sapiens cDNA clone IMAGE:2529436 3'
5703	18798	31973	2.43	6.0E-64	Y18933.1	NT	Homo sapiens MCP-1 gene and enhancer region
5703	18798	31974	2.43	6.0E-64	Y18933.1	NT	Homo sapiens MCP-1 gene and enhancer region
5725	18819	31998	6.33	6.0E-64	MT13975.1	NT	Homo sapiens protein Kinase C beta-II type (PRKCB1), mRNA, complete cds
5929	19015	32209	0.71	6.0E-64	11422189	NT	Homo sapiens calcitonin receptor (CALOR), mRNA
5929	19015	32210	0.71	6.0E-64	11422189	NT	Homo sapiens calcitonin receptor (CALOR), mRNA
7446	20412	33764	2.85	6.0E-64	11525879	NT	Homo sapiens mesenchyme homeo box 1 (MEOX1), mRNA
7446	20412	33765	2.85	6.0E-64	11525879	NT	Homo sapiens mesenchyme homeo box 1 (MEOX1), mRNA
9682	22835	36091	7.07	6.0E-64	11420555	NT	Homo sapiens acetyl-CoA synthetase (LOC55602), mRNA
9864	22800	36254	1.78	6.0E-64	AF274753.1	NT	Homo sapiens progressive ankylosis-like protein (ANK), mRNA, complete cds
10076	23003	36473	2.44	6.0E-64	S76475.1	NT	tKc [human, brain, mRNA, 2715 nt]
11121	24081	37605	4.48	6.0E-64	11420197	NT	Homo sapiens stromal antigen 3 (STAG3), mRNA
11121	24081	37606	4.48	6.0E-64	11420197	NT	Homo sapiens stromal antigen 3 (STAG3), mRNA

Table 4

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
11358	16198	29105	1.73	6.0E-64	AW026445.1	EST_HUMAN	w13e03.x1 NCI_CGAP_Bm23 Homo sapiens cDNA clone IMAGE:2529436 3'
11358	16196	29106	1.73	6.0E-64	AW026445.1	EST_HUMAN	w13e03.x1 NCI_CGAP_Bm23 Homo sapiens cDNA clone IMAGE:2529436 3'
12998	25172	31818	9.26	6.0E-64	11526198	NT	Homo sapiens interleukin 10 receptor, beta (IL10RB), mRNA
821	13879	26829	3.66	5.0E-64	AF231919.1	NT	Homo sapiens chromosome 21 unknown mRNA
821	13879	26830	3.66	5.0E-64	AF231919.1	NT	Homo sapiens chromosome 21 unknown mRNA
1341	14376	27345	0.93	5.0E-64	AB020710.1	NT	Homo sapiens mRNA for KIAA0903 protein, partial cds
1724	14754	27740	1.7	5.0E-64	U89358.1	NT	Human [3]mbt protein homolog mRNA, complete cds
2637	14509	27483	3.52	5.0E-64	7682205	NT	Homo sapiens KIAA0618 gene product (KIAA0618), mRNA
2637	14509	27484	3.52	5.0E-64	7682205	NT	Homo sapiens KIAA0618 gene product (KIAA0618), mRNA
3983	17023	29934	7.14	5.0E-64	AF017433.1	NT	Homo sapiens putative transcription factor CRE3 (CRE3) mRNA, partial cds
4132	17164	30053	0.93	5.0E-64	AB020710.1	NT	Homo sapiens mRNA for KIAA0903 protein, partial cds
8125	21062	34460	0.57	4.0E-64	BE784807.1	EST_HUMAN	607590382F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3944397 5'
11164	24122	37650	1.55	4.0E-64	AW813783.1	EST_HUMAN	RC3-ST0197-120200-015-a03 ST0197 Homo sapiens cDNA
11164	24122	37651	1.55	4.0E-64	AW813783.1	EST_HUMAN	RC3-ST0197-120200-015-a03 ST0197 Homo sapiens cDNA
2208	15223	26243	6.32	3.0E-64	C18895.1	EST_HUMAN	C18895 Human placenta cDNA (Tfujivara) Homo sapiens cDNA clone GEN-589E02 5'
3268	16322	29244	0.72	3.0E-64	BE784381.1	EST_HUMAN	607590382F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:39443577 5'
3457	16503	29422	1.85	3.0E-64	AV711714.1	EST_HUMAN	AV711714 DCA Homo sapiens cDNA clone DCAAMC01 5'
3457	16503	29423	1.85	3.0E-64	AV711714.1	EST_HUMAN	AV711714 DCA Homo sapiens cDNA clone DCAAMC01 5'
6200	19274	32508	1.35	3.0E-64	Z26273.1	NT	H. sapiens isoform 1 gene for L-type calcium channel, exon 28
6475	19540	32786	0.64	3.0E-64	AW500861.1	EST_HUMAN	UI-HF-BP0p-alk-c-05-0-UJr1 NIH_MGC_51 Homo sapiens cDNA clone IMAGE:3073161 5'
6641	19699	32975	2.78	3.0E-64	BF370000.1	EST_HUMAN	RC8-FN0019-260800-011-G11 FN0019 Homo sapiens cDNA
8809	21776	35201	1.78	3.0E-64	AF248953.1	NT	Homo sapiens golgi matrix protein GM130 (GOLGA2) mRNA, complete cds
8809	21776	35202	1.78	3.0E-64	AF248953.1	NT	Homo sapiens golgi matrix protein GM130 (GOLGA2) mRNA, complete cds
8840	21807	35225	2.73	3.0E-64	BE206521.1	EST_HUMAN	bb72h12.y1 NIH_MGC_12 Homo sapiens cDNA clone IMAGE:3047975 5' similar to gb:L08089 DNAJ
8840	21807	35226	2.73	3.0E-64	BE206521.1	EST_HUMAN	bb72h12.y1 NIH_MGC_12 Homo sapiens cDNA clone IMAGE:3047975 5' similar to gb:L08089 DNAJ
9782	22723	36177	1.54	3.0E-64	AL163246.2	NT	PROTEIN HOMOLOG 2 (HUMAN);
9782	22723	36178	1.54	3.0E-64	AL163246.2	NT	Homo sapiens chromosome 21 segment HS21C046
9872	22825	36278	0.8	3.0E-64	AW977384.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C046
9872	22825	36279	0.8	3.0E-64	AW977384.1	EST_HUMAN	EST389493 MAGe sequences, MAGO Homo sapiens cDNA
11988	24875	38471	1.87	3.0E-64	AL163227.2	NT	EST389493 MAGe sequences, MAGO Homo sapiens cDNA
1090	14134	27086	0.95	2.0E-64	AA609940.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C027
1398	14432	27401	1.2	2.0E-64	4787701	NT	af09403.x1 Scores_testis_NHT Homo sapiens cDNA clone IMAGE:1031151 3'
							Homo sapiens eIF4E-like cap-binding protein (4EHP) mRNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2530	15533		2.05	2.0E-64	AI927030.1	EST_HUMAN	wo87b01.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2462281 3' similar to contains element L1 repetitive element;
2536	15538	28560	3.13	2.0E-64	AL163246.2	NT	Homo sapiens chromosome 21 segment HS21C046
2536	15538	28561	3.13	2.0E-64	AL163246.2	NT	Homo sapiens chromosome 21 segment HS21C046
3601	16841	29748	0.67	2.0E-64	AW958145.1	EST_HUMAN	EST1370215 IMAGE resequenced, IMAGE Homo sapiens cDNA
3601	16841	29749	0.67	2.0E-64	AW958145.1	EST_HUMAN	EST1370215 IMAGE resequenced, IMAGE Homo sapiens cDNA
6121	19199	32424	2.2	2.0E-64	AU124387.1	EST_HUMAN	AU124387 NT2RM2 Homo sapiens cDNA clone NT2RM2002113 5'
6370	19438	32681	1.38	2.0E-64	AF113708.1	NT	Homo sapiens angiotensin 4 (ANG4) mRNA, partial cds
6632	19690	32969	4.02	2.0E-64	BF668337.1	EST_HUMAN	602123474F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4280395 5'
8745	19800	33080	1.5	2.0E-64	AJ078337.1	EST_HUMAN	oz29b03.x1 Soares, total Telus_N62HF8_3w Homo sapiens cDNA clone IMAGE:1676717 3'
6859	19912	33208	3.88	2.0E-64	M77185.1	NT	H.sapiens dopamine receptor D5 pseudogene 1, partial cds
8106	21043	34442	0.57	2.0E-64	11431064	NT	Homo sapiens elastin 2-binding protein 1 (A2BP1), mRNA
8164	21102	34501	0.56	2.0E-64	AW666785.1	EST_HUMAN	QV1-HT0413-010200-050-h12 HT0413 Homo sapiens cDNA
9016	21982	35400	5.69	2.0E-64	11434008	NT	Homo sapiens lymphocyte cytosolic protein 1 (L-plestin)(LCP1), mRNA
9016	21982	35401	5.69	2.0E-64	11434008	NT	Homo sapiens lymphocyte cytosolic protein 1 (L-plestin)(LCP1), mRNA
9495	22459	35899	0.43	2.0E-64	11423508	NT	Homo sapiens hypothetical protein SBB167 (LOC57115), mRNA
9586	22548	35999	0.96	2.0E-64	AU132570.1	EST_HUMAN	AU132570 NT2RP4 Homo sapiens cDNA clone NT2RP4000109 5'
11114	24074	37597	3.74	2.0E-64	BF528114.1	EST_HUMAN	602042882F1 NCI_CGAP_Brn67 Homo sapiens cDNA clone IMAGE:4180556 5'
11391	24337	37866	4.59	2.0E-64	AJ922911.1	EST_HUMAN	wn81b06.x1 NCI_CGAP_U11 Homo sapiens cDNA clone IMAGE:2452211 3'
11391	24337	37867	4.59	2.0E-64	AJ922911.1	EST_HUMAN	wn81b06.x1 NCI_CGAP_U11 Homo sapiens cDNA clone IMAGE:2452211 3'
11833	24716	38301	1.89	2.0E-64	BE269650.1	EST_HUMAN	601185078F1 NIH_MGC_8 Homo sapiens cDNA clone IMAGE:3542922 5'
11833	24716	38302	1.89	2.0E-64	BE269650.1	EST_HUMAN	601185078F1 NIH_MGC_8 Homo sapiens cDNA clone IMAGE:3542922 5'
12316	25122	31844	1.47	2.0E-64	8567387	NT	Homo sapiens period (Drosophila) homolog 3 (PER3), mRNA
12744	25393		3.54	2.0E-64	H55162.1	EST_HUMAN	GHR220101 Chromosome 22 exon Homo sapiens cDNA clone C22_132 5'
258	13355	28279	1.48	1.0E-64	AF231919.1	NT	Homo sapiens chromosome 21 unknown mRNA
1794	14823	27807	17.02	1.0E-64	AI929419.1	EST_HUMAN	au60c01.x1 Schneider fetal brain 00004 Homo sapiens cDNA clone IMAGE:2519136 3' similar to gb1:271698_cds1 PROTHYMOSIN ALPHA (HUMAN);contains element MSR1 repetitive element;
3024	16081	29004	0.81	1.0E-64	4507334	NT	Homo sapiens synaptotagmin 1 (SYNJ1), mRNA
3522	16568	29492	5.73	1.0E-64	AF196779.1	NT	Homo sapiens transcription factor IGHE enhancer 3, JM11 protein, JM4 protein, JM5 protein, T54 protein, JM10 protein, A4 differentiation-dependent protein, triple LIM domain protein 6, and synaptophysin genes, complete cds; and L-type calcium channel a2
3598	16843	29562	1.38	1.0E-64	AF228527.1	NT	Homo sapiens TRIAD3 mRNA, partial cds
3598	16843	29563	1.38	1.0E-64	AF228527.1	NT	Homo sapiens TRIAD3 mRNA, partial cds
3917	16957	29870	2	1.0E-64	8622829	NT	Homo sapiens hypothetical protein FLJ11026 (FLJ11026), mRNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10424	23346	36831	0.88	1.0E-64	AA042976.1	EST_HUMAN	zk53f08.s1 Soares_pregnant_uterus_NbHPU Homo sapiens cDNA clone IMAGE:486567 3'
12288	25104		2.03	1.0E-64	AL163246.2	NT	Homo sapiens chromosome 21 segment HS21C046
2284	15287	28321	1.84	9.0E-65	X89211.1	NT	H.sapiens DNA for endogenous retroviral like element
2284	15287	28322	1.64	9.0E-65	X89211.1	NT	H.sapiens DNA for endogenous retroviral like element
11863	24745		35.25	9.0E-65	BF330676.1	EST_HUMAN	QV4-BT0257-081199-017-403 BT0257 Homo sapiens cDNA
11837	24720	38305	7.27	8.0E-65	AI929244.1	EST_HUMAN	au58h07.x1 Schneider fetal brain 00004 Homo sapiens cDNA clone IMAGE:2519005 3' similar to
10515	23437	36936	2.13	7.0E-65	BE081653.1	EST_HUMAN	SW:RL21_HUMAN P46778 60S RIBOSOMAL PROTEIN L21.;
1059	14105	27056	2.73	6.0E-65	AV721898.1	EST_HUMAN	QV2-BT0635-240400-162-002 BT0635 Homo sapiens cDNA
1938	14962		12.23	6.0E-65	AA550929.1	EST_HUMAN	AV721898 HTB Homo sapiens cDNA clone HTBBZC06 5'
6721	19777	33056	0.87	6.0E-65	AA503892.1	EST_HUMAN	η86d10.s1 NCI_CGAP_Prl1 Homo sapiens cDNA clone IMAGE:999379 similar to gb:K03002 60S
							η837b07.s1 NCI_CGAP_Prl5 Homo sapiens cDNA clone IMAGE:954517
9098	22064	35489	2.49	6.0E-65	AW063252.1	EST_HUMAN	xc07b09.x1 NCI_CGAP_Co21 Homo sapiens cDNA clone IMAGE:2583545 3' similar to TR:Q63306 Q63306
9365	22330	35759	4.16	6.0E-65	AA427878.1	EST_HUMAN	LONG INTERSPERSED REPETITIVE DNA CONTAINING 7 ORFS. ;contains L1.b2 L1 repetitive element ;
9365	22330	35760	4.16	6.0E-65	AA427878.1	EST_HUMAN	zw53b06.s1 Soares_totat_fetus_Nb2HF8_9w Homo sapiens cDNA clone IMAGE:773747 3'
9429	22393	35832	1.08	6.0E-65	AI085314.1	EST_HUMAN	zw53b06.s1 Soares_totat_fetus_Nb2HF8_9w Homo sapiens cDNA clone IMAGE:773747 3'
9429	22393	35833	1.08	6.0E-65	AI085314.1	EST_HUMAN	qf18h05.x1 NCI_CGAP_Brm25 Homo sapiens cDNA clone IMAGE:1750425 3'
11220	24173	37699	2.59	6.0E-65	BE567816.1	EST_HUMAN	qf18h05.x1 NCI_CGAP_Brm25 Homo sapiens cDNA clone IMAGE:1750425 3'
11378	24325	37854	1.51	6.0E-65	BF340825.1	EST_HUMAN	607340485F1 NIH_MGC_53 Homo sapiens cDNA clone IMAGE:3682677 5'
11825	24708	38291	1.8	6.0E-65	AL163210.2	NT	602037721F1 NCI_CGAP_Brm64 Homo sapiens cDNA clone IMAGE:4185677 5'
632	13697	26617	1.92	5.0E-65	AF084604.1	NT	Homo sapiens chromosome 21 segment HS21C010
1355	14390	27359	1.22	5.0E-65	AF084604.1	NT	Homo sapiens KE03 protein mRNA, partial cds
1355	14390	27360	1.22	5.0E-65	AF084604.1	NT	Homo sapiens KIAA0156 gene product (KIAA0156), mRNA
2164	15180	28200	1.51	5.0E-65	AB033768.1	NT	Homo sapiens KIAA0156 gene product (KIAA0156), mRNA
3289	16323	29245	2.13	5.0E-65	4507848	NT	Homo sapiens hPAD-colony10 mRNA for peptidylarginine deiminase type I, complete cds
3269	16323	29246	2.13	5.0E-65	4507848	NT	Homo sapiens ubiquitin specific protease 13 (isopeptidase T-3) (USP13) mRNA
7052	20074	33381	1.18	5.0E-65	4504606	NT	Homo sapiens ubiquitin specific protease 13 (isopeptidase T-3) (USP13) mRNA
10833	23784	37253	1.28	5.0E-65	AF006658.1	NT	Homo sapiens interferon-related developmental regulator 1 (IFRD1), mRNA
195	13296	26224	2.33	4.0E-65	AL120419.1	EST_HUMAN	Multiple sclerosis associated retrovirus polyprotein (pol) mRNA, partial cds
747	13808	26748	1.29	4.0E-65	AL266468.1	EST_HUMAN	DKFZp761G108_r1 761 (synonym: hamy2) Homo sapiens cDNA clone DKFZp761G108 5'
							qm46e01.x1 Soares_placenta_8to8weeks_2NbpHP8c9W Homo sapiens cDNA clone IMAGE:1891800 3'

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
747	13808	26749	1.29	4.0E-65	AI266468.1	EST_HUMAN	qin46d1.x1 Soares_plecenta_8to6weeks_2NbHP8to9W Homo sapiens cDNA clone IMAGE:1891800 3'
1080	14124	27077	1.51	4.0E-65	4826735	NT	Homo sapiens fragile X mental retardation, autosomal homolog 1 (FXR1), mRNA
1482	14515	27489	15.66	4.0E-65	4506636	NT	Homo sapiens ribosomal protein L34 (RPL34) mRNA
3971	17011	29925	0.97	4.0E-65	AW993185.1	EST_HUMAN	RC2-BN0033-160200-013-a03 BN0033 Homo sapiens cDNA
6279	19351	32585	4.17	4.0E-65	AB033093.1	NT	Homo sapiens mRNA for KIAA1267 protein, partial cds
6279	19351	32586	4.17	4.0E-65	AB033093.1	NT	Homo sapiens mRNA for KIAA1267 protein, partial cds
7289	20261	33595	0.62	4.0E-65	AY008372.1	NT	Homo sapiens oxysterol binding protein-related protein 3 (ORP3) mRNA, complete cds
7324	20295	33638	0.84	4.0E-65	AY008372.1	NT	Human diaphanin 27 gene, exons 10 and 11, and L1 and Alu repeats
7429	20396	33748	2.48	4.0E-65	M19879.1	NT	Homo sapiens hypothetical protein FLJ22087 (FLJ22087), mRNA
7797	20749	34124	0.58	4.0E-65	U40372.1	NT	Human 3', 5' cyclic nucleotide phosphodiesterase (HSPDE1C3A) mRNA, partial cds
7797	20749	34125	0.58	4.0E-65	U40372.1	NT	Human 3', 5' cyclic nucleotide phosphodiesterase (HSPDE1C3A) mRNA, partial cds
8118	21055	34452	0.81	4.0E-65	U39656.1	NT	Human MAP kinase kinase 6 (MKK6) mRNA, complete cds
8174	21144	34550	0.78	4.0E-65	5453765	NT	Homo sapiens nel (chicken)-like 2 (NELL2), mRNA
8174	21144	34550	0.78	4.0E-65	5453765	NT	Homo sapiens nel (chicken)-like 2 (NELL2), mRNA
9501	22465	35905	1.34	4.0E-65	11429127	NT	Homo sapiens Janus kinase 2 (a protein tyrosine kinase) (JAK2), mRNA
10945	23865		2.65	4.0E-65	AJ277546.2	NT	Homo sapiens WEE1 gene for protein kinase and partial ZNF143 gene for zinc finger transcription factor
11301	24251	37777	2.99	4.0E-65	AV738764.1	EST_HUMAN	AV738764 CB Homo sapiens cDNA clone CBCCBE05 5'
11434	24378	37918	6.02	4.0E-65	AF119846.1	NT	Homo sapiens PRO1474 mRNA, complete cds
12608	14124	27077	1.79	4.0E-65	4826735	NT	Homo sapiens fragile X mental retardation, autosomal homolog 1 (FXR1), mRNA
13091	13296	26224	1.6	4.0E-65	AL120419.1	EST_HUMAN	DKFZp761G108.t1 781 (synonym: hamy2) Homo sapiens cDNA clone DKFZp761G108 5'
97	13214	26139	3.16	3.0E-65	5031976	NT	Homo sapiens pre-B-cell colony-enhancing factor (PBEF) mRNA
98	13214	26139	5.52	3.0E-65	5031976	NT	Homo sapiens pre-B-cell colony-enhancing factor (PBEF) mRNA
1236	15819		22.13	3.0E-65	X78932.1	NT	H. sapiens HZF9 mRNA for zinc finger protein
1840	14867	27866	1.7	3.0E-65	AJ000692.1	EST_HUMAN	ov23f03.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1638173 3' similar to contains element
3003	16061	28979	0.74	3.0E-65	D87078.2	NT	MSR1 repetitive element;
3290	16343	29264	0.68	3.0E-65	4504950	NT	Homo sapiens mRNA for KIAA0235 protein, partial cds
3734	16776	29688	1.61	3.0E-65	AJ000692.1	EST_HUMAN	Homo sapiens laminin, beta 1 (LAMB1), mRNA
4679	17700	30588	1.33	3.0E-65	6912385	NT	ov23f03.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1638173 3' similar to contains element
10429	23351	36835	1.42	3.0E-65	BE787366.1	EST_HUMAN	MSR1 repetitive element;
							Homo sapiens rab6 GTPase activating protein (GAP and centrosome-associated) (GAPCENA), mRNA
							601479686F1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3882405 5'

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
11719	23916	37433	8.57	3.0E-65	AA430006.1	EST_HUMAN	zw65a06.r1 Soares testis NHT Homo sapiens cDNA clone IMAGE:781042 5'
3415	16463	29384	6.08	2.0E-65	BF880294.1	EST_HUMAN	602155082F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4285966 5'
6686	19743		4.55	2.0E-65	BE263373.1	EST_HUMAN	601190883F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3534741 5'
7399	20310	33653	27.84	2.0E-65	BF576922.1	EST_HUMAN	602134339F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4289295 5'
9197	22163	35592	1.26	2.0E-65	AK024463.1	NT	Homo sapiens mRNA for FLJ00056 protein, partial cds
9197	22163	35593	1.26	2.0E-65	AK024463.1	NT	Homo sapiens mRNA for FLJ00056 protein, partial cds
12238	25089		2.75	2.0E-65	AA307904.1	EST_HUMAN	EST:178755 Colon carcinoma (HCC) cell line Homo sapiens cDNA 5' end similar to endogenous retrovirus
12708	25728		1.95	2.0E-65	BF246086.1	EST_HUMAN	601854033F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4073769 5'
540	13611	26530	1.54	1.0E-65	7657495	NT	Homo sapiens putative Rab5 GDP/GTP exchange factor homologue (RABEX5), mRNA
2056	15075	28095	1.07	1.0E-65	AB040946.1	NT	Homo sapiens mRNA for KIAA1513 protein, partial cds
3385	16434	29361	0.8	1.0E-65	BE466681.1	EST_HUMAN	h224a03.x1 NCI_CGAP_GC8 Homo sapiens cDNA clone IMAGE:3208888 3'
4023	17061	29962	1.71	1.0E-65	4504082	NT	Homo sapiens glycican 4 (GPC4) mRNA
4023	17061	29963	1.71	1.0E-65	4504082	NT	Homo sapiens glycican 4 (GPC4) mRNA
4234	17263	30147	2.4	1.0E-65	AW029340.1	EST_HUMAN	wx09c09.x1 NCI_CGAP_Gas4 Homo sapiens cDNA clone IMAGE:2543152 3'
4234	17263	30148	2.4	1.0E-65	AW029340.1	EST_HUMAN	wx09c09.x1 NCI_CGAP_Gas4 Homo sapiens cDNA clone IMAGE:2543152 3'
5358	18463	31332	0.54	1.0E-65	BE089508.1	EST_HUMAN	QV0-BT0702-170400-194-09 BT0702 Homo sapiens cDNA
5358	18463	31333	0.54	1.0E-65	BE089509.1	EST_HUMAN	QV0-BT0702-170400-194-09 BT0702 Homo sapiens cDNA
5554	18651	31595	0.61	1.0E-65	AI243738.1	EST_HUMAN	qh88h07.x1 Soares_NFL_T_GBC_51 Homo sapiens cDNA clone IMAGE:1854109 3' similar to TR:Q07823
8597	21565	34980	5.47	1.0E-65	AW820481.1	EST_HUMAN	Q07823 MAC30 PROTEIN;
8597	21565	34981	5.47	1.0E-65	AW820481.1	EST_HUMAN	QV2-ST0298-140200-042-112 ST0298 Homo sapiens cDNA
8623	21591	35009	2.16	1.0E-65	BE732118.1	EST_HUMAN	QV2-ST0298-140200-042-112 ST0298 Homo sapiens cDNA
8623	21591	35010	2.16	1.0E-65	BE732118.1	EST_HUMAN	601566124F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3841012 5'
8662	21630	35050	2.14	1.0E-65	AU141295.1	EST_HUMAN	601566124F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3841012 5'
8662	21630	35051	2.14	1.0E-65	AU141295.1	EST_HUMAN	AU141295 THYRO1 Homo sapiens cDNA clone THYRO1000356 5'
9192	22158	35588	1.94	1.0E-65	BF698707.1	EST_HUMAN	AU141295 THYRO1 Homo sapiens cDNA clone THYRO1000356 5'
9374	22339	35769	2.25	1.0E-65	AU129040.1	EST_HUMAN	602126239F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4283313 5'
9374	22339	35770	2.25	1.0E-65	AU129040.1	EST_HUMAN	AU129040 NT2RP2 Homo sapiens cDNA clone NT2RP2004714 5'
9386	22351		2.52	1.0E-65	11431894	NT	AU129040 NT2RP2 Homo sapiens cDNA clone NT2RP2004714 5'
9386	22351		2.52	1.0E-65	11431894	NT	Homo sapiens incitol 1,4,5-triphosphate receptor, type 1 (ITPR1), mRNA
9832	22681	36136	5.48	1.0E-65	AI191716.1	EST_HUMAN	q45a02.x1 Soares testis NHT Homo sapiens cDNA clone IMAGE:1733450 3' similar to gb:M29581 ZINC
10245	23170	36659	1.28	1.0E-65	AU153793.1	EST_HUMAN	FINGER PROTEIN 8 (HUMAN); contains MER19.1 MER19 repetitive element;
10665	23587	37085	0.64	1.0E-65	AA089559.1	EST_HUMAN	AU153793 NT2RP3 Homo sapiens cDNA clone NT2RP3004016 3'
							z75a04.r1 Soares_pituitary_gland_N3HPG Homo sapiens cDNA clone IMAGE:382734 5'

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10935	23855	37371	1.02	1.0E-65	AB037832.1	NT	Homo sapiens mRNA for KIAA1411 protein, partial cds
11011	23976	37501	7.57	1.0E-65	M26187.1	NT	Human platelet factor 4 variation 1 (PF4var1) gene, complete cds
11131	24091	37620	10.37	1.0E-65	4506660	NT	Homo sapiens ribosomal protein L7a (RPL7A) mRNA
11465	24408	37955	2.43	1.0E-65	BF698707.1	EST_HUMAN	602125239F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4283313 5'
11545	24486	38040	1.89	1.0E-65	AI621017.1	EST_HUMAN	ts7a06.x1 NCJ CGAP_G06 Homo sapiens cDNA clone IMAGE:2237170 3' similar to gb1.15533_mna1
12289	25105	31815	3.13	1.0E-65	11418041	NT	PANCREATITIS ASSOCIATED PROTEIN 1 PRECURSOR (HUMAN);
12391	25168	31815	7.2	1.0E-65	11418322	NT	Homo sapiens TNF-inducible protein CG12-1 (CG12-1), mRNA
12799	25427	26110	1.87	1.0E-65	11418248	NT	Homo sapiens cadherin EGF LAG seven-pass G-type receptor 1 (CELSR1), mRNA
72	13190	26110	0.94	9.0E-66	AL160311.1	NT	Homo sapiens sulfoltransferase-related protein (SULTX3), mRNA
72	13190	26111	0.94	9.0E-66	AL160311.1	NT	Novel human gene mapping to chromosome 22
1356	14391	27381	0.93	9.0E-66	5031980	NT	Homo sapiens 26S proteasome-associated pad1 homolog (POH1) mRNA
1356	14391	27382	0.93	9.0E-66	5031980	NT	Homo sapiens 26S proteasome-associated pad1 homolog (POH1) mRNA
1480	14513		6.17	9.0E-66	M87299.1	NT	Human transposon-like element, partial
3916	16956	29858	0.74	9.0E-66	M72393.1	NT	Human calcium-dependent phospholipid-binding protein (PLA2) mRNA, complete cds
3916	16956	29859	0.74	9.0E-66	M72393.1	NT	Human calcium-dependent phospholipid-binding protein (PLA2) mRNA, complete cds
4719	17739	30631	0.73	9.0E-66	AL137163.1	NT	Novel human gene mapping to chromosome X
4717	17737	30629	1.59	8.0E-66	AA424304.1	EST_HUMAN	z60c05.r1 Soares_NHMPu_ST Homo sapiens cDNA clone IMAGE:767048 5'
11675	24641		1.48	7.0E-66	BE064410.1	EST_HUMAN	RC4-BT0311-141199-011-h06 BT0311 Homo sapiens cDNA
4393	17421	30304	1.01	8.0E-66	AI924653.1	EST_HUMAN	wn57h07.x1 NCJ CGAP_Lu19 Homo sapiens cDNA clone IMAGE:2446597 3' similar to WP:F15G9.4A
4393	17421	30305	1.01	8.0E-66	AI924653.1	EST_HUMAN	CE18595;
4393	17421	30306	1.01	8.0E-66	AI924653.1	EST_HUMAN	wn57h07.x1 NCJ CGAP_Lu19 Homo sapiens cDNA clone IMAGE:2446597 3' similar to WP:F15G9.4A
8777	21744	37985	0.82	6.0E-66	BE178563.1	EST_HUMAN	CE18595;
11493	24436	37985	4.18	6.0E-66	X69181.1	NT	PM2-HT0604-030300-001-b06 HT0604 Homo sapiens cDNA
1369	14403	27373	1.94	5.0E-66	BE064410.1	EST_HUMAN	H.sapiens mRNA for ribosomal protein L31
9649	22593	38041	15.54	5.0E-66	11420557	NT	RC4-BT0311-141199-011-h06 BT0311 Homo sapiens cDNA
791	13550	26797	1.39	4.0E-66	6679816	NT	Homo sapiens thyroid hormone receptor binding protein (AIB3), mRNA
1750	14779	27764	1.16	4.0E-66	AW897798.1	EST_HUMAN	Mus musculus fragile X mental retardation syndrome 1 homolog (Fmr1), mRNA
2288	15301	28325	1.84	4.0E-66	X89211.1	NT	RC1-NN0063-100500-022-a02 NN0063 Homo sapiens cDNA
2481	15485		2.82	4.0E-66	AJ223364.1	NT	H.sapiens DNA for endogenous retroviral like element
4823	17840		3.19	4.0E-66	9635487	NT	Homo sapiens germ-line DNA upstream of Jkappa locus
							Human endogenous retrovirus, complete genome

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5630	18726	31887	3.86	4.0E-68	11428843	NT	Homo sapiens methylene tetrahydrofolate dehydrogenase (NAD+ dependent), methenyltetrahydrofolate
5835	18925	32109	0.78	4.0E-66	AW939119.1	EST_HUMAN	cyclohydrolase (MTHFD2), mRNA
7036	18368	31255	4.89	4.0E-68	AW985473.1	EST_HUMAN	Q1V1-DT0069-110200-067-q10 DT0069 Homo sapiens cDNA
7338	20309	33852	7.18	4.0E-68	U78188.1	NT	EST377548 MAGI resequences, MAGI Homo sapiens cDNA
7891	18726	31887	0.98	4.0E-68	11428843	NT	Homo sapiens cAMP-regulated guanine nucleotide exchange factor 1 (GAMP-GEF1) mRNA, complete cds
8413	21382	34789	6.46	4.0E-66	11421838	NT	Homo sapiens methylene tetrahydrofolate dehydrogenase (NAD+ dependent), methenyltetrahydrofolate
8472	21441	34859	1.46	4.0E-68	X57147.1	NT	cyclohydrolase (MTHFD2), mRNA
11020	23985	37512	1.75	4.0E-66	BF507488.1	EST_HUMAN	Homo sapiens hypodermal protein FLJ20118 (FLJ20118), mRNA
11706	24871	38248	1.53	4.0E-68	AB023215.1	NT	Human endogenous retrovirus pHE.1 (ERV8)
1424	14457	27432	5.89	3.0E-66	4502098	NT	U1H-BW1-arr-a-10-0-JL1.1 NCL CGAP_Sub7 Homo sapiens cDNA clone IMAGE:3070747 3'
1424	14457	27433	5.89	3.0E-66	4502098	NT	Homo sapiens mRNA for KIAA0998 protein, partial cds
1999	15020	28027	1.07	3.0E-66	NE5323.1	EST_HUMAN	Homo sapiens solute carrier family 25 (mitochondrial carrier; adenine nucleotide translocator), member 5 (SLC25A5), nuclear gene encoding mitochondrial protein, mRNA
1999	15020	28028	1.07	3.0E-66	NE5323.1	EST_HUMAN	Homo sapiens solute carrier family 25 (mitochondrial carrier; adenine nucleotide translocator), member 5 (SLC25A5), nuclear gene encoding mitochondrial protein, mRNA
1999	15020	28029	1.07	3.0E-66	NE5323.1	EST_HUMAN	yz27g12.1 Soares_multiple_sclerosis_2NBHMSF Homo sapiens cDNA clone IMAGE:284326 5' similar to SW:H2B1_JTGCA P35068 HISTONE H2B.1/H2B.2 [2] PIR:B56612;
2718	15712	28729	4.78	3.0E-66	11141880	NT	SW:H2B1_JTGCA P35068 HISTONE H2B.1/H2B.2 [2] PIR:B56612;
3134	16191	29101	6.79	3.0E-66	7682223	NT	SW:H2B1_JTGCA P35068 HISTONE H2B.1/H2B.2 [2] PIR:B56612;
5542	18639	31679	0.78	3.0E-68	AB020699.1	NT	yz27g12.1 Soares_multiple_sclerosis_2NBHMSF Homo sapiens cDNA clone IMAGE:284326 5' similar to SW:H2B1_JTGCA P35068 HISTONE H2B.1/H2B.2 [2] PIR:B56612;
5657	18753	31920	0.79	3.0E-66	M13975.1	NT	yz27g12.1 Soares_multiple_sclerosis_2NBHMSF Homo sapiens cDNA clone IMAGE:284326 5' similar to SW:H2B1_JTGCA P35068 HISTONE H2B.1/H2B.2 [2] PIR:B56612;
5867	18956	32143	1.49	3.0E-66	11417946	NT	Homo sapiens TGF-beta-induced transcription factor 2 (TGIF2), mRNA
5867	18956	32144	1.49	3.0E-66	11417946	NT	Homo sapiens mRNA for KIAA0892 protein, partial cds
7660	20620	33985	4.07	3.0E-66	X92211.1	NT	Homo sapiens protein kinase C beta-II type (PRKCB1) mRNA, complete cds
9883	22836	36290	0.71	3.0E-66	AK024453.1	NT	Homo sapiens NIPSNAP, C. elegans, homolog 1 (NIPSNAP1), mRNA
10077	23004	36474	0.62	3.0E-66	11417118	NT	H. sapiens geminine immunoglobulin heavy chain, variable region, (15-1)
10433	23355	36841	0.69	3.0E-66	7019480	NT	Homo sapiens mRNA for FLJ00045 protein, partial cds
10889	23809	37315	0.97	3.0E-66	AF155659.1	NT	Homo sapiens KIAA0493 protein (KIAA0493), mRNA
							Homo sapiens protocadherin beta 1 (PCDH-beta1), mRNA
							Homo sapiens molybdenum cofactor biosynthesis protein E (MCBPE) mRNA, complete cds

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Table 4
Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
11838	24721	38306	5.1	3.0E-66	5453949	NT	Homo sapiens protein phosphatase 2, regulatory subunit B (B56), alpha isoform (PPP2R5A) mRNA
13109	25629	31647	1.38	3.0E-66	11417862	NT	Homo sapiens calcitriol binding protein 1 (KIAA0330), mRNA
53	13173	26082	1.94	2.0E-66	7657334	NT	Homo sapiens Mitshapen/NIK-related kinase (MINK), mRNA
53	13173	26083	1.94	2.0E-66	7657334	NT	Homo sapiens Mitshapen/NIK-related kinase (MINK), mRNA
422	13117	26015	0.7	2.0E-66	4505524	NT	Homo sapiens origin recognition complex, subunit 5 (yeast homolog)-like (ORC5L) mRNA, and translated products
422	13117	26016	0.7	2.0E-66	4505524	NT	Homo sapiens origin recognition complex, subunit 5 (yeast homolog)-like (ORC5L) mRNA, and translated products
1843	14869	27867	2.18	2.0E-66	AL163301.2	NT	Homo sapiens chromosome 21 segment HS21C101
2241	15255	28279	2.33	2.0E-66	X65859.1	NT	H sapiens pseudogene for the low affinity IL-8 receptor
2986	16044	28665	1.39	2.0E-66	X65859.1	NT	H sapiens pseudogene for the low affinity IL-8 receptor
3632	16578	29501	0.79	2.0E-66	8923290	NT	Homo sapiens hypothetical protein FLJ20309 (FLJ20309), mRNA
3777	16919	29727	0.9	2.0E-66	AL117233.1	NT	Novel human gene mapping to chromosome 1
4685	17706	30598	36.62	2.0E-66	AJ133267.2	NT	Homo sapiens HLA-B gene for human leukocyte antigen B
4685	17706	30599	36.62	2.0E-66	AJ133267.2	NT	Homo sapiens HLA-B gene for human leukocyte antigen B
5914	19000	32191	0.82	2.0E-66	AW968854.1	EST_HUMAN	EST380930 IMAGE resequences, MAGJ Homo sapiens cDNA
5914	19000	32192	0.82	2.0E-66	AW968854.1	EST_HUMAN	EST380930 IMAGE resequences, MAGJ Homo sapiens cDNA
9199	22165	35595	2.86	2.0E-66	N45480.1	EST_HUMAN	y59c02.1 Soares multiple sclerosis 2/NbHMSF Homo sapiens cDNA clone IMAGE:277826 5'
12614	25941		2.61	2.0E-66	11418318	NT	Homo sapiens G-2 and S-phase expressed 1 (GTSE1), mRNA
2904	15963	28885	1.58	1.0E-66	AV717817.1	EST_HUMAN	AV717817 DCB Homo sapiens cDNA clone DCBADC07 5'
2904	15963	28886	1.58	1.0E-66	AV717817.1	EST_HUMAN	AV717817 DCB Homo sapiens cDNA clone DCBADC07 5'
4412	15963	28885	3.59	1.0E-66	AV717817.1	EST_HUMAN	AV717817 DCB Homo sapiens cDNA clone DCBADC07 5'
4412	15963	28886	3.59	1.0E-66	AV717817.1	EST_HUMAN	AV717817 DCB Homo sapiens cDNA clone DCBADC07 5'
5455	18557	31468	5.82	1.0E-66	BF673088.1	EST_HUMAN	602152896F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4284151 5'
5875	18964	32154	0.64	1.0E-66	BE765232.1	EST_HUMAN	IL2-NT0101-280700-116-E04 NT0101 Homo sapiens cDNA
5876	18964	32155	0.64	1.0E-66	BE765232.1	EST_HUMAN	IL2-NT0101-280700-116-E04 NT0101 Homo sapiens cDNA
7125	20058	33364	1.09	1.0E-66	BF328623.1	EST_HUMAN	RC5-BN0193-010800-034-G06 BN0193 Homo sapiens cDNA
8801	21768	35192	1.2	1.0E-66	AA663868.1	EST_HUMAN	aa30e04.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:327262 3'
9781	22722	36176	0.7	1.0E-66	AA018828.1	EST_HUMAN	ze57e12.1 Soares retina N2b-4HR Homo sapiens cDNA clone IMAGE:363118 5'
10737	23659	37153	0.9	1.0E-66	AV748749.1	EST_HUMAN	AV748749 NPC Homo sapiens cDNA clone NPCBVA05 5'
10737	23659	37154	0.9	1.0E-66	AV748749.1	EST_HUMAN	AV748749 NPC Homo sapiens cDNA clone NPCBVA05 5'
10993	23913	37429	0.44	1.0E-66	BE044595.1	EST_HUMAN	ho47h02.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:3040563 3'

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Table 4
Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
11290	24240	37787	2.47	1.0E-66	AF111167.2	NT	Homo sapiens jun dimerization protein gene, partial cds; cfos gene, complete cds; and unknown gene
11853	24735	38322	1.69	1.0E-68	AW988744.1	EST_HUMAN	EST380820 IMAGE resequences, MAGJ Homo sapiens cDNA
12398	25170		2.75	9.0E-67	11418177	NT	Homo sapiens Ran GTPase activating protein 1 (RANGAP1), mRNA
380	13493	26425	2.51	7.0E-67	AW182232.1	EST_HUMAN	au7502.x1 Schneider fetal brain 00004 Homo sapiens cDNA clone IMAGE:2782083 3' similar to gb:M37104
1382	14418	27386	1.23	7.0E-67	AA388416.1	EST_HUMAN	ATP SYNTHASE COUPLING FACTOR 6, MITOCHONDRIAL PRECURSOR (HUMAN);
1558	14590	27561	1.19	7.0E-67	W85947.1	EST_HUMAN	EST96812 Testis I Homo sapiens cDNA 5' end similar to C. elegans hypothetical protein, cosmid
1558	14590	27562	1.18	7.0E-67	W85947.1	EST_HUMAN	ZK353
2048	15067	28086	1.02	7.0E-67	7657243	NT	zhs6005.r1 Soares fetal_liver_spleen_INFLS_S1 Homo sapiens cDNA clone IMAGE:418049 5'
2048	15067	28087	1.02	7.0E-67	7657243	NT	zhs6005.r1 Soares fetal_liver_spleen_INFLS_S1 Homo sapiens cDNA clone IMAGE:418049 5'
2821	13493	26425	2.76	7.0E-67	AW182232.1	EST_HUMAN	Homo sapiens inositol 1,3,4-triphosphate 5/6 kinase (ITPK1), mRNA
6199	19273	32507	0.96	7.0E-67	10190695	NT	Homo sapiens inositol 1,3,4-triphosphate 5/6 kinase (ITPK1), mRNA
6401	19469	32716	1.92	7.0E-67	11425572	NT	Homo sapiens inositol 1,3,4-triphosphate 5/6 kinase (ITPK1), mRNA
6401	19469	32717	1.92	7.0E-67	11425572	NT	Homo sapiens inositol 1,3,4-triphosphate 5/6 kinase (ITPK1), mRNA
6885	19937	33233	1.14	7.0E-67	4885084	NT	au7502.x1 Schneider fetal brain 00004 Homo sapiens cDNA clone IMAGE:2782083 3' similar to gb:M37104
7893	20836	34216	1.13	7.0E-67	11419212	NT	ATP SYNTHASE COUPLING FACTOR 6, MITOCHONDRIAL PRECURSOR (HUMAN);
7893	20836	34217	1.13	7.0E-67	11419212	NT	Homo sapiens zinc finger protein 304 (ZNF304), mRNA
8666	21634	35055	0.69	7.0E-67	4557732	NT	Homo sapiens adaptor-related protein complex 2, beta 1 subunit (AP2B1), mRNA
9284	22250	35681	0.73	7.0E-67	10835044	NT	Homo sapiens adaptor-related protein complex 2, beta 1 subunit (AP2B1), mRNA
11985	24862	38458	2.45	7.0E-67	U82486.1	NT	Homo sapiens ATPase, H ⁺ -transporting, lysosomal (vacuolar proton pump) non-catalytic accessory protein
12169	25019	38619	1.92	7.0E-67	11430480	NT	1A (110/118KD) (ATP6N1A), mRNA
12169	25019	38620	1.92	7.0E-67	11430480	NT	Homo sapiens mitochondrial carrier family protein (LOC55972), mRNA
12639	25323	31789	1.86	7.0E-67	AB011399.1	NT	Homo sapiens mitochondrial carrier family protein (LOC55972), mRNA
13009	25661		1.44	7.0E-67	11421527	NT	Homo sapiens latent transforming growth factor beta binding protein 2 (LTBP2) mRNA
561	13631	26548	1.19	6.0E-67	X68988.1	NT	Homo sapiens retinaldehyde dehydrogenase 2 (RALDH2), mRNA
796	13855	26802	1.7	6.0E-67	Z1727.1	NT	Human cytochrome oxidase subunit VIa (COX6A1P) pseudogene, complete cds
1278	14313	27274	2.06	6.0E-67	Y14320.1	NT	Homo sapiens low density lipoprotein-related protein 2 (LRP2), mRNA
3183	16238	29156	1.16	6.0E-67	4506434	NT	Homo sapiens low density lipoprotein-related protein 2 (LRP2), mRNA
3451	16497	29414	1.33	6.0E-67	4507332	NT	Homo sapiens gene for AF-6, complete cds
3451	16497	29415	1.33	6.0E-67	4507332	NT	Homo sapiens gene for AF-6, complete cds
							Homo sapiens calcium channel, voltage-dependent, alpha 2(delta subunit 1 (CACNA2D1), mRNA
							H. sapiens mRNA for acetyl-CoA carboxylase
							Homo sapiens mRNA for transmembrane receptor protein
							Homo sapiens PMP69 gene, exons 3,4,5,6 & 7
							Homo sapiens retinoblastoma 1 (including osteosarcoma) (RB1) mRNA
							Homo sapiens Synapsin III (SYN3) mRNA, and translated products
							Homo sapiens Synapsin III (SYN3) mRNA, and translated products

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4152	17183	30069	0.79	6.0E-67	AL163201.2	NT	Homo sapiens chromosome 21 segment HS21C001
4152	17183	30070	0.79	6.0E-67	AL163201.2	NT	Homo sapiens chromosome 21 segment HS21C001
4734	17754	30647	3.56	6.0E-67	7657020	NT	Homo sapiens DKFZp434P211 protein (DKFZP434P211), mRNA
4734	17754	30648	3.56	6.0E-67	7657020	NT	Homo sapiens DKFZp434P211 protein (DKFZP434P211), mRNA
5242	18250	31121	0.99	6.0E-67	AF018898.1	NT	Homo sapiens B-ATF gene, complete cds
5242	18250	31122	0.99	6.0E-67	AF018898.1	NT	Homo sapiens B-ATF gene, complete cds
3235	16290	29212	2.02	6.0E-67	AF009660.1	NT	Homo sapiens T cell receptor beta locus, TCRBV7S3A2 to TCRBV12S2 region
11329	24279		13.19	5.0E-67	BE010038.1	EST_HUMAN	PM3-BN0176-100400-001-g04 BN0176 Homo sapiens cDNA
1331	14366	27335	2.25	4.0E-67	R90819.1	EST_HUMAN	yo2411.1 Soares adult brain N2b4HB55Y Homo sapiens cDNA clone IMAGE:167253 5'
8355	21324	34736	0.89	4.0E-67	A1733032.1	EST_HUMAN	q26c05.x5 NC1 CGAP Kid3 Homo sapiens cDNA clone IMAGE:1493288 3' similar to SW:Z33A_HUMAN
8725	21693		1.18	4.0E-67	BF357321.1	EST_HUMAN	RC0-HT0934-130900-026-c03 HT0934 Homo sapiens cDNA
11403	24347		1.46	4.0E-67	AA714294.1	EST_HUMAN	rw06a01.st NC1 CGAP SS1 Homo sapiens cDNA clone IMAGE:1238472 3' similar to TR:O10385 O10385
2824	13699	26620	1.16	3.0E-67	AA333768.1	EST_HUMAN	PRO-POL-DUTPASE POLYPROTEIN ;
4723	17743	30634	2.52	3.0E-67	AW869159.1	EST_HUMAN	EST137903 Embryo, 9 week Homo sapiens cDNA 5' end
4753	17773		1.08	3.0E-67	AL163276.2	NT	MR3-SN0066-040500-008-01 SN0066 Homo sapiens cDNA
8522	21490	34905	1.15	3.0E-67	BF196068.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C079
11958	24526		15.35	3.0E-67	AA827874.1	EST_HUMAN	hr8105.x1 NC1 CGAP Kid11 Homo sapiens cDNA clone IMAGE:3134913 3' similar to SW:RHOP_MOUSE
190	13291	28217	0.97	2.0E-67	BE348354.1	EST_HUMAN	Q61085 GTP-RHO BINDING PROTEIN 1 ;
846	13902	28860	6.48	2.0E-67	AW816405.1	EST_HUMAN	om18b07.s1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1541365 3'
1107	14151		1.26	2.0E-67	AF167460.1	NT	hwr16g09.x1 NC1 CGAP Lu24 Homo sapiens cDNA clone IMAGE:3183136 3' similar to WP:F23H11.9
1901	14925	27922	1.26	2.0E-67	BE303037.1	EST_HUMAN	CE09617 ;
1901	14925		1.28	2.0E-67	BE303037.1	EST_HUMAN	QV4-ST0234-181199-037-005 ST0234 Homo sapiens cDNA
2251	15265	28291	0.9	2.0E-67	11422946	NT	Homo sapiens double stranded RNA activated protein kinase (PKR) gene, exons 2a, 2, 3, and 4
2251	15265	28292	0.9	2.0E-67	11422946	NT	ba72g05.y1 NIH_MGC 20 Homo sapiens cDNA clone IMAGE:2905976 5' similar to TR:O84892 O84892
2394	15401	28428	1.16	2.0E-67	AF309561.1	NT	KIAA0798 PROTEIN ;
2438	15445	28463	1.36	2.0E-67	4758795	NT	ba72g05.y1 NIH_MGC 20 Homo sapiens cDNA clone IMAGE:2905976 5' similar to TR:O84892 O84892
3481	16527	29452	3.78	2.0E-67	AA625755.1	EST_HUMAN	KIAA0798 PROTEIN ;
4027	17065	29966	2.7	2.0E-67	AL163300.2	NT	ba72g05.y1 NIH_MGC 20 Homo sapiens cDNA clone IMAGE:2905976 5' similar to TR:O84892 O84892

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6190	19284	32500	0.77	2.0E-67	AL049784.1	NT	Novel human gene mapping to chromosome 13
6247	19320	32550	4.91	2.0E-67	BF240759.1	EST_HUMAN	601875351F1 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:4091893 5'
6428	19494	32746	2.19	2.0E-67	AB051763.1	NT	Homo sapiens mRNA for NADPH-cytochrome P-450 reductase, complete cds
6428	19494	32747	2.19	2.0E-67	AB051763.1	NT	Homo sapiens mRNA for NADPH-cytochrome P-450 reductase, complete cds
6798	19852	33137	0.77	2.0E-67	AL120542.1	EST_HUMAN	DKFZp761A229_r1 761 (synonym: ham2) Homo sapiens cDNA clone DKFZp761A228 5'
8804	21870	35295	0.83	2.0E-67	AA334609.1	EST_HUMAN	EST38850 Embryo, 9 week Homo sapiens cDNA 5' end similar to cerebellin
8904	21870	35296	0.83	2.0E-67	AA334609.1	EST_HUMAN	EST38850 Embryo, 9 week Homo sapiens cDNA 5' end similar to cerebellin
9348	22313	35737	1.11	2.0E-67	AW602635.1	EST_HUMAN	RC4-BT0566-170100-011-c07 BT0566 Homo sapiens cDNA
9348	22313	35738	1.11	2.0E-67	AW602635.1	EST_HUMAN	RC4-BT0566-170100-011-c07 BT0566 Homo sapiens cDNA
9925	22809	36261	1.05	2.0E-67	AV731333.1	EST_HUMAN	AV731333 HTF Homo sapiens cDNA clone HTFARD03 5'
10067	22894	36463	1.01	2.0E-67	AW293824.1	EST_HUMAN	UI-H-B12-ahin-e-10-0-JL.st NCL CGAP_Sub4 Homo sapiens cDNA clone IMAGE:2727283 3'
10984	23904	37418	0.44	2.0E-67	AA928089.1	EST_HUMAN	on88607.st Scores_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1563541 3'
11249	24202	37724	1.47	2.0E-67	BF685768.1	EST_HUMAN	602140470F1 NIH_MGC_46 Homo sapiens cDNA clone IMAGE:4301705 5'
11380	24327	37856	1.58	2.0E-67	BF034485.1	EST_HUMAN	601456282F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3858975 5'
11396	26011		2.51	2.0E-67	11436448	NT	Homo sapiens KIAA0985 protein (KIAA0985), mRNA
11562	24502	38060	1.83	2.0E-67	BE295714.1	EST_HUMAN	601175762F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3531038 5'
11784	23939	37481	1.63	2.0E-67	BF377189.1	EST_HUMAN	PM2-TN0103-040900-001-c02 TN0103 Homo sapiens cDNA
12808	25434	31741	1.73	2.0E-67	11417877	NT	Homo sapiens gamma-glutamyltransferase 1 (GGT1), mRNA
253	13350	26276	1.82	1.0E-67	4502166	NT	Homo sapiens amyloid beta (A4) precursor protein (protease nexin-II, Alzheimer disease) (APP), mRNA
709	13771	26705	1.34	1.0E-67	AA702784.1	EST_HUMAN	z80b04.s1 Scores_fetal_liver_spleen_infls_S1 Homo sapiens cDNA clone IMAGE:448015 3'
10597	23509	37001	0.44	1.0E-67	Q93075	SWISSPROT	HYPOTHETICAL PROTEIN KIAA0218
10587	23509	37002	0.44	1.0E-67	Q93075	SWISSPROT	HYPOTHETICAL PROTEIN KIAA0218
2186	15201	28221	2.37	8.0E-68	BE970732.1	EST_HUMAN	601448558F1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3852254 5'
3883	16923	29831	4.25	8.0E-68	AA209456.1	EST_HUMAN	z82h10.r1 Stratagene hNT neuron (#937233) Homo sapiens cDNA clone IMAGE:648163 5' similar to SW-SAV_SULAC Q07590 SAV PROTEIN ;
3883	16923	29832	4.25	8.0E-68	AA209456.1	EST_HUMAN	z82h10.r1 Stratagene hNT neuron (#937233) Homo sapiens cDNA clone IMAGE:648163 5' similar to SW-SAV_SULAC Q07590 SAV PROTEIN ;
8438	21407	34819	0.57	7.0E-68	AI810505.1	EST_HUMAN	w889e03.x1 NCL CGAP_P28 Homo sapiens cDNA clone IMAGE:2312860 3'
10816	23737	37240	2.46	6.0E-68	BE612554.1	NT	Homo sapiens brefeldin A-inhibited guanine nucleotide-exchange protein 2 (BIG2), mRNA
12811	25436		2.18	6.0E-68	BE612554.1	EST_HUMAN	601452067F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3855761 5'
13058	25594	31686	1.52	6.0E-68	BF310675.1	EST_HUMAN	601894635F2 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4124144 5'
803	15815	26810	0.88	5.0E-68	AF231918.1	NT	Homo sapiens chromosome 21 unknown mRNA
803	15815	26811	0.88	5.0E-68	AF231918.1	NT	Homo sapiens chromosome 21 unknown mRNA

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820	13678	28827	4.72	5.0E-68	AF231919.1	NT	Homo sapiens chromosome 21 unknown mRNA
820	13878	28828	4.72	5.0E-68	AF231919.1	NT	Homo sapiens chromosome 21 unknown mRNA
2791	15783	28799	1.23	5.0E-68	AF231919.1	NT	Homo sapiens chromosome 21 unknown mRNA
3162	16218	29133	3.08	5.0E-68	AB037852.1	NT	Homo sapiens mRNA for KIAA1431 protein, partial cds
4210	17239		0.8	5.0E-68	4826987	NT	Homo sapiens retinoblastoma-binding protein 2 (RBBP2) mRNA
4518	17543	30429	0.75	5.0E-68	AL157645.1	EST_HUMAN	DKFZp647D207.1 547 (synonym: hfor-1) Homo sapiens cDNA clone DKFZp647D207.5
6889	19941	33236	0.67	5.0E-68	7019512	NT	Homo sapiens RAB3A interacting protein (rab33)-like 1 (RAB33L1), mRNA
6889	19941	33237	0.67	5.0E-68	7019512	NT	Homo sapiens RAB3A interacting protein (rab33)-like 1 (RAB33L1), mRNA
2532	15535	28555	0.94	4.0E-68	11421388	NT	Homo sapiens transcription factor NRF (NRF), mRNA
2532	15535	28556	0.94	4.0E-68	11421388	NT	Homo sapiens transcription factor NRF (NRF), mRNA
5011	18025		7.63	4.0E-68	P04406	SWISSPROT	GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE, LIVER
6075	19156	32369	0.67	4.0E-68	AF157063.1	NT	Homo sapiens sedlin (SED1) gene, exon 4
6939	20163	33485	5.5	4.0E-68	11055991	NT	Homo sapiens serine carboxypeptidase 1 precursor protein (HSCP1), mRNA
6939	20163	33486	5.5	4.0E-68	11055991	NT	Homo sapiens serine carboxypeptidase 1 precursor protein (HSCP1), mRNA
7946	20887	34278	0.72	4.0E-68	7661683	NT	Homo sapiens DKFZP586L0724 protein (DKFZP586L0724), mRNA
9395	22360	35790	5.91	4.0E-68	D63479.2	NT	Homo sapiens mRNA for KIAA0145 protein, partial cds
9395	22360	35791	5.91	4.0E-68	D63479.2	NT	Homo sapiens mRNA for KIAA0145 protein, partial cds
9333	22496	35944	2.83	4.0E-68	AB040918.1	NT	Homo sapiens mRNA for KIAA1485 protein, partial cds
11345	24295	37821	1.55	4.0E-68	4508282	NT	Homo sapiens protein tyrosine phosphatase type IVA, member 1 (PTP4A1) mRNA
11345	24295	37822	1.55	4.0E-68	4508282	NT	Homo sapiens protein tyrosine phosphatase type IVA, member 1 (PTP4A1) mRNA
3673	16716	29630	5.02	3.0E-68	AF236082.1	NT	Mus musculus G-protein coupled receptor GPR73 (Gpr73) mRNA, complete cds
5299	18303	31164	0.93	3.0E-68	AF236082.1	NT	Mus musculus G-protein coupled receptor GPR73 (Gpr73) mRNA, complete cds
9812	21135		5.47	3.0E-68	A1342323.1	EST_HUMAN	q38h02.x1 Soares_fetal_lung_NbHL19W Homo sapiens cDNA clone IMAGE:1950291 3' similar to contains THR-2 THR repetitive element;
10868	23788	37288	2.01	3.0E-68	F28784.1	EST_HUMAN	HSPD18178 HM8 Homo sapiens cDNA clone s3000023D09
13012	25725		1.99	3.0E-68	AW939485.1	EST_HUMAN	QV1-DT0072-010200-056-h08 D10072 Homo sapiens cDNA
2873	18321		27.9	2.0E-68	D00522.1	NT	Cricetulus longicaudatus mRNA for EF-1 alpha, complete cds
4055	17092	29987	0.75	2.0E-68	BE675766.1	EST_HUMAN	HYPOTHETICAL 88.8 KD PROTEIN. ;
4708	17729	30623	1.86	2.0E-68	AB008881.1	NT	Homo sapiens gene for activin receptor type IIB, complete cds
7059	20081		9.21	2.0E-68	R45088.1	EST_HUMAN	y938g04.s1 Soares Infant brain IN1B Homo sapiens cDNA clone IMAGE:34898 3'
7265	20000	33289	4.51	2.0E-68	BF035316.1	EST_HUMAN	601458514F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3862034 5'
7425	20392		0.61	2.0E-68	11525737	NT	Homo sapiens UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylglucosaminyltransferase 8 (GalNAc-T8) (GALNT8), mRNA

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Table 4
Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7595	20556	33916	0.61	2.0E-68	BF336745.1	EST_HUMAN	IL3-CT0534-180900-273-A01 CT0534 Homo sapiens cDNA
8301	22268	35698	0.67	2.0E-68	Q05869	SWISSPROT	FORMIN 4 (LIMB DEFORMITY PROTEIN)
80	13196	26120	0.75	1.0E-68	4505222	NT	Homo sapiens meningioma (disrupted in balanced translocation) 1 (MN1), mRNA
296	13390	26318	17.69	1.0E-68	AW818405.1	EST_HUMAN	QV4-ST0234-181199-037-f05 ST0234 Homo sapiens cDNA
2263	15277	28301	1.27	1.0E-68	AB011149.1	NT	Homo sapiens mRNA for KIAA0577 protein, complete cds
2263	15277	28302	1.27	1.0E-68	AB011149.1	NT	Homo sapiens mRNA for KIAA0577 protein, complete cds
2767	15759	28781	1.04	1.0E-68	AW451832.1	EST_HUMAN	U1-H-B13-alk-f01-Q-U1 et NCI_CGAP_Sub5 Homo sapiens cDNA clone IMAGE:2737272 3'
4037	17075	29975	1.01	1.0E-68	BE286032.1	EST_HUMAN	601177002F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3632344 5'
5066	18076	30957	0.69	1.0E-68	AA807343.1	EST_HUMAN	sk47g12.s1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1460518 3'
5395	18498	31376	1.8	1.0E-68	7662349	NT	Homo sapiens cell recognition molecule Caspr2 (KIAA0868), mRNA
7938	20880	34270	0.56	1.0E-68	11436716	NT	Homo sapiens sentrin/SUMO-specific protease (SENP1), mRNA
11196	24153	37884	1.48	1.0E-68	11418869	NT	Homo sapiens phosphodiesterase 7B (PDE7B), mRNA
11198	24153	37885	1.48	1.0E-68	11418869	NT	Homo sapiens phosphodiesterase 7B (PDE7B), mRNA
11250	24203	37725	3.37	1.0E-68	L76416.1	NT	Homo sapiens MIF2 suppressor (HSMIT3) mRNA, complete cds
11631	24568	38131	2.13	1.0E-68	U50310.1	NT	Human protein kinase C substrate 80K-H (PRKCSH) gene, exon 4-5
11631	24568	38132	2.13	1.0E-68	U50310.1	NT	Human protein kinase C substrate 80K-H (PRKCSH) gene, exon 4-5
11975	24852	38449	1.73	1.0E-68	11418431	NT	Homo sapiens CGI-76 protein (LOC51632), mRNA
11975	24852	38450	1.73	1.0E-68	11418431	NT	Homo sapiens CGI-76 protein (LOC51632), mRNA
12790	13198	26120	2.19	1.0E-68	4506222	NT	Homo sapiens meningioma (disrupted in balanced translocation) 1 (MN1), mRNA
13005	25896	31419	2.07	1.0E-68	11430460	NT	Homo sapiens low density lipoprotein-related protein 2 (LRP2), mRNA
13057	25863		1.61	1.0E-68	11418213	NT	Homo sapiens ADP-ribosylation factor GTPase activating protein 1 (ARFGAP1), mRNA
22	13142	26040	5.15	9.0E-69	5031976	NT	Homo sapiens pre-B-cell colony-enhancing factor (PBEF) mRNA
22	13142	26041	5.15	9.0E-69	5031976	NT	Homo sapiens pre-B-cell colony-enhancing factor (PBEF) mRNA
1029	14075	27025	0.78	9.0E-69	5031980	NT	Homo sapiens 26S proteasome-associated pad1 homolog (POH1) mRNA
1029	14075	27026	0.78	9.0E-69	5031980	NT	Homo sapiens 26S proteasome-associated pad1 homolog (POH1) mRNA
4155	17186	30074	0.97	9.0E-69	4757867	NT	Homo sapiens v-rat murine sarcoma viral oncogene homolog B1 (BRAF) mRNA
4175	17206	30092	1.02	9.0E-69	4504010	NT	Homo sapiens glutamate-cysteine ligase (gamma-glutamylcysteine synthetase), regulatory (30.8kD) (GLCLR) mRNA
5241	18249	31120	0.93	9.0E-69	AF097177.1	NT	Homo sapiens T-cell receptor gamma V1 gene region
11236	24189		5.51	9.0E-69	AU117241.1	EST_HUMAN	AU117241 HEMBA1 Homo sapiens cDNA clone HEMBA1000968 5'
3387	16446		1.77	8.0E-69	AJ237744.1	NT	Homo sapiens RIBIR gene (partial), exon 12
6487	19552	32802	5.65	7.0E-69	9669912	NT	Homo sapiens actin-related protein 3-beta (ARP3BETA), mRNA
8195	21165	34574	15.42	8.0E-69	AI192764.1	EST_HUMAN	q662h01.x1 Soares_fetal_lung_NHL19W Homo sapiens cDNA clone IMAGE:1743601 3' similar to gb:U11566.60S RIBOSOMAL PROTEIN L18 (HUMAN);

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8195	21165	34575	15.42	6.0E-69	A192764.1	EST_HUMAN	q62h01.x1 Soares_fetal_lung_NbH19W Homo sapiens cDNA clone IMAGE:1743801 3' similar to
9325	22290	35720	1.04	5.0E-69	A4826039.1	EST_HUMAN	gbL11566 60S RIBOSOMAL PROTEIN L18 (HUMAN);
521	13592		1.27	4.0E-69	A1873830.1	EST_HUMAN	cd60a03.s1 NCI_CGAP_GCBT Homo sapiens cDNA clone IMAGE:1372300 3'
5855	25846	32130	1.38	4.0E-69	BE561063.1	EST_HUMAN	wm28h11.x1 NCI_CGAP_U4 Homo sapiens cDNA clone IMAGE:2437125 3'
							601344705F1 NIH_MGC_8 Homo sapiens cDNA clone IMAGE:3677641 5'
5943	19029	32223	5	4.0E-69	A1764973.1	EST_HUMAN	wh57606.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2384819 3' similar to TR-O55137
6783	19838	33123	2.77	4.0E-69	4557732	NT	O55137 ACYL-CoA THIOESTERASE.1
9265	22231	35692	0.55	4.0E-69	AU119634.1	EST_HUMAN	Homo sapiens latent transforming growth factor beta binding protein 2 (LTBP2) mRNA
388	13499	26432	3.2	3.0E-69	BE258012.1	EST_HUMAN	Homo sapiens latent transforming growth factor beta binding protein 2 (LTBP2) mRNA
614	13679	26595	2.56	3.0E-69	AF221712.1	NT	AU119634 HEMBA1 Homo sapiens cDNA clone HEMBA1006283 5'
2388	15394		0.93	3.0E-69	5729910	NT	601110371F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3351352 5'
4618	17639		0.93	3.0E-69	T96234.1	EST_HUMAN	Homo sapiens Smad- and Olf-interacting zinc finger protein mRNA, partial cds
5266	17639		0.93	3.0E-69	T96234.1	EST_HUMAN	Homo sapiens lymphatic vessel endothelial hyaluronan receptor 1 (LYVE-1) mRNA
5314	18330	36613	1.79	3.0E-69	11418185	NT	ye48h04.r1 Soares fetal liver spleen 1NF1S Homo sapiens cDNA clone IMAGE:121015 5'
5712	18806	31883	0.54	3.0E-69	U14178.1	NT	ye48h04.r1 Soares fetal liver spleen 1NF1S Homo sapiens cDNA clone IMAGE:121015 5'
6972	20195		0.58	3.0E-69	AJ277557.1	NT	Homo sapiens aconitase 2, mitochondrial (ACO2) mRNA
7038	18370	31257	0.6	3.0E-69	11426786	NT	Human type II IL-1 receptor gene, exon 1B
7597	20558	33918	0.82	3.0E-69	AF095703.1	NT	Homo sapiens dNT-2 gene for mitochondrial 5(3')-deoxyribonucleotidase (dNT-2 gene), exons 1-5.
7651	20611	33977	1.52	3.0E-69	U52351.1	NT	Homo sapiens sperm surface protein (HSS), mRNA
7800	20752	34428	8.4	3.0E-69	AF268075.1	NT	Homo sapiens short chain L-3-hydroxyacyl-CoA dehydrogenase precursor (HADHSC) gene, nuclear gene
8715	21683	35111	1.05	3.0E-69	AW138846.1	EST_HUMAN	Homo sapiens short chain L-3-hydroxyacyl-CoA dehydrogenase precursor (HADHSC) gene, nuclear gene
9120	22086		1.38	3.0E-69	AA376399.1	EST_HUMAN	encoding mitochondrial protein, complete cds
9328	22293	35722	0.5	3.0E-69	8923248	NT	Homo sapiens arm-repeat protein NPRAP/neurojulin (CTNND2) mRNA, partial cds
9768	22709	36164	1.64	3.0E-69	X13223.1	NT	Homo sapiens TRAF6-binding protein T6BP mRNA, complete cds
9891	22844	36301	59.4	3.0E-69	X06233.1	NT	U1-HB11-40w-g01-0-UI.s1 NCI_CGAP_Sub3 Homo sapiens cDNA clone IMAGE:2715840 3'
10188	23113	36597	0.71	3.0E-69	5730036	NT	ES T88807 HSC172 cells II Homo sapiens cDNA 5' and similar to similar to ribosomal protein S18
11003	23969	37493	3.29	3.0E-69	11432120	NT	Homo sapiens hypochlorite protein FLJ20275 (FLJ20275), mRNA
11190	24146		12.51	3.0E-69	AA376399.1	EST_HUMAN	Homo sapiens mRNA for N-acetylglucosaminide-(beta 1-4)-galactosyltransferase
12300	25111		7.34	3.0E-69	11419157	NT	Human mRNA for calcium-binding protein in macrophages (MRP-14) macrophage migration inhibitory factor (MIF)-related protein

Table 4

Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
129	13477	26411	1.06	2.0E-69	AF160252.1	NT	Homo sapiens KIAA0553 protein gene, complete cds; and alpha1b protein gene, partial cds
129	13477	26412	1.06	2.0E-69	AF160252.1	NT	Homo sapiens KIAA0553 protein gene, complete cds; and alpha1b protein gene, partial cds
404	13477	26411	4.75	2.0E-69	AF160252.1	NT	Homo sapiens KIAA0553 protein gene, complete cds; and alpha1b protein gene, partial cds
404	13477	26412	4.75	2.0E-69	AF160252.1	NT	Homo sapiens KIAA0553 protein gene, complete cds; and alpha1b protein gene, partial cds
1902	14926	27924	1.46	2.0E-69	BE257857.1	EST_HUMAN	601109444F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3350074 5'
2856	15916		3.8	2.0E-69	AA431157.1	EST_HUMAN	zw71g02.1 Scores, testis, NHT Homo sapiens cDNA clone IMAGE:781682 5'
8900	21866	35289	0.97	2.0E-69	AA114270.1	EST_HUMAN	zn29g01.1 Stratagene pancreas (#937208) Homo sapiens cDNA clone IMAGE:527088 5'
1714	14744	27728	2.69	1.0E-69	AF033768.1	NT	Rattus norvegicus brain specific cortactin-binding protein CBP80 mRNA, partial cds
5059	18089		0.73	1.0E-69	BE409094.1	EST_HUMAN	601301284F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3633781 5'
6169	19243	32474	0.78	1.0E-69	BE902501.1	EST_HUMAN	601875789F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3958532 5'
6168	19243	32478	0.78	1.0E-69	BE902501.1	EST_HUMAN	601875789F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3958532 5'
6768	19812	33092	4.09	1.0E-69	AW393959.1	EST_HUMAN	QV0-TT0010-031195-045-c07 TT0010 Homo sapiens cDNA
6992	20216	33544	1.4	1.0E-69	7662263	NT	Homo sapiens KIAA0716 gene product (KIAA0716), mRNA
6992	20216	33545	1.4	1.0E-69	7662263	NT	Homo sapiens KIAA0716 gene product (KIAA0716), mRNA
7011	20137	33453	2.78	1.0E-69	AB032973.1	NT	Homo sapiens mRNA for KIAA1147 protein, partial cds
7011	20137	33454	2.78	1.0E-69	AB032973.1	NT	Homo sapiens mRNA for KIAA1147 protein, partial cds
7065	20087	33396	0.62	1.0E-69	BE531007.1	EST_HUMAN	601278532F1 NIH_MGC_39 Homo sapiens cDNA clone IMAGE:3610614 5'
7065	20087	33397	0.62	1.0E-69	BE531007.1	EST_HUMAN	601278532F1 NIH_MGC_39 Homo sapiens cDNA clone IMAGE:3610614 5'
10534	23456	36952	4.31	1.0E-69	BE245070.1	EST_HUMAN	TCBAP1E2678 Pediatric pre-B cell acute lymphoblastic leukemia Baylor-HGSC project=TCBA Homo sapiens cDNA clone TCBAP2678
10534	23456	36953	4.31	1.0E-69	BE245070.1	EST_HUMAN	TCBAP1E2678 Pediatric pre-B cell acute lymphoblastic leukemia Baylor-HGSC project=TCBA Homo sapiens cDNA clone TCBAP2678
10631	23553	37053	1.48	1.0E-69	AB074607.1	NT	Homo sapiens mRNA for KIAA0707 protein, partial cds
10779	23700	37198	0.53	1.0E-69	BF528429.1	EST_HUMAN	602043782F1 NCL_CGAP_Bm87 Homo sapiens cDNA clone IMAGE:4181325 5'
11219	24172		2.78	1.0E-69	4804918	NT	Homo sapiens keratin 8 (KRT8) mRNA
12234	25068	38167	1.89	1.0E-69	BF125887.1	EST_HUMAN	601762902F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:4026785 5'
12848	25331		6.78	1.0E-69	AI809994.1	EST_HUMAN	wf64e08.x1 Scores, NFL, T, GBC, S1 Homo sapiens cDNA clone IMAGE:2360390 3' similar to contains Alu repetitive element; contains element M/R repetitive element;
2339	15980	28370	1.61	8.0E-70	AA230303.1	EST_HUMAN	nc13d12.1 NCL_CGAP_P1 Homo sapiens cDNA clone IMAGE:1008023
4401	17428	30314	2.11	8.0E-70	L77566.1	NT	Homo sapiens DGS-1 mRNA, 3' end
1830	14857	27854	2.26	7.0E-70	AI497807.1	EST_HUMAN	hm85f01.x1 NCL_CGAP_Bm25 Homo sapiens cDNA clone IMAGE:2165305 3'
1830	14857	27855	2.26	7.0E-70	AI497807.1	EST_HUMAN	hm85f01.x1 NCL_CGAP_Bm25 Homo sapiens cDNA clone IMAGE:2165305 3'
1947	14971	27969	1.87	7.0E-70	AA282955.1	EST_HUMAN	zf15n04.1 NCL_CGAP_GC81 Homo sapiens cDNA clone IMAGE:713239 5'
2078	15095		2.97	7.0E-70	5031669	NT	Homo sapiens tumor suppressor deleted in oral cancer-related 1 (DOC-1R) mRNA

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Table 4

Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4252	17281	30162	4.29	7.0E-70	4757723	NT	Homo sapiens adenylate cyclase 3 (ADCY3) mRNA
5560	18657	31602	5.36	7.0E-70	AB032369.1	NT	Homo sapiens MIST mRNA, partial cds
5560	18657	31603	5.36	7.0E-70	AB032369.1	NT	Homo sapiens MIST mRNA, partial cds
7110	20044	33346	2.38	7.0E-70	AJ000052.1	NT	Homo sapiens gene encoding splicing factor SF1, exons 2-8
8045	20982	34379	0.74	7.0E-70	11417308	NT	Homo sapiens tlin immunoglobulin domain protein (myelitin) (TITID), mRNA
8774	21741	35162	2.43	7.0E-70	AB037715.1	NT	Homo sapiens mRNA for KIAA1294 protein, partial cds
8774	21741	35163	2.43	7.0E-70	AB037715.1	NT	Homo sapiens mRNA for KIAA1294 protein, partial cds
9072	22038	35482	4.26	7.0E-70	M74099.1	NT	Human displacement protein (CCAAT) mRNA
9072	22038	35483	4.26	7.0E-70	M74099.1	NT	Human displacement protein (CCAAT) mRNA
9512	22475	35919	2.79	7.0E-70	X59841.1	NT	Human PBX3 mRNA
9512	22475	35920	2.79	7.0E-70	X59841.1	NT	Human PBX3 mRNA
9790	21133	34513	3.51	7.0E-70	AF153715.1	NT	Homo sapiens phospholipid scramblase 1 gene, exon 1 and 5' flanking region
9816	21138	34542	2.05	7.0E-70	11525964	NT	Homo sapiens karyopherin beta 2b, transportin (TRN2), mRNA
9816	21138	34543	2.05	7.0E-70	11525964	NT	Homo sapiens karyopherin beta 2b, transportin (TRN2), mRNA
10014	22941	36407	0.93	7.0E-70	4557624	NT	Homo sapiens glutamate-cysteine ligase (gamma-glutamylcysteine synthetase), catalytic (72.8kD) (GLCLC) mRNA
10661	23583	37079	0.6	7.0E-70	AB036429.1	NT	Homo sapiens NDST4 mRNA for N-deacetylase/N-sulfotransferase 4, complete cds
10661	23583	37080	0.6	7.0E-70	AB036429.1	NT	Homo sapiens NDST4 mRNA for N-deacetylase/N-sulfotransferase 4, complete cds
11923	24804	38396	2.36	7.0E-70	11526319	NT	Homo sapiens HIR (histone cell cycle regulation defective, S. cerevisiae) homolog A (HIRA), mRNA
11923	24804	38397	2.36	7.0E-70	11526319	NT	Homo sapiens HIR (histone cell cycle regulation defective, S. cerevisiae) homolog A (HIRA), mRNA
12893	25882	31414	13.53	7.0E-70	Z00040.1	NT	Human kappa-immunoglobulin germ line pseudogene variable region (subgroup V kappa I)
13071	25605	31688	34.82	7.0E-70	Z00040.1	NT	Human kappa-immunoglobulin germ line pseudogene variable region (subgroup V kappa I)
872	13928	28886	2.38	6.0E-70	4502166	NT	Homo sapiens amyloid beta (A4) precursor protein (protease nexin-II, Alzheimer disease) (APP), mRNA
2147	15163	28179	1.7	6.0E-70	M30938.1	NT	Human Ku (p70/p80) subunit mRNA, complete cds
2516	15519	28542	1.17	6.0E-70	8923899	NT	Homo sapiens CMP-N-acetylneuraminate acid synthase (LOC55907), mRNA
2559	15997	28577	1.76	5.0E-70	7662307	NT	Homo sapiens KIAA0792 gene product (KIAA0792), mRNA
2559	15997	28578	1.76	5.0E-70	7662307	NT	Homo sapiens KIAA0792 gene product (KIAA0792), mRNA
12243	25073	33265	2.52	5.0E-70	BE166034.1	EST_HUMAN	MR3-HT0487-150200-115-a06 HT0487 Homo sapiens cDNA
6918	19869	33265	1.24	4.0E-70	T06037.1	EST_HUMAN	EST03928 Fetal brain, Stralagene (cath936206) Homo sapiens cDNA clone HFBDN25
6961	20186	33510	0.78	4.0E-70	AW793226.1	EST_HUMAN	CM4-UM0003-010300-105-g08 UM0003 Homo sapiens cDNA
6961	20186	33511	0.78	4.0E-70	AW793226.1	EST_HUMAN	CM4-UM0003-010300-105-g08 UM0003 Homo sapiens cDNA

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Table 4
Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1593	14625	27598	1.56	3.0E-70	BE071796.1	EST_HUMAN	RCO-BT0522-071299-011-a12 BT0522 Homo sapiens cDNA
1593	14625	27599	1.56	3.0E-70	BE071796.1	EST_HUMAN	RCO-BT0522-071299-011-a12 BT0522 Homo sapiens cDNA
5701	18796	31970	0.63	3.0E-70	11430988	NT	Homo sapiens plakophilin 4 (PKP4), mRNA
5701	18796	31971	0.63	3.0E-70	11430988	NT	Homo sapiens plakophilin 4 (PKP4), mRNA
6055	19136	32346	1.1	3.0E-70	AI831975.1	EST_HUMAN	wh90d03.x1 NCI_CGAP_OLL1 Homo sapiens cDNA clone IMAGE:2385005 3'
6509	19573	32826	1.27	3.0E-70	BF685233.1	EST_HUMAN	602141661F1 NIH_MGC_46 Homo sapiens cDNA clone IMAGE:4302805 5'
6509	19573	32827	1.27	3.0E-70	BF685233.1	EST_HUMAN	602141661F1 NIH_MGC_46 Homo sapiens cDNA clone IMAGE:4302805 5'
10467	23389	36883	0.55	3.0E-70	BE502973.1	EST_HUMAN	hzb1h02.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3214419 3'
40	13160	26063	2.14	2.0E-70	AF012872.1	NT	Homo sapiens phosphatidylinositol 4-kinase 230 (p4K230) mRNA, complete cds
690	13763	26680	14.23	2.0E-70	N42181.1	EST_HUMAN	W07a10.r1 Scores melanocyte 2N5HM Homo sapiens cDNA clone IMAGE:270522 5' similar to SW:D3HL_RAT P29268 3-HYDROXYISOBUTYRATE DEHYDROGENASE PRECURSOR ;
690	13763	26681	14.23	2.0E-70	N42181.1	EST_HUMAN	W07a10.r1 Scores melanocyte 2N5HM Homo sapiens cDNA clone IMAGE:270522 5' similar to SW:D3HL_RAT P29268 3-HYDROXYISOBUTYRATE DEHYDROGENASE PRECURSOR ;
706	13768	26704	1.39	2.0E-70	A246899.1	EST_HUMAN	qp51h01.x1 NCI_CGAP_Pan1 Homo sapiens cDNA clone IMAGE:2004913 3'
1023	14069	27020	1.23	2.0E-70	8923669	NT	Homo sapiens hypothetical protein FLJ20768 (FLJ20768), mRNA
1188	14228	27184	1.73	2.0E-70	7661983	NT	Homo sapiens KIAA0193 gene product (KIAA0193), mRNA
1188	14228	27185	1.73	2.0E-70	7661983	NT	Homo sapiens KIAA0193 gene product (KIAA0193), mRNA
1664	14696	27671	1.53	2.0E-70	AA180093.1	EST_HUMAN	zp45h05.r1 StrataGene HeLa cell s3 837216 Homo sapiens cDNA clone IMAGE:612441 5' similar to TR:G1041293.G1041293.D2085.5 ;
1664	14696	27672	1.53	2.0E-70	AA180093.1	EST_HUMAN	zp45h05.r1 StrataGene HeLa cell s3 837216 Homo sapiens cDNA clone IMAGE:612441 5' similar to TR:G1041293.G1041293.D2085.5 ;
1757	14786	27771	1.73	2.0E-70	AL163202.2	NT	Homo sapiens chromosome 21 segment HS21C002
2328	15339		5.47	2.0E-70	AA054010.1	EST_HUMAN	zf48g04.r1 Scores retina N2b4-HR Homo sapiens cDNA clone IMAGE:380214 5' similar to SW:GAG_HTL1A
3641	16694	29600	1.06	2.0E-70	H37988.1	EST_HUMAN	P03345 GAG POLYPROTEIN ;
3833	16873	29774	0.86	2.0E-70	AL133207.2	NT	yp58b04.r1 Scores fetal liver spleen 1NfLS Homo sapiens cDNA clone IMAGE:191599 5'
4079	17114	30010	5.63	2.0E-70	M69181.1	NT	Novel human gene mapping to chromosome X
4221	17260	30135	0.96	2.0E-70	L78810.1	NT	Human nonmuscle myosin heavy chain-B (MYH10) mRNA, partial cds
4221	17260	30136	0.96	2.0E-70	L78810.1	NT	Homo sapiens ADP/ATP carrier protein (ANT-2) gene, complete cds
5593	16698	31658	9.14	2.0E-70	X72662.1	NT	Homo sapiens ADP/ATP carrier protein (ANT-2) gene, complete cds
5593	16699	31659	9.14	2.0E-70	X72662.1	NT	H. sapiens gene for schwannomin (CS8)
6328	19398	32840	1.1	2.0E-70	AF310105.1	NT	H. sapiens gene for schwannomin (CS8)
6780	19844	33128	3.84	2.0E-70	D12625.1	NT	Homo sapiens NALP1 mRNA, complete cds
8824	19878	33167	11.3	2.0E-70	AF123074.1	NT	Human mRNA for NF1 protein isoform (neurofibromin isoform), complete cds
						NT	Homo sapiens cytoplasmic dynein intermediate chain 1 mRNA, complete cds

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Single Exon Probes Expressed in Bone Marrow.

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6824	19878	33168	11.3	2.0E-70	AF123074.1	NT	Homo sapiens cytoplasmic dynein intermediate chain 1 mRNA, complete cds
7190	18421	31223	1.44	2.0E-70	11422642	NT	Homo sapiens sialyltransferase 6 (N-acetylglucosaminidase alpha 2,3-sialyltransferase) (SIAT6), mRNA
7633	20593	33956	0.58	2.0E-70	AF288207.1	NT	Homo sapiens cysteinyl-L-proline synthetase mRNA, complete cds, alternatively spliced
8251	21220	34629	5.38	2.0E-70	M21741.1	NT	Human guanine nucleotide-binding protein alpha-subunit gene (G-s-alpha), exons 4 and 5
8564	21532	34952	0.45	2.0E-70	11423599	NT	Homo sapiens amylo-1,6-glucosidase, 4-alpha-glucanotransferase (glycogen debranching enzyme, glycogen storage disease type III) (AGL), mRNA
9007	21973		0.76	2.0E-70	H47959.1	EST_HUMAN	yo78902.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:193682 5'
9524	22487	35935	0.95	2.0E-70	11528355	NT	Homo sapiens dynactin p62 subunit (LOC31164), mRNA
10497	23419	36918	1.42	2.0E-70	AF123303.1	NT	Homo sapiens calcium-binding transporter mRNA, partial cds
10963	23983	37396	0.49	2.0E-70	AB033042.1	NT	Homo sapiens mRNA for KIAA1216 protein, partial cds
11408	24352	37884	3.11	2.0E-70	8923420	NT	Homo sapiens hypothetical protein FLJ20450 (FLJ20450), mRNA
11408	24352	37885	3.11	2.0E-70	8923420	NT	Homo sapiens hypothetical protein FLJ20450 (FLJ20450), mRNA
11956	24835	38431	11.5	2.0E-70	4503520	NT	Homo sapiens eukaryotic translation initiation factor 3, subunit 6 (48kD) (EIF3S6) mRNA
12637	25321	31786	2.64	2.0E-70	11430460	NT	Homo sapiens low density lipoprotein-related protein 2 (LRP2), mRNA
12637	25321	31787	2.64	2.0E-70	11430460	NT	Homo sapiens low density lipoprotein-related protein 2 (LRP2), mRNA
3404	16453		3.08	1.0E-70	4507476	NT	Homo sapiens transglutaminase 3 (E polypeptide, protein-glutamine-gamma-glutamyltransferase) (TGM3) mRNA
9635	22579		0.78	1.0E-70	W85795.1	EST_HUMAN	zh55g05.r1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:416024 5'
10158	23083		0.64	1.0E-70	AA442292.1	EST_HUMAN	zv54c03.r1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:767444 5'
11281	24231	37157	8.6	1.0E-70	AV735538.1	EST_HUMAN	AV738538 CB Homo sapiens cDNA clone CBLGB10 5'
6054	19135	32344	7.1	9.0E-71	AI143870.1	EST_HUMAN	qe04f01.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1738009 3' similar to TR:O14045
6054	19135	32345	7.1	9.0E-71	AI143870.1	EST_HUMAN	qe04f01.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1738009 3' similar to TR:O14045
7231	20253	33587	1.98	9.0E-71	AI654903.1	EST_HUMAN	O14045 PHOSPHOTRANSFERASE ;
11852	20253	33587	3.67	9.0E-71	AI654903.1	EST_HUMAN	Wb52c05.x1 NCI_CGAP_GC6 Homo sapiens cDNA clone IMAGE:2309288 3' similar to TR:P97213 P97213
9425	22389		3.62	8.0E-71	AA171451.1	EST_HUMAN	CDU2, CDU1, TCDD, TCDB, TCDE, TCDA, TCDC, CDD1, CDD2, CDD3, AND CDD4 GENES. ;
10967	23887	37398	0.45	8.0E-71	AW273820.1	EST_HUMAN	Wb52c05.x1 NCI_CGAP_GC6 Homo sapiens cDNA clone IMAGE:2309288 3' similar to TR:P97213 P97213
7601	20562	33923	8.17	7.0E-71	AA442230.1	EST_HUMAN	CDU2, CDU1, TCDD, TCDB, TCDE, TCDA, TCDC, CDD1, CDD2, CDD3, AND CDD4 GENES. ;
							zp21d11.r1 Stratagene neuroepithelium (#837321) Homo sapiens cDNA clone IMAGE:610101 5' similar to TR:G1143061 G1143061 STRAIN XA34 POL. ;
							xv24d01.x1 Soares_NFL_I_GBC_S1 Homo sapiens cDNA clone IMAGE:2814049 3' similar to TR:O54730
							O54730 TRANSPLANTABILITY ASSOCIATED PROTEIN 1 ;
							zv60h06.r1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:758075 5'

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Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9028	21892	35412	1.61	7.0E-71	AA705487.1	EST_HUMAN	zfp1a06.s1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:462228 3'
11658	24594	38168	1.78	7.0E-71	AL163210.2	NT	Homo sapiens chromosome 21 segment HS21C010
2220	15234	28258	8.79	5.0E-71	AF056322.1	NT	Homo sapiens SP100-HMG nuclear autoantigen (SP100) mRNA, complete cds
4145	17177	30068	1.1	5.0E-71	AW818409.1	EST_HUMAN	QV4-ST0234-181189-037-705 ST0234 Homo sapiens cDNA
5981	19068	32264	2.02	5.0E-71	4502740	NT	Homo sapiens cyclin-dependent kinase 6 (CDK6) mRNA
8819	19873	33162	1.15	5.0E-71	11641408	NT	Homo sapiens keratin, hair, acidic, 7 (KRT1A7), mRNA
7105	20039	33341	0.72	5.0E-71	7662209	NT	Homo sapiens KIAA0623 gene product (KIAA0623), mRNA
7167	18398	31243	0.64	5.0E-71	AB033106.1	NT	Homo sapiens mRNA for KIAA1280 protein, partial cds
7167	18398	31244	0.64	5.0E-71	AB033106.1	NT	Homo sapiens mRNA for KIAA1280 protein, partial cds
7353	20323	33871	0.69	5.0E-71	11431590	NT	Homo sapiens protein kinase C, beta 1 (PRKCB1), mRNA
7753	20706	34075	1.62	5.0E-71	M38108.1	NT	Human neurofibromatosis protein type 1 mRNA, 3' end of cds
7974	20913	34304	0.84	5.0E-71	11626445	NT	Homo sapiens MAGUK protein p55T; Protein Associated with Lins 2 (LOC51678), mRNA
8007	20945	34340	22.85	5.0E-71	AF072810.1	NT	Homo sapiens transcription factor WSTF mRNA, complete cds
8868	21835	35258	0.61	5.0E-71	5453777	NT	Homo sapiens nuclear factor related to kappa B binding protein (NFKB) mRNA
8868	21835	35257	0.61	5.0E-71	5453777	NT	Homo sapiens nuclear factor related to kappa B binding protein (NFKB) mRNA
10271	23196		2.45	5.0E-71	X13467.1	NT	Human PEA4 gene for Alzheimer's disease A4 amyloid protein precursor (exon 2)
11325	24275	37803	7.5	5.0E-71	11436514	NT	Homo sapiens pro-platelet basic protein (includes platelet basic protein, beta-thromboglobulin, connective tissue-activating peptide III, neutrophil-activating peptide-2) (PPBP), mRNA
11525	24468	38020	2.01	5.0E-71	11438069	NT	Homo sapiens similar to hypothetical protein FLJ20163 (H. sapiens) (LOC63325), mRNA
12198	25043	38624	1.81	5.0E-71	11417862	NT	Homo sapiens calcineurin binding protein 1 (KIAA0330), mRNA
104	13220	26145	1.04	4.0E-71	4507592	NT	Homo sapiens tumor necrosis factor (ligand) superfamily, member 10 (TNFSF10) mRNA
350	13439	26363	58.4	4.0E-71	AF157628.1	NT	Equus caballus glyceraldehyde-3-phosphate dehydrogenase mRNA, partial cds
350	13439	26364	58.4	4.0E-71	AF157628.1	NT	Equus caballus glyceraldehyde-3-phosphate dehydrogenase mRNA, partial cds
2897	15956	28873	1.9	4.0E-71	4505880	NT	Homo sapiens plasminogen (PLG) mRNA
4459	17485	30372	4.75	4.0E-71	AF056322.1	NT	Homo sapiens SP100-HMG nuclear autoantigen (SP100) mRNA, complete cds
5022	18036	30921	6.04	4.0E-71	7657602	NT	Homo sapiens putative heme-binding protein (SOL), mRNA
8368	21337		1.34	3.0E-71	AU135734.1	EST_HUMAN	AU135734 PLACE1 Homo sapiens cDNA clone PLACE1002775 5'
11051	24014	37538	2.84	3.0E-71	AA657683.1	EST_HUMAN	nt45ht0.s1 NC1_CGAP_Pra Homo sapiens cDNA clone IMAGE:1043683 similar to contains PTR5.13 PTR6 repetitive element;
1234	14271	27231	5.56	2.0E-71	AL163206.2	NT	Homo sapiens chromosome 21 segment HS21C006
5393	18496	31374	8.35	2.0E-71	D87462.1	NT	Human mRNA for KIAA0272 gene, partial cds
5393	18496	31375	8.35	2.0E-71	D87462.1	NT	Human mRNA for KIAA0272 gene, partial cds
7160	18392	31236	0.67	2.0E-71	AL042439.1	EST_HUMAN	DKFZp434D1721_r1 434 (synonym: htas3) Homo sapiens cDNA clone DKFZp434D1721 5'

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9359	22324	35752	0.5	2.0E-71	BF195585.1	EST_HUMAN	7n85c11.x1 NCL CGAP_Ov18 Homo sapiens cDNA clone IMAGE:3571221 3' similar to TR:Q8Z185 Q8Z185 PUTATIVE FOUR REPEAT ION CHANNEL 1
10950	23870	37382	4.19	2.0E-71	AF095703.1	NT	Homo sapiens short chain L-3-hydroxyacyl-CoA dehydrogenase precursor (HADHSC) gene, nuclear gene encoding mitochondrial protein, complete cds
10950	23870	37383	4.19	2.0E-71	AF095703.1	NT	Homo sapiens short chain L-3-hydroxyacyl-CoA dehydrogenase precursor (HADHSC) gene, nuclear gene encoding mitochondrial protein, complete cds
11053	24016	37539	3.41	2.0E-71	BE018477.1	EST_HUMAN	bb81a06.y1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3048754 5' similar to SW:R238_HUMAN P54727 UV EXCISION REPAIR PROTEIN RAD23 HOMOLOG B
11907	24768	38377	2.27	2.0E-71	R55926.1	EST_HUMAN	377c11.11 Soares breast 2NblHst Homo sapiens cDNA clone IMAGE:154772 5'
12315	25121		7.13	2.0E-71	T95489.1	EST_HUMAN	ye43e09.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:120520 5'
839	13705	26826	1.69	1.0E-71	A1077927.1	EST_HUMAN	oy15e03.s1 Soares senescent_fibroblasts_NbHSF Homo sapiens cDNA clone IMAGE:1665916 3' similar to contains LOR1.b2 LOR1 repetitive element
940	13993	26945	1.58	1.0E-71	7706281	NT	Homo sapiens neuronal cell death-related protein (LOC51616), mRNA
1102	14148	27096	6.21	1.0E-71	AF205890.1	NT	Homo sapiens disabled-2 gene, exons 2 through 15 and complete cds
1343	14378	27347	9.86	1.0E-71	AF012872.1	NT	Homo sapiens phosphatidylinositol 4-kinase 230 (p4K230) mRNA, complete cds
2094	15111	28131	1.29	1.0E-71	AB017007.1	NT	Homo sapiens PMS2L16 mRNA, partial cds
2094	15111	28132	1.29	1.0E-71	AB017007.1	NT	Homo sapiens PMS2L16 mRNA, partial cds
2703	15899	28714	4.81	1.0E-71	7657153	NT	Homo sapiens hairy/enhancer-of-split related with YRPW motif-like (HEYL), mRNA
3610	16655	29572	5.11	1.0E-71	AF246219.1	NT	Homo sapiens SNARE protein kinase SNAK mRNA, complete cds
3610	16655	29573	5.11	1.0E-71	AF246219.1	NT	Homo sapiens SNARE protein kinase SNAK mRNA, complete cds
3662	16705	29819	1.18	1.0E-71	BE122850.1	EST_HUMAN	02_15 Human Epidermal Keratinocyte Subtraction Library- Upregulated Transcripts Homo sapiens cDNA clone 02_15 5' similar to Homo sapiens chromosome 19
3662	16705	29820	1.18	1.0E-71	BE122850.1	EST_HUMAN	02_15 Human Epidermal Keratinocyte Subtraction Library- Upregulated Transcripts Homo sapiens cDNA clone 02_15 5' similar to Homo sapiens chromosome 19
3754	16706	29707	1.56	1.0E-71	AF218904.1	NT	Homo sapiens attractin precursor (ATRIN) gene, exon 19
4497	17522	30409	2.16	1.0E-71	D28476.1	NT	Human mRNA for KIAA0045 gene, complete cds
4622	17643	30531	0.88	1.0E-71	H23176.1	EST_HUMAN	ym56h10.r1 Soares infant brain 1N1B Homo sapiens cDNA clone IMAGE:52528 5'
6906	19958	33255	1.38	1.0E-71		NT	Homo sapiens GCN5 (general control of amino-acid synthesis, yeast, homdog)-like 2 (GCN5L2), mRNA
7292	20264	33598	1.28	1.0E-71	AB011131.1	NT	Homo sapiens mRNA for KIAA0559 protein, partial cds
7533	20496	33857	12.87	1.0E-71	U80753.1	NT	Homo sapiens CAGL79 mRNA, partial cds
8466	21454	34871	0.76	1.0E-71	AF105297.1	NT	Homo sapiens glycylcan-6 (GPO6) mRNA, complete cds
8509	21477	34890	2.14	1.0E-71	11425430	NT	Homo sapiens myomesin (M-protein) 2 (168kD) (MYOM2), mRNA
8789	21756	35177	4.49	1.0E-71	8922811	NT	Homo sapiens hypothetical protein FLJ10998 (FLJ10998), mRNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Description
8789	21766	35178	4.49	1.0E-71	8922811	NT	Homo sapiens hypothetical protein FLJ10998 (FLJ10998), mRNA
9584	22546	35997	0.83	1.0E-71	S72393.1	NT	CSNK2A1-casein kinase II (CKII) subunit alpha [human, Genomic, 18862 nt]
10367	23290	36767	9.49	1.0E-71	AY007643.1	NT	Homo sapiens cytochrome c oxidase subunit VIIa-related protein gene, complete cds
10428	23350		3.08	1.0E-71	AV761217.1	EST_HUMAN	AV761217 MDS Homo sapiens cDNA clone MDSEIA03 5'
10904	23824	37336	1.52	1.0E-71	11433142	NT	Homo sapiens activated leucocyte cell adhesion molecule (ALCAM), mRNA
11137	24097		2.43	1.0E-71	AV761217.1	EST_HUMAN	AV761217 MDS Homo sapiens cDNA clone MDSEIA03 5'
11228	24181	37706	2.12	1.0E-71	11418903	NT	Homo sapiens coagulation factor XIII, A1 polypeptide (F13A1), mRNA
11481	24424	37973	2.27	1.0E-71	11417191	NT	Homo sapiens leucyl/cystinyl aminopeptidase (LNPEP), mRNA
11481	24424	37974	2.27	1.0E-71	11417191	NT	Homo sapiens leucyl/cystinyl aminopeptidase (LNPEP), mRNA
12681	25349		3.13	1.0E-71	AB011399.1	NT	Homo sapiens gene for AP-6, complete cds
407	13480	26414	1.23	9.0E-72	AB87635.1	EST_HUMAN	wk95g03.x1 NCL_CGAP_Lu19 Homo sapiens cDNA clone IMAGE:2423188 3' similar to TR:O86705 O86705 HYPOTHETICAL 38.6 KD PROTEIN, contains Alu repetitive element.
407	13480	26415	1.23	9.0E-72	AB87635.1	EST_HUMAN	wk95g03.x1 NCL_CGAP_Lu19 Homo sapiens cDNA clone IMAGE:2423188 3' similar to TR:O86705 O86705 HYPOTHETICAL 38.6 KD PROTEIN, contains Alu repetitive element.
6232	19306	32538	0.89	8.0E-72	BF035762.1	EST_HUMAN	601458747F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3862451 5'
11444	24387	37927	2.55	8.0E-72	11424480	NT	Homo sapiens nuclear RNA helicase, DECD variant of DEAD box family (DDXL), mRNA
11444	24387	37928	2.55	8.0E-72	11424480	NT	Homo sapiens nuclear RNA helicase, DECD variant of DEAD box family (DDXL), mRNA
11444	24387	37929	2.55	8.0E-72	11424480	NT	Homo sapiens nuclear RNA helicase, DECD variant of DEAD box family (DDXL), mRNA
4139	17170	30056	1.24	7.0E-72	4501866	NT	Homo sapiens aconitase 2, mitochondrial (ACO2), nuclear gene encoding mitochondrial protein, mRNA
4139	17170	30057	1.24	7.0E-72	4501866	NT	Homo sapiens aconitase 2, mitochondrial (ACO2), nuclear gene encoding mitochondrial protein, mRNA
4139	17170	30058	1.24	7.0E-72	4501866	NT	Homo sapiens aconitase 2, mitochondrial (ACO2), nuclear gene encoding mitochondrial protein, mRNA
7331	20302	33646	2.87	7.0E-72	S41894.1	NT	Homo sapiens aconitase 2, mitochondrial (ACO2), nuclear gene encoding mitochondrial protein, mRNA
12800	25428		1.52	7.0E-72	F26259.1	EST_HUMAN	(pseudogene) PTMAP2-prothymosin alpha [human, Genomic, 1192 nt, segment 2 of 3]
8727	21695		4.9	6.0E-72	AL163246.2	NT	HSPD13670 HM3 Homo sapiens cDNA clone s4000051G02 Homo sapiens chromosome 21 segment HS21C046
65	13184	26102	4.86	5.0E-72	BF333707.1	EST_HUMAN	QV0-CS0010-150900-398-e11 CS0010 Homo sapiens cDNA
65	13184	26103	4.86	5.0E-72	BF333707.1	EST_HUMAN	QV0-CS0010-150900-398-e11 CS0010 Homo sapiens cDNA
66	13184	26102	13.05	5.0E-72	BF333707.1	EST_HUMAN	QV0-CS0010-150900-398-e11 CS0010 Homo sapiens cDNA
66	13184	26103	13.05	5.0E-72	BF333707.1	EST_HUMAN	QV0-CS0010-150900-398-e11 CS0010 Homo sapiens cDNA
1141	14184		2.75	5.0E-72	L11645.1	NT	Homo sapiens alpha-tubulin mRNA, complete cds
7138	20114	33427	1.65	5.0E-72	AU128594.1	EST_HUMAN	AU128594 NT2RP2 Homo sapiens cDNA clone NT2RP2003751 5'

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Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1198	14238	27193	0.71	3.0E-72	U80226.1	NT	Human gamma-aminobutyric acid transaminase mRNA, partial cds
1198	14238	27194	0.71	3.0E-72	U80226.1	NT	Human gamma-aminobutyric acid transaminase mRNA, partial cds
1523	14555	27526	1.45	3.0E-72	BE242161.1	EST_HUMAN	TCAAP1E1252 Pediatric acute myelogenous leukemia cell (FAB M1) Baylor-HGSC project=TCAA Homo sapiens cDNA clone TCAAP1-252
3060	16148	29062	13.29	3.0E-72	AJ229043.1	NT	Homo sapiens 959 kb contig between AML1 and CBR1 on chromosome 21q22, segment 3/3
3292	16345	29265	2.41	3.0E-72	8923548	NT	Homo sapiens hypothetical protein FLJ20586 (FLJ20586), mRNA
3836	18876	29778	2.52	3.0E-72	S77599.1	NT	TCR V delta 2-C alpha = T-cell receptor delta and C alpha fusion gene (alternatively spliced, splice junction)
4576	17598	30492	3.77	3.0E-72	11416196	NT	[human, precursor B-cell line REH, mRNA Partial, 211 nt]
4800	17817	30710	1.31	3.0E-72	AF167572.1	NT	Homo sapiens hypothetical protein (FLJ11127), mRNA
4800	17817	30711	1.31	3.0E-72	AF167572.1	NT	Homo sapiens protein methyltransferase (JBP1) mRNA, complete cds
5149	18168	31037	1.02	3.0E-72	AW959677.1	EST_HUMAN	Homo sapiens protein methyltransferase (JBP1) mRNA, complete cds
5598	18694		1.06	3.0E-72	4756093	NT	EST371747 IMAGE resequences, MAGF Homo sapiens cDNA
6092	19171	32386	1.91	3.0E-72	AF073367.1	NT	Homo sapiens semaphorin W (SEMAW) mRNA
6092	19171	32387	1.91	3.0E-72	AF073367.1	NT	Homo sapiens growth factor receptor-bound protein 10 (GRB10) gene, exon 5
6290	19362	32600	4.78	3.0E-72	AB029004.1	NT	Homo sapiens growth factor receptor-bound protein 10 (GRB10) gene, exon 5
6290	19362	32601	4.78	3.0E-72	AB029004.1	NT	Homo sapiens mRNA for KIAA1081 protein, partial cds
6767	19821	33103	3.89	3.0E-72	4826987	NT	Homo sapiens ribosomal protein L3-like (RPL3L) mRNA
7838	20785	34190	1.87	3.0E-72	U80017.1	NT	Homo sapiens basic transcription factor 2 p44 (btf2p44) gene, partial cds, neuronal apoptosis inhibitory protein (naip) and survival motor neuron protein (smn) genes, complete cds
8516	21484	34898	1.07	3.0E-72	5031892	NT	Homo sapiens nuclear receptor subfamily 1, group H, member 3 (NR1H3), mRNA
10797	23718	37220	7.09	3.0E-72	X68289.1	NT	Homo sapiens nuclear receptor subfamily C, exon 2 and joined cds
11912	24793	38388	3.23	3.0E-72	11424091	NT	Homo sapiens CD37 antigen (CD37), mRNA
11912	24793	38384	3.23	3.0E-72	11424091	NT	Homo sapiens CD37 antigen (CD37), mRNA
12078	24950	38546	3.56	3.0E-72	AF190864.1	NT	Homo sapiens ADP-ribosylation factor binding protein GGA3 (GGA3) mRNA, complete cds
6069	19150	32362	1.53	2.0E-72	11426671	NT	Homo sapiens solute carrier family 13 (sodium-dependent dicarboxylate transporter), member 2 (SLC13A2), mRNA
9451	22415	35852	0.82	2.0E-72	BF308660.1	EST_HUMAN	601890419F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4131461 5'
9451	22415	35853	0.82	2.0E-72	BF308660.1	EST_HUMAN	601890419F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4131461 5'
11092	24052	37575	2.4	2.0E-72	AA789277.1	EST_HUMAN	a28b09.s1 Soares testis NHT Homo sapiens cDNA clone 1391609 3' similar to gb:X02067 H.sapiens mRNA for 7SL RNA pseudogene (HUMAN);
12726	28379	31745	6.47	2.0E-72	AF182714.1	NT	Rattus norvegicus putative phosphate/phosphoenolpyruvate translocator mRNA, complete cds
5881	18950	32136	3.78	1.0E-72	7637676	NT	Homo sapiens vacuolar protein sorting 41 (yeast homolog) (VPS41), mRNA
6711	19787	33046	1.24	1.0E-72	11321578	NT	Homo sapiens myosin, heavy polypeptide 13, skeletal muscle (MYH13), mRNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6711	19767	33047	1.24	1.0E-72	11321578	NT	Homo sapiens myosin, heavy polypeptide 13, skeletal muscle (MYH13), mRNA
6788	25668	33126	1.3	1.0E-72	AV751818.1	EST_HUMAN	AV751818 NPd Homo sapiens cDNA clone NPDAIE11 5'
7899	20842	34224	3.72	1.0E-72	BE175434.1	EST_HUMAN	RC4-HT0578-170300-012-g02 HT0578 Homo sapiens cDNA
7899	20842	34225	3.72	1.0E-72	BE175434.1	EST_HUMAN	RC4-HT0578-170300-012-g02 HT0578 Homo sapiens cDNA
9949	22876	36338	7.79	1.0E-72	AF222742.1	NT	Homo sapiens synaptic glycoprotein SC2 (SC2) mRNA, complete cds
9949	22876	36339	7.79	1.0E-72	AF222742.1	NT	Homo sapiens synaptic glycoprotein SC2 (SC2) mRNA, complete cds
1455	14488	27463	1.53	9.0E-73	AW374968.1	EST_HUMAN	MIR0-CT0063-071099-002-h11 CT0063 Homo sapiens cDNA
6156	19231	32462	0.94	9.0E-73	11525883	NT	Homo sapiens membrane protein, palmitoylated 3 (MAGUK p55 subfamily member 3) (MPP3), mRNA
11297	24247		18.46	9.0E-73	11424099	NT	Homo sapiens ribosomal protein L13a (RPL13A), mRNA
1039	14084	27035	0.93	8.0E-73	AW071755.1	EST_HUMAN	ws55c06.x1 NCL_CGAP_Bm25 Homo sapiens cDNA clone IMAGE:2501088 3' similar to TR:Q59050
5660	18756	31924	0.79	8.0E-73	4505798	NT	Q59050 HYPOTHETICAL PROTEIN MJ1866. ;
6724	19780	33059	5.01	8.0E-73	11426469	NT	Homo sapiens phosphatidylinositol 3-kinase, class 2, alpha polypeptide (PIK3C2A), mRNA
8432	21401	34814	2.3	8.0E-73	AF113129.1	NT	Homo sapiens lysosomal homologue (LOC57151), mRNA
							Homo sapiens vacuolar ATPase isoform VA68 mRNA, complete cds
9708	22681	36117	7.24	8.0E-73	BE019900.1	EST_HUMAN	bb62a06.y1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3030034 5' similar to gb:X04098_cds1 ACTIN, CYTOPLASMIC 2 (HUMAN); gb:M21495 Mouse cytoskeletal gamma-actin mRNA, complete cds (MOUSE);
10097	23023	36487	2.34	8.0E-73	11526037	NT	Homo sapiens interleukin 12 receptor, beta 1 (IL12RB1), mRNA
10097	23023	36498	2.34	8.0E-73	11526037	NT	Homo sapiens interleukin 12 receptor, beta 1 (IL12RB1), mRNA
12010	24887	38483	3.54	8.0E-73	AF084620.1	NT	Homo sapiens brefeldin A-inhibited guanine nucleotide-exchange protein 1 mRNA, complete cds
12785	25418	31735	3.45	8.0E-73	11418189	NT	Homo sapiens thyroid autoantigen 70kD (Ku antigen) (G22P1), mRNA
1136	14179	27130	1.3	7.0E-73	8923290	NT	Homo sapiens hypothetical protein FLJ20309 (FLJ20309), mRNA
3312	16365	26285	1	7.0E-73	AL163206.2	NT	Homo sapiens chromosome 21 segment HS21C006
4981	17996		1.74	7.0E-73	AL163206.2	NT	Homo sapiens chromosome 21 segment HS21C082
159	13262		2.28	6.0E-73	AL163218.2	NT	Homo sapiens chromosome 21 segment HS21C018
7378	20348	33699	3.58	6.0E-73	BE166874.1	EST_HUMAN	QV0-HT0494-020300-137-403 HT0494 Homo sapiens cDNA
5326	18432	31184	2.11	4.0E-73	11422159	NT	Homo sapiens HELG protein (FAM44A1), mRNA
1344	14379	27348	1.16	3.0E-73	AW1843789.1	EST_HUMAN	GMO-CN0044-260100-164-f08 CN0044 Homo sapiens cDNA
1879	14904	27904	1.34	3.0E-73	11435913	NT	Homo sapiens heme-binding protein (HBBP), mRNA
1879	14904	27905	1.34	3.0E-73	11435913	NT	Homo sapiens heme-binding protein (HBBP), mRNA
6856	19909	33204	0.86	3.0E-73	AA136403.1	EST_HUMAN	z195e04.s1 Stratagene fetal refina 937202 Homo sapiens cDNA clone IMAGE:565950 3' similar to gb:Z23064_cds1 HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN G (HUMAN);
9111	22077	35503	0.54	3.0E-73	AV729428.1	EST_HUMAN	AV729428 HTc Homo sapiens cDNA clone HTCAAF071 5'

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9111	22077	35504	0.54	3.0E-73	AV729428.1	EST_HUMAN	AV729428 HTC Homo sapiens cDNA clone HTCAAF071 5'
11047	24011		1.65	3.0E-73	X69660.1	NT	H.sapiens SH3GLP2 pseudogene, 5' end
13017	25567		1.35	3.0E-73	AL163246.2	NT	Homo sapiens chromosome 21 segment HS21C046
13021	25569		1.97	3.0E-73	AW898081.1	EST_HUMAN	RC3-NN0066-270400-011-c04 NN0066 Homo sapiens cDNA
852	13908	26966	1.9	2.0E-73	AF139897.1	NT	Homo sapiens BASS1 (BASS1) mRNA, partial cds
1963	14985		2.95	2.0E-73	AW898081.1	EST_HUMAN	RC3-NN0066-270400-011-c04 NN0066 Homo sapiens cDNA
2306	15318		1.58	2.0E-73	U01317.1	NT	Human beta globin region on chromosome 11
3196	16251	29170	3.89	2.0E-73	4502592	NT	Homo sapiens caspase 8, apoptosis-related cysteine protease (CASP8) mRNA
3561	16607	29527	0.77	2.0E-73	7669539	NT	Homo sapiens Parkinson disease (autosomal recessive, juvenile) 2, parkin (PARK2), transcript variant 3, mRNA
3561	16607	29528	0.77	2.0E-73	7669539	NT	Homo sapiens Parkinson disease (autosomal recessive, juvenile) 2, parkin (PARK2), transcript variant 3, mRNA
6577	19637	32902	0.7	2.0E-73	AF088824.1	NT	Mus musculus rho/rac-interacting citron kinase (Crik) mRNA, complete cds
6577	19637	32903	0.7	2.0E-73	AF088824.1	NT	Mus musculus rho/rac-interacting citron kinase (Crik) mRNA, complete cds
6827	19685	32964	6.38	2.0E-73	AB048811.1	NT	Homo sapiens mRNA for KIAA1591 protein, partial cds
6858	19911	33206	1.52	2.0E-73	11431471	NT	Homo sapiens interleukin 4 receptor (IL4R), mRNA
6858	19911	33207	1.52	2.0E-73	11431471	NT	Homo sapiens interleukin 4 receptor (IL4R), mRNA
8092	21028	34427	0.59	2.0E-73	M94048.1	NT	Human peripheral myelin protein 22 mRNA, complete cds
8099	21035	34435	0.77	2.0E-73	AB037760.1	NT	Homo sapiens mRNA for KIAA1329 protein, partial cds
8980	22843	36299	0.55	2.0E-73	AF198349.1	NT	Gallus gallus Dach2 protein (Dach2) mRNA, complete cds
9890	22843	36300	0.55	2.0E-73	AF198349.1	NT	Gallus gallus Dach2 protein (Dach2) mRNA, complete cds
10788	23709	37211	1.12	2.0E-73	4504168	NT	Homo sapiens glutathione synthetase (GSS) mRNA
10863	23783	37284	1.99	2.0E-73	11496980	NT	Homo sapiens supervillin (SVIL), transcript variant 1, mRNA
10863	23783	37285	1.99	2.0E-73	11496980	NT	Homo sapiens supervillin (SVIL), transcript variant 1, mRNA
11107	24087	37589	1.49	2.0E-73	11431598	NT	Homo sapiens KIAA1080 protein; Golgi-associated, gamma-actin binding protein 2 (KIAA1080), mRNA
11395	24341	37872	2.64	2.0E-73	4557612	NT	Homo sapiens galactosylceramidase (Krabbe disease) (GALC), mRNA
11395	24341	37873	2.64	2.0E-73	4557612	NT	Homo sapiens galactosylceramidase (Krabbe disease) (GALC), mRNA
11420	24354	37896	1.81	2.0E-73	AB028982.1	NT	Homo sapiens mRNA for KIAA1059 protein, partial cds
12681	14995		1.91	2.0E-73	AW898081.1	EST_HUMAN	RC3-NN0066-270400-011-c04 NN0066 Homo sapiens cDNA
1798	14827	27814	2.81	1.0E-73	AU121585.1	EST_HUMAN	AU121585 MAMMA1 Homo sapiens cDNA clone MAMMA1000490 5'
6495	19559	32810	1.2	1.0E-73	BE161283.1	EST_HUMAN	GM1-HT0282-111199-042-H10 HT0282 Homo sapiens cDNA
9857	22793	36244	1.47	1.0E-73	A1147427.1	EST_HUMAN	cg61607.r1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1839637 5' similar to contains element MER22 repetitive element;

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11779	23934	37455	2.1	1.0E-73	BE385477.1	EST_HUMAN	601276071F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3617105 5'
742	13803	26742	1.47	8.0E-74	4657426	NT	Homo sapiens CD39-like 4 (CD39L-4) mRNA
6021	19104	32306	1.84	8.0E-74	S83194.1	NT	Ca2+/calmodulin-dependent protein kinase IV kinase isoform [rats, brain, mRNA, 3429 nt]
6021	19104	32307	1.84	8.0E-74	S83194.1	NT	Ca2+/calmodulin-dependent protein kinase IV kinase isoform [rats, brain, mRNA, 3429 nt]
1966	14987	27989	4.43	7.0E-74	AJ001689.1	NT	Homo sapiens NKG2D gene, exon 10
3339	16390	29311	2.01	7.0E-74	AL163246.2	NT	Homo sapiens chromosome 21 segment HS21C046
8598	22602	36051	2.25	7.0E-74	BE967432.1	EST_HUMAN	601648284F1 NIH_MGC_73 Homo sapiens cDNA clone IMAGE:3932997 5'
12784	25417	31734	4.84	7.0E-74	BE268305.1	EST_HUMAN	601191927F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3335855 5'
1124	14168	27120	5.19	6.0E-74	AF109907.1	NT	Homo sapiens S164 gene, partial cds; P51 and hypothetical protein genes, complete cds; and S171 gene, partial cds
1631	14664	27639	1.03	6.0E-74	AW263177.1	EST_HUMAN	601283521F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:2700636 3'
2324	15335	28357	7.92	6.0E-74	BE388260.1	EST_HUMAN	601283521F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3605453 5'
2324	15335	28358	7.92	6.0E-74	BE388260.1	EST_HUMAN	601283521F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3605453 5'
2875	15934	28852	1.12	6.0E-74	AW014039.1	EST_HUMAN	U1-H-B10-aat-h-03-0-U1.s1 NCI CGAP_Sub1 Homo sapiens cDNA clone IMAGE:2709365 3'
2875	15934	28853	1.12	6.0E-74	AW014039.1	EST_HUMAN	U1-H-B10-aat-h-03-0-U1.s1 NCI CGAP_Sub1 Homo sapiens cDNA clone IMAGE:2709365 3'
3726	16768	29679	1.28	6.0E-74	BE048846.1	EST_HUMAN	h54e11.x1 NCI CGAP_Kid11 Homo sapiens cDNA clone IMAGE:3132332 3'
3726	16768	29680	1.28	6.0E-74	BE048846.1	EST_HUMAN	h54e11.x1 NCI CGAP_Kid11 Homo sapiens cDNA clone IMAGE:3132332 3'
5065	18075	30955	4.18	6.0E-74	4758135	NT	Homo sapiens DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 11 (S.cerevisiae CHL1-like helicase) (DDX11) mRNA
5065	18075	30956	4.18	6.0E-74	4758135	NT	Homo sapiens DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 11 (S.cerevisiae CHL1-like helicase) (DDX11) mRNA
5439	18541	31451	3.08	6.0E-74	11056013	NT	Homo sapiens actin filament associated protein (AFAP), mRNA
906	13981	26917	2.09	5.0E-74	AW020986.1	EST_HUMAN	df17c09.y1 Morton Fetal Cochlea Homo sapiens cDNA clone IMAGE:2483704 5'
2713	15707		3.68	5.0E-74	AW382766.1	EST_HUMAN	PM0-CT0289-271099-001-h07 CT0289 Homo sapiens cDNA
5481	18581	31492	1.76	5.0E-74	11425417	NT	Homo sapiens phosphatidylinositol glycan, class L (PIGL), mRNA
5887	18976	32168	12.05	5.0E-74	X89670.1	NT	H.sapiens mRNA for TPCR16 protein
5938	19024	32218	7.23	5.0E-74	4507966	NT	Homo sapiens VAMP (vesicle-associated membrane protein)-associated protein A (33kD) (VAPA), mRNA, and translated products
6013	19096	32296	2.71	5.0E-74	11431471	NT	Homo sapiens interleukin 4 receptor (IL4R), mRNA
6013	19096	32297	2.71	5.0E-74	11431471	NT	Homo sapiens interleukin 4 receptor (IL4R), mRNA
7080	20101	33412	2.18	5.0E-74	7662263	NT	Homo sapiens KIAA0716 gene product (KIAA0716), mRNA
7932	20101	33412	0.54	5.0E-74	7662263	NT	Homo sapiens KIAA0716 gene product (KIAA0716), mRNA
8371	21340	34751	3.05	5.0E-74	11345483	NT	Homo sapiens hypothetical protein FLJ13222 (FLJ13222), mRNA
11087	24048	37570	4.06	5.0E-74	Y09420.1	NT	H.sapiens mRNA for HIP-1

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
11087	24048	37571	4.08	5.0E-74	Y09420.1	NT	H. sapiens mRNA for HIP-1
278	13374	26303	1.85	4.0E-74	D87675.1	NT	Homo sapiens DNA for amyloid precursor protein, complete cds
853	13909	26687	5.8	4.0E-74	AB028942.1	NT	Homo sapiens mRNA for KIAA1019 protein, partial cds
1979	15000	28002	2.21	4.0E-74	AB026898.1	NT	Homo sapiens DNA, DLEC1 to ORCTL4 gene region, section 1/2 (DLEC1, ORCTL3, ORCTL4 genes, complete cds)
1979	15000	28003	2.21	4.0E-74	AB026898.1	NT	Homo sapiens DNA, DLEC1 to ORCTL4 gene region, section 1/2 (DLEC1, ORCTL3, ORCTL4 genes, complete cds)
2086	15103	28120	2.38	4.0E-74	4508192	NT	Homo sapiens proteasome (prosome, macropain) subunit, beta type, 1 (PSMB1) mRNA
2086	15103	28121	2.38	4.0E-74	4508192	NT	Homo sapiens proteasome (prosome, macropain) subunit, beta type, 1 (PSMB1) mRNA
2142	15159	28175	1.51	4.0E-74	AB032894.1	NT	Homo sapiens mRNA for KIAA1168 protein, partial cds
2434	15441	28459	0.81	4.0E-74	AJ006976.1	NT	Homo sapiens PLP gene
3107	18184	28078	5.45	4.0E-74	AJ006976.1	NT	Homo sapiens PLP gene
4091	17125	30018	1.23	4.0E-74	AL163247.2	NT	Homo sapiens chromosome 21 segment HS21C047
4587	17609	30504	2.06	4.0E-74	7682183	NT	Homo sapiens KIAA0569 gene product (KIAA0569), mRNA
4848	17687	30554	0.99	4.0E-74	Z17227.1	NT	Homo sapiens mRNA for transmembrane receptor protein
5055	18087	30846	0.74	4.0E-74	AB040909.1	NT	Homo sapiens mRNA for KIAA1478 protein, partial cds
8895	21861		21.81	3.0E-74	AA300378.1	EST_HUMAN	EST13131 Thymus tumor III Homo sapiens cDNA 5' end similar to similar to ribosomal protein L37
9727	22755	36208	2.57	3.0E-74	M78984.1	EST_HUMAN	EST01132 Subtracted Hippocampus, Striatum (cat. #936205) Homo sapiens cDNA clone HHCPF91
10703	23625	37122	2.69	3.0E-74	AA801493.1	EST_HUMAN	nc17g05.s1 NC1_CGAP_Phe1 Homo sapiens cDNA clone IMAGE:1100984 3'
959	14012	26965	58.94	2.0E-74	7689491	NT	Homo sapiens glyceraldehyde-3-phosphate dehydrogenase (GAPD), mRNA
959	14012	26966	58.94	2.0E-74	7689491	NT	Homo sapiens glyceraldehyde-3-phosphate dehydrogenase (GAPD), mRNA
1179	14220	27178	0.9	2.0E-74	AF020092.1	NT	Human endogenous retrovirus HERV-K-147D
1249	14285	27251	1.32	2.0E-74	AI950528.1	EST_HUMAN	wx51e07.x1 NC1_CGAP_Lu28 Homo sapiens cDNA clone IMAGE:2547204 3' similar to SW:GG95_HUMAN Q08379 GOLGIN-95; contains element MER22 repetitive element;
1599	14631	27606	3.54	2.0E-74	4885198	NT	Homo sapiens epidermal growth factor receptor (avian erythroblastic leukemia viral (v-erb-b) oncogene homolog) (EGFR) mRNA
1599	14631	27607	3.54	2.0E-74	4885198	NT	Homo sapiens epidermal growth factor receptor (avian erythroblastic leukemia viral (v-erb-b) oncogene homolog) (EGFR) mRNA
2608	15808	28632	3.02	2.0E-74	AI557280.1	EST_HUMAN	PT2.1_15_G11.1.tumor2 Homo sapiens cDNA 3'
5042	18055	30933	3.87	2.0E-74	AL355092.1	NT	Novel human gene mapping to chromosome 22
5042	18055	30934	3.87	2.0E-74	AL355092.1	NT	Novel human gene mapping to chromosome 22
5046	18059	30938	0.93	2.0E-74	J02963.1	NT	Human platelet glycoprotein IIb mRNA, 3' end
5898	25847	32174	2.03	2.0E-74	BE711134.1	EST_HUMAN	RC8-HT0678-220500-011-C03 HT0678 Homo sapiens cDNA

Table 4

Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5999	26650	32280	1.93	2.0E-74	11439587	NT	Homo sapiens PDZ-73 protein (PDZ-73/NY-CO-38), mRNA
5999	26650	32281	1.93	2.0E-74	11439587	NT	Homo sapiens PDZ-73 protein (PDZ-73/NY-CO-38), mRNA
6077	26650	32280	2.58	2.0E-74	11439587	NT	Homo sapiens PDZ-73 protein (PDZ-73/NY-CO-38), mRNA
6077	26650	32281	2.58	2.0E-74	11439587	NT	Homo sapiens PDZ-73 protein (PDZ-73/NY-CO-38), mRNA
7310	20281	33621	1.14	2.0E-74	BF030788.1	EST_HUMAN	601557524F1 NIH_MGC 58 Homo sapiens cDNA clone IMAGE:3827549 5'
8272	21241	34652	1.35	2.0E-74	AB037816.1	NT	Homo sapiens mRNA for KIAA1395 protein, partial cds
9737	22765	36220	8.08	2.0E-74	AL163204.2	NT	Homo sapiens chromosome 21 segment HS21C004
12058	24931	38523	1.72	2.0E-74	AA196181.1	EST_HUMAN	Homo sapiens protein kinase, AMP-activated, alpha 2 catalytic subunit (PRKAA2) mRNA
12521	28352	26086	3.11	2.0E-74	7657334	NT	z96a06.s1 Stragene muscle 937209 Homo sapiens cDNA clone IMAGE:628018 3'
55	13175	26348	2.22	1.0E-74	AW816405.1	EST_HUMAN	Homo sapiens MitshapenNIK-related kinase (MINK), mRNA
337	13426	26348	3.95	1.0E-74	AW816405.1	EST_HUMAN	QV4-ST0234-181199-037-f05 ST0234 Homo sapiens cDNA
500	13572	26494	1.1	1.0E-74	8922829	NT	Homo sapiens hypothetical protein FLJ11026 (FLJ11026), mRNA
507	13578	26499	8.18	1.0E-74	X02344.1	NT	Homo sapiens beta 2 gene
603	13670	26584	2.15	1.0E-74	4508020	NT	Homo sapiens zinc finger protein 259 (ZNF259) mRNA
1001	14052	27004	2.21	1.0E-74	AL163246.2	NT	Homo sapiens chromosome 21 segment HS21C046
2235	15249	28273	3.56	1.0E-74	AB002059.1	NT	Homo sapiens DNA for Human P2XM, complete cds
3156	16212	28127	2.83	1.0E-74	4759697	NT	Homo sapiens mannosidase, alpha, class 2A, member 1 (MAN2A1), mRNA
3943	16983	28998	0.79	1.0E-74	4504116	NT	Homo sapiens glutamate receptor, ionotropic, kainate 1 (GRIK1) mRNA
3943	16983	28999	0.79	1.0E-74	4504116	NT	Homo sapiens glutamate receptor, ionotropic, kainate 1 (GRIK1) mRNA
3992	17032	28941	5.75	1.0E-74	AL163268.2	NT	Homo sapiens chromosome 21 segment HS21C088
4092	17126	30019	0.96	1.0E-74	BE083080.1	EST_HUMAN	RC2-BT0642-270300-019-f06 BT0642 Homo sapiens cDNA
							h273h08.x1 NCL_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3213683 3' similar to WP-B0511.12
							CE17951:
4296	17325	30205	0.71	1.0E-74	BE467769.1	EST_HUMAN	Homo sapiens DQRR1 mRNA, partial cds
5217	18226	31100	1.36	1.0E-74	D83327.1	NT	Homo sapiens neurofibromin (NF1) gene, complete cds
6863	19916	33210	0.97	1.0E-74	M89914.1	NT	Homo sapiens KIAA0852 protein (KIAA0852), mRNA
7888	20832	34211	1.17	1.0E-74	11417977	NT	Homo sapiens KIAA0852 protein (KIAA0852), mRNA
8391	21360	34767	1.1	1.0E-74	BE549105.1	EST_HUMAN	601070088F1 NIH_MGC_12 Homo sapiens cDNA clone IMAGE:3456260 5'
8391	21360	34768	1.1	1.0E-74	BE549105.1	EST_HUMAN	601070088F1 NIH_MGC_12 Homo sapiens cDNA clone IMAGE:3456260 5'
9157	22123	35552	3.86	1.0E-74	AF214562.1	NT	Homo sapiens tracheal epithelium enriched protein (PLUNC) gene, complete cds
9186	22152	35581	0.71	1.0E-74	AJ251550.1	EST_HUMAN	MRQ-HT0559-230500-021-a03 HT0559 Homo sapiens cDNA
10600	23522	37015	0.55	1.0E-74	AJ251550.1	NT	Homo sapiens partial AK155 gene for AK155 protein, exons 1-3 and joined CDS
10600	23522	37016	0.55	1.0E-74	AJ251550.1	NT	Homo sapiens partial AK155 gene for AK155 protein, exons 1-3 and joined CDS
10847	23767	37266	1.51	1.0E-74	11420549	NT	Homo sapiens hypothetical protein FLJ10783 (FLJ10783), mRNA
12100	24971	38568	1.5	1.0E-74	AB007941.1	NT	Homo sapiens mRNA for KIAA0472 protein, partial cds

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Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
12154	25012	38616	3.9	1.0E-74	11417856	NT	Homo sapiens glutathione S-transferase theta 2 (GSTT2), mRNA
12235	25067		7.14	1.0E-74	11417856	NT	Homo sapiens glutathione S-transferase theta 2 (GSTT2), mRNA
12848	25458		1.52	1.0E-74	AF240786.1	NT	Homo sapiens glutathione S-transferase theta 2 (GSTT2) and glutathione S-transferase theta 1 (GSTT1) genes, complete cds
2652	15549		6.34	8.0E-75	AF176228.1	NT	Homo sapiens DNA cytosine-5 methyltransferase 3B (DNMT3B) mRNA, complete cds
12543	25286		1.81	8.0E-75	AL163202.2	NT	Homo sapiens chromosome 21 segment HS21C002
2329	15340	28362	1.16	6.0E-75	AI817415.1	EST_HUMAN	wk38a08.x1 NCL CGAP_P222 Homo sapiens cDNA clone IMAGE:2417854 3' similar to gb:M14123_cds4 RETROVIRUS-RELATED POL. POLYPROTEIN (HUMAN);
5201	18210	31084	0.91	5.0E-75	BE841305.1	EST_HUMAN	MRO-SN0040-080600-008-g06 SN0040 Homo sapiens cDNA
8075	21012	34411	0.51	5.0E-75	AA573446.1	EST_HUMAN	nk99d03.s1 NCL CGAP_C03 Homo sapiens cDNA clone IMAGE:1028833 3'
8075	21012	34412	0.51	5.0E-75	AA573446.1	EST_HUMAN	nk99d03.s1 NCL CGAP_C03 Homo sapiens cDNA clone IMAGE:1028833 3'
9259	22225	35654	1.13	5.0E-75	BE272325.1	EST_HUMAN	601126068F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:2989865 5'
9472	22436	35874	0.64	5.0E-75	AA132811.1	EST_HUMAN	zot1e08.r1 Stratagene colon (#937204) Homo sapiens cDNA clone IMAGE:567174 5'
9549	22512	35961	0.89	5.0E-75	BE561655.1	EST_HUMAN	601346909F1 NIH_MGC_8 Homo sapiens cDNA clone IMAGE:3687458 5'
9549	22512	35962	0.89	5.0E-75	BE561655.1	EST_HUMAN	601346909F1 NIH_MGC_8 Homo sapiens cDNA clone IMAGE:3687458 5'
9728	22756	36209	1.42	5.0E-75	BF690254.1	EST_HUMAN	602186616T1 NIH_MGC_49 Homo sapiens cDNA clone IMAGE:4296738 3'
10594	23516	37007	2.9	5.0E-75	AI636623.1	EST_HUMAN	l331c12.x1 NCL CGAP_GC8 Homo sapiens cDNA clone IMAGE:2242390 3' similar to TR:P97361 P97361 HYPOTHETICAL 20.1 KD PROTEIN ;
112	13223	26147	1.88	4.0E-75	BE081333.1	EST_HUMAN	QY1-BT0632-210200-078-e02 BT0632 Homo sapiens cDNA
459	13532		2.66	4.0E-75	N39757.1	EST_HUMAN	yx80h08.r1 Soares melanocyte 2NbhM Homo sapiens cDNA clone IMAGE:269055 5'
1780	14809	27765	1.73	4.0E-75	AW897230.1	EST_HUMAN	CNO-NN0057-150400-335-at1 NN0057 Homo sapiens cDNA
2851	15921	28841	4.5	4.0E-75	BE409464.1	EST_HUMAN	601303866F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3683344 5'
3512	16568	29482	0.93	4.0E-75		8922837	Homo sapiens hypothetical protein FLJ10747, mRNA
5607	18703	31859	0.65	4.0E-75	11417946	NT	Homo sapiens NIPSNAP, C. elegans, homolog 1 (NIPSNAP1), mRNA
5607	18703	31860	0.65	4.0E-75	11417946	NT	Homo sapiens NIPSNAP, C. elegans, homolog 1 (NIPSNAP1), mRNA
6400	19488	32716	6.35	4.0E-75	5579457	NT	Homo sapiens eukaryotic translation initiation factor 3, subunit 8 (104D) (EIF3S8), mRNA
6923	19973	33270	1.61	4.0E-75	11417946	NT	Homo sapiens NIPSNAP, C. elegans, homolog 1 (NIPSNAP1), mRNA
6923	19973	33271	1.61	4.0E-75	11417946	NT	Homo sapiens NIPSNAP, C. elegans, homolog 1 (NIPSNAP1), mRNA
11044	24008	37534	15.05	4.0E-75	7669505	NT	Homo sapiens myosin, heavy polypeptide 1, skeletal muscle, adult (MYH1), mRNA
1004	14055	27007	4.38	3.0E-75	AF157623.1	NT	Homo sapiens HTRA serine protease (PRSS11) gene, complete cds
1005	14055	27007	3.22	3.0E-75	AF157623.1	NT	Homo sapiens HTRA serine protease (PRSS11) gene, complete cds
1653	14879	27875	2.36	3.0E-75	AB011165.1	NT	Homo sapiens mRNA for KIAA0561 protein, partial cds
2430	15437	28454	5.12	3.0E-75	4759153	NT	Homo sapiens synaptosomal-associated protein, 29kD (SNAP29) mRNA
3034	16092	29010	1.06	3.0E-75	AL183201.2	NT	Homo sapiens chromosome 21 segment HS21C001

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Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3203	16258	29177	1.13	3.0E-75	AB011153.1	NT	Homo sapiens mRNA for KIAA0581 protein, partial cds
3361	16411	29334	0.95	3.0E-75	M72393.1	NT	Human calcium-dependent phospholipid-binding protein (PLA2) mRNA, complete cds
3361	16411	29335	0.95	3.0E-75	M72393.1	NT	Human calcium-dependent phospholipid-binding protein (PLA2) mRNA, complete cds
3752	16794	29705	0.78	3.0E-75	M72393.1	NT	Human calcium-dependent phospholipid-binding protein (PLA2) mRNA, complete cds
4197	17228	30118	1.03	3.0E-75	D87675.1	NT	Homo sapiens DNA for amyloid precursor protein, complete cds
4466	17492	30379	0.71	3.0E-75	7662421	NT	Homo sapiens KIAA0971 protein (KIAA0971), mRNA
5323	18429	31179	1.15	3.0E-75	11420956	NT	Homo sapiens adaptor-related protein complex 1, sigma 2 subunit (AP1S2), mRNA
5323	18429	31180	1.15	3.0E-75	11420956	NT	Homo sapiens adaptor-related protein complex 1, sigma 2 subunit (AP1S2), mRNA
6657	19714	32991	0.51	3.0E-75	AF123074.1	NT	Homo sapiens cytoplasmic dynein intermediate chain 1 mRNA, complete cds
6657	19714	32992	0.51	3.0E-75	AF123074.1	NT	Homo sapiens cytoplasmic dynein intermediate chain 1 mRNA, complete cds
6935	20159	33479	1.76	3.0E-75	11526319	NT	Homo sapiens HIR (histone cell cycle regulation defective, S. cerevisiae) homolog A (HIRA), mRNA
6935	20159	33480	1.76	3.0E-75	11526319	NT	Homo sapiens HIR (histone cell cycle regulation defective, S. cerevisiae) homolog A (HIRA), mRNA
7342	20313	33656	4.47	3.0E-75	7662209	NT	Homo sapiens KIAA0623 gene product (KIAA0623), mRNA
7342	20313	33657	4.47	3.0E-75	7662209	NT	Homo sapiens KIAA0623 gene product (KIAA0623), mRNA
7884	20828	34204	2.82	3.0E-75	4885632	NT	Homo sapiens Oncogene TIM (TIM) mRNA
7884	20828	34205	2.82	3.0E-75	4885632	NT	Homo sapiens Oncogene TIM (TIM) mRNA
9336	22301	35730	1.21	3.0E-75	11420804	NT	Homo sapiens snail 1 (drosophila homolog), zinc finger protein (SNA1), mRNA
10037	22664	36431	0.85	3.0E-75	11420222	NT	Homo sapiens Drosophila Kelch like protein (DKELCHL), mRNA
10908	23828	37341	4.16	3.0E-75	11436430	NT	Homo sapiens synuclein, alpha (non A4 component of amyloid precursor) (SNCA), mRNA
12085	24957	38552	1.73	3.0E-75	6715588	NT	Homo sapiens brefeldin A-inhibited guanine nucleotide-exchange protein 1 (BIG1), mRNA
12085	24957	38553	1.73	3.0E-75	6715588	NT	Homo sapiens brefeldin A-inhibited guanine nucleotide-exchange protein 1 (BIG1), mRNA
5756	18850		1.41	2.0E-75	AV734680.1	EST_HUMAN	AV734680 cDNA Homo sapiens cDNA clone IMAGE:1915898 3' similar to TR:Q69386 Q69386
9103	22069	35495	2.56	2.0E-75	AI311783.1	EST_HUMAN	q91e02.x1 NCL CGAP_Kid5 Homo sapiens cDNA clone IMAGE:2632707 3' similar to contains PTR7.11
2311	15323	28345	7.79	1.0E-75	AW168135.1	EST_HUMAN	PTK7 repetitive element;
2957	16015	28943	3.35	1.0E-75	X52221.1	NT	H. sapiens ERCC2 gene, exons 1 & 2 (partial)
4718	17738	30630	0.65	1.0E-75	BE279301.1	EST_HUMAN	601157633F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3504272 5'
5224	18232	31107	0.7	1.0E-75	BE894192.1	EST_HUMAN	601437130F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3922303 5'
7843	20790	34165	0.76	1.0E-75	BE082528.1	EST_HUMAN	RCS-BT0640-020300-031-H03 BT0640 Homo sapiens cDNA
7843	20790	34166	0.76	1.0E-75	BE082528.1	EST_HUMAN	RCS-BT0640-020300-031-H03 BT0640 Homo sapiens cDNA

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Table 4
Single Exon Probes Expressed In Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8757	21724		12.42	1.0E-75	AA399270.1	EST_HUMAN	z157h03.s1 Scores_testis_NHT Homo sapiens cDNA clone IMAGE:726485 3' similar to gb:M13932 40S
9783	22724	36179	4.03	1.0E-75	BF313645.1	EST_HUMAN	RIBOSOMAL PROTEIN S17 (HUMAN);
9783	22724	36180	4.03	1.0E-75	BF313645.1	EST_HUMAN	601900294F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4129678 5'
11229	24182		3.79	1.0E-75	AA694377.1	EST_HUMAN	601900294F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4129678 5'
							ac77b08.s1 Stratagene lung (#937210) Homo sapiens cDNA clone IMAGE:868599 3'
11428	24372	37910	2.13	1.0E-75	AF223391.1	NT	Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced
12438	18232	31107	1.72	1.0E-75	BE894192.1	EST_HUMAN	601437130F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3922303 5'
46	13166	26070	2.23	9.0E-76	AI652648.1	EST_HUMAN	wk30b10.x1 NCI_OGAP_G06 Homo sapiens cDNA clone IMAGE:2307163 3' similar to TR:O75235 O75235
46	13166	26071	2.23	9.0E-76	AI652648.1	EST_HUMAN	TRAP1;
2425	15432		0.96	9.0E-76	AA702415.1	EST_HUMAN	wk30b10.x1 NCI_OGAP_G06 Homo sapiens cDNA clone IMAGE:2307163 3' similar to TR:O75235 O75235
10261	23186	36670	37.43	9.0E-76	M12937.1	NT	TRAP1;
937	13990	26941	0.98	8.0E-76	4504374	NT	z155b07.s1 Scores_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:447541 3'
937	13990	26942	0.98	8.0E-76	4504374	NT	Human ferritin Heavy subunit mRNA, complete cds
2921	16879	28904	1.28	8.0E-76	7706724	NT	Homo sapiens H factor 1 (complement) (HF1) mRNA
6295	19367	32606	4.79	8.0E-76	11421442	NT	Homo sapiens H factor 1 (complement) (HF1) mRNA
7731	20886	34049	1.41	8.0E-76	11436215	NT	Homo sapiens mediator (Sur2), mRNA
7816	20765	34141	0.97	8.0E-76	11419212	NT	Homo sapiens LIM domain kinase 1 (LMK1), mRNA
8638	21607	35030	0.64	8.0E-76	11416961	NT	Homo sapiens serine/threonine kinase 2 (STK2), mRNA
9453	22417	35655	0.45	8.0E-76	AB046764.1	NT	Homo sapiens mitochondrial carrier family protein (LOC55972), mRNA
10744	23666	37161	1.41	8.0E-76	M13792.1	NT	Homo sapiens AIM-1 protein (LOC51151), mRNA
11026	23991	37518	4.09	8.0E-76	10442821	NT	Homo sapiens mRNA for KIAA1544 protein, partial cds
12767	25408		2.29	8.0E-76	11417862	NT	Human adenosine deaminase (ADA) gene, complete cds
							Homo sapiens baculoviral IAP repeat-containing 6 (BIRC6), mRNA
							Homo sapiens calcineurin binding protein 1 (KIAA0330), mRNA
777	13836	26782	1.41	7.0E-76	5016092	NT	Homo sapiens dihydropyrimidine dehydrogenase (E3 component of pyruvate dehydrogenase complex, 2-oxo-glutarate complex, branched chain keto acid dehydrogenase complex) (DLD) mRNA
3305	16358	29277	28.65	7.0E-76	AF056490.1	NT	Homo sapiens cAMP-specific phosphodiesterase 8A (PDE8A) mRNA, partial cds
3311	16364	29284	8.23	7.0E-76	4505052	NT	Homo sapiens lymphocyte antigen 75 (LY75) mRNA, and translated products
4399	17427	30311	4.52	7.0E-76	4507184	NT	Homo sapiens septaplatin reductase (7,8-dihydrobiopterin:NADP+ oxidoreductase) (SPR) mRNA
4399	17427	30312	4.52	7.0E-76	4507184	NT	Homo sapiens septaplatin reductase (7,8-dihydrobiopterin:NADP+ oxidoreductase) (SPR) mRNA
1238	14274		12.96	6.0E-76	BE399253.1	EST_HUMAN	601312019F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3658757 5'
11783	23948	37469	2.36	6.0E-76	BE273201.1	EST_HUMAN	601142253F1 NIH_MGC_14 Homo sapiens cDNA clone IMAGE:3506029 5'

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Single Exon Probes Expressed In Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1960	14982	27983	8.97	5.0E-76	D63874.1	NT	Human mRNA for HMG-1, complete cds
1960	14982	27984	8.97	5.0E-76	D63874.1	NT	Human mRNA for HMG-1, complete cds
1960	14982	27985	8.97	5.0E-76	D63874.1	NT	Human mRNA for HMG-1, complete cds
3220	16276	29199	1.01	4.0E-76	BE814096.1	EST_HUMAN	QV3-BN0047-270700-283-q08 BN0047 Homo sapiens cDNA
5342	18447	31200	1.08	4.0E-76	BE783412.1	EST_HUMAN	601471725F1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:3874470 5'
10384	23306	36783	6.89	4.0E-76	D81625.1	EST_HUMAN	HUM178G01B Human fetal brain (T Fujitara) Homo sapiens cDNA clone GEN-178G01 5'
10384	23306	36784	6.89	4.0E-76	D81625.1	EST_HUMAN	HUM178G01B Human fetal brain (T Fujitara) Homo sapiens cDNA clone GEN-178G01 5'
630	13695	26614	1.94	3.0E-76	BF516262.1	EST_HUMAN	UIH-BW1-anz-b-04-U1.s1 NCI CGAP_Sub7 Homo sapiens cDNA clone IMAGE:3083862 3'
630	13695	26615	1.94	3.0E-76	BF516262.1	EST_HUMAN	UIH-BW1-anz-b-04-U1.s1 NCI CGAP_Sub7 Homo sapiens cDNA clone IMAGE:3083862 3'
1603	14635	27611	9.36	3.0E-76	4503476	NT	Homo sapiens eukaryotic translation elongation factor 1 beta 2 (EEF1B2) mRNA
1603	14635	27612	9.36	3.0E-76	4503476	NT	Homo sapiens eukaryotic translation elongation factor 1 beta 2 (EEF1B2) mRNA
3442	16489	29407	5.03	3.0E-76	BF375689.1	EST_HUMAN	RC5-ST0300-180100-033-A03 ST0300 Homo sapiens cDNA
3442	16489	29408	5.03	3.0E-76	BF375689.1	EST_HUMAN	RC5-ST0300-180100-033-A03 ST0300 Homo sapiens cDNA
4105	17139	30034	14.72	3.0E-76	BE348693.1	EST_HUMAN	h87112.x1 NCI CGAP_L242 Homo sapiens cDNA clone IMAGE:3161823 3' similar to TR:O94886 O94886 KIAA0792 PROTEIN ;
5301	18304	31165	0.88	3.0E-76	AV702881.1	EST_HUMAN	AV702881 ADB Homo sapiens cDNA clone ADBBSC02 5'
5309	18327	38612	2.12	3.0E-76	Z41314.1	EST_HUMAN	HSCZQD042 normalized infant brain cDNA Homo sapiens cDNA clone c-zqd04 3'
5822	18912	32095	1	3.0E-76	AA160811.1	EST_HUMAN	z073c07.r1 Strelagene pancreas (#937208) Homo sapiens cDNA clone IMAGE:592524 5' similar to gb:L32976 MIXED LINEAGE KINASE 1 (HUMAN);
6102	19181	32400	0.71	3.0E-76	AW027705.1	EST_HUMAN	hw75c05.x1 Soares_thymus_NHFT1 Homo sapiens cDNA clone IMAGE:2536388 3'
6504	19568	32820	8.03	3.0E-76	AF286598.1	NT	Homo sapiens angiotensin binding protein 1 mRNA, complete cds
8460	21458	34876	0.83	3.0E-76	N42871.1	EST_HUMAN	y20g10.t1 Soares_melanocyte_2NblHM Homo sapiens cDNA clone IMAGE:271842 5'
10074	23001	38471	3.32	3.0E-76	AW298353.1	EST_HUMAN	xs49h01.x1 NCI CGAP_Ki671 Homo sapiens cDNA clone IMAGE:2773009 3'
10098	23024	36499	1.08	3.0E-76	AA442309.1	EST_HUMAN	zs45d11.t1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:757481 5'
10098	23024	36500	1.08	3.0E-76	AA442309.1	EST_HUMAN	zs45d11.t1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:757481 5'
12143	25760	31519	2.43	3.0E-76	AW967984.1	EST_HUMAN	EST380059 MAGe resequences, MAGJ Homo sapiens cDNA
12248	25971	31301	4.4	3.0E-76	AW956455.1	EST_HUMAN	EST388525 MAGe resequences, MAGD Homo sapiens cDNA
281	13376	26305	1.46	2.0E-76	D64295.1	NT	Human mRNA for possible protein TPRDII, complete cds
342	13431	26352	2.6	2.0E-76	D64295.1	NT	Human mRNA for possible protein TPRDII, complete cds
342	13431	26353	2.6	2.0E-76	D64295.1	NT	Human mRNA for possible protein TPRDII, complete cds
461	13534		1.14	2.0E-76	4557662	NT	Homo sapiens immunoglobulin (IGD78A) binding protein 1 (IGBP1) mRNA
692	13659	26573	1.12	2.0E-76	4503944	NT	Homo sapiens glucagon (GCG) mRNA
1032	14078	27031	1.37	2.0E-76	4758053	NT	Homo sapiens cAMP responsive element binding protein 1 (CREB1) mRNA
1537	14570	27542	1.74	2.0E-76	4504028	NT	Homo sapiens GM2 ganglioside activator protein (GM2A) mRNA

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Table 4
Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1537	14570	27543	1.74	2.0E-76	4504028	NT	Homo sapiens GM2 ganglioside activator protein (GM2A) mRNA
1945	14869	27967	1.03	2.0E-76	AA253654.1	EST_HUMAN	z680h11.s1 Stralagene schizo brain S11 Homo sapiens cDNA clone IMAGE:701925 3'
2854	15914	28837	3.73	2.0E-76	P23266	SWISSPROT	OLFACTORY RECEPTOR-LIKE PROTEIN F5
3308	16361	29281	1.87	2.0E-76	AA445992.1	EST_HUMAN	z64e02.s1 Soares testis NHT Homo sapiens cDNA clone IMAGE:780986 3' similar to SW:ITB5_HUMAN P18084 INTEGRIN BETA-5 SUBUNIT PRECURSOR ;
3308	16361	29282	1.87	2.0E-76	AA445992.1	EST_HUMAN	z64e02.s1 Soares testis NHT Homo sapiens cDNA clone IMAGE:780986 3' similar to SW:ITB5_HUMAN P18084 INTEGRIN BETA-5 SUBUNIT PRECURSOR ;
4561	17584	30476	1.01	2.0E-76	AL163283.2	NT	Homo sapiens chromosome 21 segment HS21C083
4984	17999	30888	7.6	2.0E-76	AW870618.1	EST_HUMAN	QV3-OT0028-220300-132-b11 OT0028 Homo sapiens cDNA
5382	18486		0.97	2.0E-76	AF127845.1	NT	Gorilla gorilla olfactory receptor (GGO18) gene, partial cds
5700	18795	31969	5.35	2.0E-76	AB029004.1	NT	Homo sapiens mRNA for KIAA1081 protein, partial cds
7643	20603	33968	0.55	2.0E-76	11421326	NT	Homo sapiens KIAA0783 gene product (KIAA0783), mRNA
7668	20627	33991	0.76	2.0E-76	11426908	NT	Homo sapiens A kinase (PRKA) anchor protein 10 (AKAP10), mRNA
7924	20867	34255	1.66	2.0E-76	11427410	NT	Homo sapiens TPCR86 protein (HSTPCR86P), mRNA
10845	23567	37064	7.03	2.0E-76	11437211	NT	Homo sapiens similar to ribosomal protein S28 (H. sapiens) (LOC63150), mRNA
11266	24218	37742	2.64	2.0E-76	7549807	NT	Homo sapiens HIRA interacting protein 4 (dnal-like) (HIRIP4), mRNA
4328	17355	30241	3.37	1.0E-76	D63874.1	NT	Human mRNA for HMG-1, complete cds
4326	17355	30242	3.37	1.0E-76	D63874.1	NT	Human mRNA for HMG-1, complete cds
5523	18622	31557	6.74	1.0E-76	BE796637.1	EST_HUMAN	601589896F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3944302 5'
6372	19440		0.64	1.0E-76	AA333207.1	EST_HUMAN	EST137301 Embryo, 8 week 1 Homo sapiens cDNA 5' end
7109	20043	33345	4.09	9.0E-77	BE889525.1	EST_HUMAN	601512435F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3913737 5'
12923	25499		1.36	9.0E-77	BE410354.1	EST_HUMAN	601302333F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3636763 5'
189	13289	26215	1.35	8.0E-77	R83144.1	EST_HUMAN	yp11h02.r1 Soares breast 3NBHst Homo sapiens cDNA clone IMAGE:187155 5' similar to
4950	17573	30463	1.25	8.0E-77	BF205181.1	EST_HUMAN	SP-ANKB_HUMAN Q01484 ANKYRIN, BRAIN VARIANT 1 ;
5528	18627	31563	1.83	8.0E-77			601866926F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4109503 5'
11716	24679	38257	1.82	8.0E-77	AA019770.1	EST_HUMAN	Homo sapiens proteasome (prosome, macropain) 26S subunit, non-ATPase, 7 (Mav34 homolog) (PSMD7) mRNA
11716	24679	38258	1.82	8.0E-77	AA019770.1	EST_HUMAN	z62e02.r1 Soares retina N2b4HR Homo sapiens cDNA clone IMAGE:363578 5'
12900	25484	31732	4.66	8.0E-77	R00245.1	EST_HUMAN	z62e02.r1 Soares retina N2b4HR Homo sapiens cDNA clone IMAGE:363578 5'
1946	14970	27968	2.43	7.0E-77	AA625756.1	EST_HUMAN	ye69f04.s1 Soares fetal liver spleen 'NFLS Homo sapiens cDNA clone IMAGE:123007 3' similar to contains
2421	15428	28451	1.88	7.0E-77			MER10 repetitive element ;
2421	15428	28452	1.88	7.0E-77	4505944	NT	z691g01.s1 Soares testis NHT Homo sapiens cDNA clone IMAGE:745392 3'
							Homo sapiens polymerase (RNA) II (DNA directed) polypeptide E (25kD) (POLR2E) mRNA
							Homo sapiens polymerase (RNA) II (DNA directed) polypeptide E (25kD) (POLR2E) mRNA

Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
262	13358	26283	4.64	6.0E-77	4504600	NT	Homo sapiens interferon (alpha, beta and omega) receptor 2 (IFNAR2) mRNA
1144	14187	27138	20.18	6.0E-77	AW957753.1	EST_HUMAN	EST369823 IMAGE resequences, IMAGE Homo sapiens cDNA
1545	14578	27531	3.97	6.0E-77	A1204066.1	EST_HUMAN	qe7h12.x1 Soares_fetal_lung_NbHL19W Homo sapiens cDNA clone IMAGE:1745063 3'
1240	14276	27236	2.34	5.0E-77	AFO41016.1	NT	7 Homo sapiens glucokinase (GCK) gene, exon 2
1362	14396	27387	1.41	5.0E-77	4557250	NT	Homo sapiens disintegrin and metalloprotease domain 10 (ADAM10) mRNA
2895	15691	28709	1.03	5.0E-77	AF162666.1	NT	Homo sapiens toubled-like kinase 1 (TLK1) mRNA, complete cds
2774	15766	28786	0.96	5.0E-77	4503160	NT	Homo sapiens cullin 1 (CUL1) mRNA
3534	16580	29504	0.64	5.0E-77	8394518	NT	Homo sapiens ubiquitin specific protease 18 (USP18), mRNA
4732	17752	30644	0.92	5.0E-77	5031660	NT	Homo sapiens EGF-like repeats and discoidin I-like domains 3 (EDIL3), mRNA
4732	17752	30645	0.92	5.0E-77	5031660	NT	Homo sapiens EGF-like repeats and discoidin I-like domains 3 (EDIL3), mRNA
4975	17990	30880	3.64	5.0E-77	AL043953.1	EST_HUMAN	DKFZp434G1728_r1 434 (synonym: htes3) Homo sapiens cDNA clone DKFZp434G1728 5'
6951	20175	33499	0.84	5.0E-77	M13975.1	NT	Homo sapiens protein kinase C beta-II type (PRKCBT) mRNA, complete cds
7548	20511	33869	0.52	5.0E-77	X98296.1	NT	H. sapiens mRNA for ubiquitin hydrolase
7849	20511	33869	0.67	5.0E-77	X98296.1	NT	H. sapiens mRNA for ubiquitin hydrolase
8711	21679	35104	1.22	5.0E-77	11428849	NT	Homo sapiens 3-hydroxyisobutyryl-Coenzyme A hydrolase (HIBCH), mRNA
8711	21679	35105	1.22	5.0E-77	11428849	NT	Homo sapiens 3-hydroxyisobutyryl-Coenzyme A hydrolase (HIBCH), mRNA
9928	22811	36264	3	5.0E-77	11421928	NT	Homo sapiens sorting nexin 5 (SNX5), mRNA
9928	22811	36265	3	5.0E-77	11421928	NT	Homo sapiens sorting nexin 5 (SNX5), mRNA
10857	23777	37276	0.82	5.0E-77	AB002297.1	NT	Human mRNA for KIAA0299 gene, partial cds
10857	23777	37277	0.82	5.0E-77	AB002297.1	NT	Human mRNA for KIAA0299 gene, partial cds
1989	15010	28015	1.26	3.0E-77	5730038	NT	Homo sapiens SET domain and mariner transposase fusion gene (SETMAR) mRNA
1989	15010	28016	1.26	3.0E-77	5730038	NT	Homo sapiens SET domain and mariner transposase fusion gene (SETMAR) mRNA
10652	23574	37069	0.71	3.0E-77	H65167.1	EST_HUMAN	yu64g01.r1 Weizmann Olfactory Epithelium Homo sapiens cDNA clone IMAGE:238608 5' similar to SP-S17447 S17447 PROBABLE LIGAND-BINDING PROTEIN RY2G5 - ;
10652	23574	37070	0.71	3.0E-77	H65167.1	EST_HUMAN	yu64g01.r1 Weizmann Olfactory Epithelium Homo sapiens cDNA clone IMAGE:238608 5' similar to SP-S17447 S17447 PROBABLE LIGAND-BINDING PROTEIN RY2G5 - ;
10988	23888	37399	0.66	3.0E-77	A1017333.1	EST_HUMAN	SP-S17447 S17447 PROBABLE LIGAND-BINDING PROTEIN RY2G5 - ;
10988	23888	37400	0.66	3.0E-77	A1017333.1	EST_HUMAN	alpha31h07.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1638973 3'
11222	24175	37701	3.68	3.0E-77	BF35917.1	EST_HUMAN	alpha31h07.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1638973 3'
1354	14389	27368	1.66	2.0E-77	AV764617.1	EST_HUMAN	PM3-MT0078-080900-005-g03 MT 0078 Homo sapiens cDNA
1428	14462	27439	2.31	2.0E-77	AW997112.1	EST_HUMAN	AV764617 MDS Homo sapiens cDNA clone MDSBT10 5'
2102	15119	28140	1.01	2.0E-77	L41825.1	NT	RC3-BN0053-170200-011-h01 BN0053 Homo sapiens cDNA
2113	15130	28150	2.48	2.0E-77	L41825.1	NT	Homo sapiens CYP17 gene, 5' end
2600	15898	28620	2.28	2.0E-77	AB037836.1	NT	Homo sapiens CGI-79 protein (LOC51634), mRNA
							Homo sapiens mRNA for KIAA1415 protein, partial cds

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Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2600	15898	28621	2.28	2.0E-77	AB037836.1	NT	Homo sapiens mRNA for KIAA1415 protein, partial cds
4064	17100	29992	1.25	2.0E-77	BE044316.1	EST_HUMAN	h043b05.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:3040113 3' similar to SW:GAG2_HUMAN P10264 RETROVIRUS-RELATED GAG POLYPROTEIN ;
4442	17468	30357	0.88	2.0E-77	AI613519.1	EST_HUMAN	hw22g02.x1 NCL_CGAP_Brn52 Homo sapiens cDNA clone IMAGE:2260466 3' similar to TR:O65245
4442	17468	30358	0.88	2.0E-77	AI613519.1	EST_HUMAN	O65245 F21E10.7 PROTEIN ;
							hw22g02.x1 NCL_CGAP_Brn52 Homo sapiens cDNA clone IMAGE:2260466 3' similar to TR:O65245
4802	17819	30713	2.32	2.0E-77	AA653025.1	EST_HUMAN	ns68g12.s1 NCL_CGAP_P12 Homo sapiens cDNA clone IMAGE:1188838 similar to SW:RL29_HUMAN P47914 60S RIBOSOMAL PROTEIN L29. [1] contains element MSR1 repetitive element ;
5158	17468	30357	0.65	2.0E-77	AI613519.1	EST_HUMAN	hw22g02.x1 NCL_CGAP_Brn52 Homo sapiens cDNA clone IMAGE:2260466 3' similar to TR:O65245
5158	17468	30358	0.65	2.0E-77	AI613519.1	EST_HUMAN	hw22g02.x1 NCL_CGAP_Brn52 Homo sapiens cDNA clone IMAGE:2260466 3' similar to TR:O65245
6065	19146	32358	2.06	2.0E-77	BE298940.1	EST_HUMAN	O65245 F21E10.7 PROTEIN ;
6296	19368	32607	1.62	2.0E-77	BE787143.1	EST_HUMAN	hw22g02.x1 NCL_CGAP_Brn52 Homo sapiens cDNA clone IMAGE:2260466 3' similar to TR:O65245
7380	20350	33701	14.21	2.0E-77	AI833003.1	EST_HUMAN	hw22g02.x1 NCL_CGAP_Brn52 Homo sapiens cDNA clone IMAGE:2260466 3' similar to TR:O65245
8874	21841	35264	0.75	2.0E-77	AI362707.1	EST_HUMAN	O65245 F21E10.7 PROTEIN ;
9886	22839	36295	5.64	2.0E-77	U50321.1	NT	601178852F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3028436 5'
9886	22839	36296	5.64	2.0E-77	U50321.1	NT	601178852F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3028436 5'
10354	23278	36753	0.5	2.0E-77	BF310349.1	EST_HUMAN	601478802F1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3878505 5'
10354	23278	36754	0.5	2.0E-77	BF310349.1	EST_HUMAN	601895183F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4124541 5'
45	13165	26068	0.94	1.0E-77	AB033102.1	NT	601895183F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4124541 5'
45	13165	26069	0.94	1.0E-77	AB033102.1	NT	Homo sapiens mRNA for KIAA1276 protein, partial cds
							Homo sapiens mRNA for KIAA1276 protein, partial cds
272	13368	26294	1.33	1.0E-77	4502166	NT	Homo sapiens amyloid beta (A4) precursor protein (protease nexin-II, Alzheimer disease) (APP), mRNA
272	13368	26295	1.33	1.0E-77	4502166	NT	Homo sapiens amyloid beta (A4) precursor protein (protease nexin-II, Alzheimer disease) (APP), mRNA
876	15853	26891	2.31	1.0E-77	4502166	NT	Homo sapiens amyloid beta (A4) precursor protein (protease nexin-II, Alzheimer disease) (APP), mRNA
876	15853	26892	2.31	1.0E-77	4502166	NT	Homo sapiens amyloid beta (A4) precursor protein (protease nexin-II, Alzheimer disease) (APP), mRNA

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Table 4
Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2450	15455	28477	1.73	1.0E-77	AB029024.1	NT	Homo sapiens mRNA for KIAA1101 protein, complete cds
3058	16115	29028	2.01	1.0E-77	4503300	NT	Homo sapiens 2,4-dienoyl CoA reductase 1, mitochondrial (DEGR1), mRNA
4380	17408	30288	3.92	1.0E-77	7706299	NT	Homo sapiens CGI-60 protein (LOC51626), mRNA
4525	17550	30438	0.73	1.0E-77	4758053	NT	Homo sapiens cAMP responsive element binding protein 1 (CREB1) mRNA
4552	17575	30465	16.98	1.0E-77	AJ229041.1	NT	Homo sapiens 958 kb contig between AML1 and CBR1 on chromosome 21q22; segment 1/3
4880	17701	30588	2.11	1.0E-77	6552322	NT	Homo sapiens breast cancer 1, early onset (BRCA1), transcript variant BRCA1-exon4, mRNA
4721	17741	30632	0.72	1.0E-77	AI273014.1	EST_HUMAN	q109g04.x1 NCJ_CGAP_Kid8 Homo sapiens cDNA clone IMAGE:1981110 3'
5000	17550	30438	0.95	1.0E-77	4758053	NT	Homo sapiens cAMP responsive element binding protein 1 (CREB1) mRNA
5219	17550	30438	0.68	1.0E-77	4758053	NT	Homo sapiens cAMP responsive element binding protein 1 (CREB1) mRNA
5246	18254	32324	1.12	1.0E-77	AL163247.2	NT	Homo sapiens chromosome 21 segment HS21C047
6038	19120	32325	1.61	1.0E-77	AF086944.1	NT	Homo sapiens dynactin 1 (DCTN1) gene, exons 27 and 28
6038	19120	32325	1.39	1.0E-77	AF086944.1	NT	Homo sapiens dynactin 1 (DCTN1) gene, exons 27 and 28
6165	19240	32471	1.61	1.0E-77	M25844.1	NT	Human von Willebrand factor gene, exon 20
6590	19650	32921	1.26	1.0E-77	4885182	NT	Homo sapiens diaphanous (Drosophila, homolog) 1 (DIAPH1), mRNA
7254	19889	33286	14.51	1.0E-77	5881412	NT	Homo sapiens elastin (supravalvular aortic stenosis, Williams-Beuren syndrome) (ELN), mRNA
7928	20871	34260	0.91	1.0E-77	11420159	NT	Homo sapiens cullin 1 (CUL1), mRNA
8040	20877	34373	0.69	1.0E-77	X04571.1	NT	Human mRNA for kidney epidermal growth factor (EGF) precursor
9620	22564	36013	0.65	1.0E-77	X94354.1	NT	H.sapiens DNA for Cone cGMP-PDE gene
9620	22564	36014	0.65	1.0E-77	X94354.1	NT	H.sapiens DNA for Cone cGMP-PDE gene
10890	23810	37316	0.92	1.0E-77	AB029396.1	NT	Homo sapiens hu-GlcAT-P mRNA for glucuronyltransferase, complete cds
10890	23810	37317	0.92	1.0E-77	AB029396.1	NT	Homo sapiens hu-GlcAT-P mRNA for glucuronyltransferase, complete cds
10916	23836	37352	3	9.0E-78	AW753302.1	EST_HUMAN	RC3-CT0254-280988-011-405 CT0254 Homo sapiens cDNA
6589	19549	32919	2.93	8.0E-78	AW947061.1	EST_HUMAN	RC2-ET0023-080500-012-405 ET0023 Homo sapiens cDNA
6589	19549	32920	2.93	8.0E-78	AW947061.1	EST_HUMAN	RC2-ET0023-080500-012-405 ET0023 Homo sapiens cDNA
86	13202	26128	2.14	6.0E-78	AU118789.1	EST_HUMAN	AU118789 HEMBA1 Homo sapiens cDNA clone HEMBA1004354 5'
86	13202	26128	2.14	6.0E-78	AU118789.1	EST_HUMAN	AU118789 HEMBA1 Homo sapiens cDNA clone HEMBA1004354 5'
3325	16376	29297	8.56	6.0E-78	BF344101.1	EST_HUMAN	602016926f1 NCJ_CGAP_Brn84 Homo sapiens cDNA clone IMAGE:4152511 5'
6712	19768	26244	2.34	6.0E-78	11432710	NT	Homo sapiens GDNF family receptor alpha 1 (GFRAL), mRNA
219	13319	26244	1.79	5.0E-78	11422486	NT	Homo sapiens hypothetical protein FLJ11316 (FLJ11316), mRNA
2569	15570	28590	5.46	5.0E-78	AW673424.1	EST_HUMAN	be54h03.y3 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:2900405 5' similar to WP.Y48B6A.6
3396	16445	29372	3.94	5.0E-78	M55586.1	NT	CE22121 ;
5486	18586	31497	2.45	5.0E-78	AF038536.1	NT	Human collagenase type IV (CLG4) gene, exon 6
5655	18751	31917	24.78	5.0E-78	11416585	NT	Homo sapiens Best's macular dystrophy related protein mRNA, partial cds
							Homo sapiens transforming growth factor, beta-induced, 68KD (TGFB), mRNA

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Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7361	20331	33681	2.22	5.0E-78	AW953120.1	EST_HUMAN	EST365190 IMAGE resequences, MAGB Homo sapiens cDNA
9438	22402	35840	6.85	5.0E-78	U60889.1	NT	Human lysosomal alpha-mannosidase (manB) gene, exon 7
9439	22403	35841	3.51	5.0E-78	BE980836.1	EST_HUMAN	601648061F1 NIH_MGC_82 Homo sapiens cDNA clone IMAGE:3931887 5'
11614	24552	38112	1.64	5.0E-78	BE241639.1	EST_HUMAN	TCAAP1E0686 Pediatric acute myelogenous leukemia cell (FAB M1) Baylor-HGSC project=TCAA Homo sapiens cDNA clone TCAAP0686
11614	24552	38113	1.64	5.0E-78	BE241639.1	EST_HUMAN	TCAAP1E0686 Pediatric acute myelogenous leukemia cell (FAB M1) Baylor-HGSC project=TCAA Homo sapiens cDNA clone TCAAP0686
1139	14182	27133	1.86	4.0E-78	AL043314.2	EST_HUMAN	DKFZp434N0323_1 434 (synonym: htes3) Homo sapiens cDNA clone DKFZp434N0323 5'
1521	14553	27524	2.74	4.0E-78	AL355841.1	NT	Novel human gene mapping to chromosome 22
1656	14688	27663	1.11	4.0E-78	AI985094.1	EST_HUMAN	w87b12.x1 NCI_CGAP Kid11 Homo sapiens cDNA clone IMAGE:2495615 3' similar to SW:WAP_PIG
2328	15337	28360	3.31	4.0E-78	AF107405.1	NT	O46655 WHEY ACIDIC PROTEIN PRECURSOR ; Homo sapiens pre-mRNA splicing factor (SFRS3) mRNA, complete cds
4350	17377	30256	1.47	4.0E-78	7658876	NT	Homo sapiens synctin (LOC30816), mRNA
4807	17824	30719	2.16	4.0E-78	4505806	NT	Homo sapiens phosphatidylinositol 4-kinase, catalytic, alpha polypeptide (PIK4CA) mRNA
4807	17824	30720	2.16	4.0E-78	4505806	NT	Homo sapiens phosphatidylinositol 4-kinase, catalytic, alpha polypeptide (PIK4CA) mRNA
5862	18951	32137	1.13	4.0E-78	11420732	NT	Homo sapiens SFRS protein kinase 2 (SRPK2), mRNA
6297	19369	32608	0.61	4.0E-78	7682109	NT	Homo sapiens KIAA0426 gene product (KIAA0426), mRNA
6297	19369	32609	0.61	4.0E-78	7682109	NT	Homo sapiens KIAA0426 gene product (KIAA0426), mRNA
6725	19781	33060	0.59	4.0E-78	4508736	NT	Homo sapiens ribosomal protein S6 kinase, 70kD, polypeptide 1 (RPS6KB1) mRNA
7733	20688	34052	0.58	4.0E-78	4508736	NT	Homo sapiens ribosomal protein S6 kinase, 70kD, polypeptide 1 (RPS6KB1) mRNA
9205	22171	35601	1.66	4.0E-78	AF012872.1	NT	Homo sapiens phosphatidylinositol 4-kinase 230 (p14K230) mRNA, complete cds
9205	22171	35602	1.66	4.0E-78	AF012872.1	NT	Homo sapiens phosphatidylinositol 4-kinase 230 (p14K230) mRNA, complete cds
9723	22751	36204	0.64	4.0E-78	11417251	NT	Homo sapiens X-ray repair complementing defective repair in Chinese hamster cells 4 (XRCC4), mRNA
10811	23732	37233	1.97	4.0E-78	11560151	NT	Homo sapiens hypothetical C2H2 zinc finger protein FLJ22504 (FLJ22504), mRNA
10811	23732	37234	1.97	4.0E-78	11560151	NT	Homo sapiens hypothetical C2H2 zinc finger protein FLJ22504 (FLJ22504), mRNA
11749	24634	38213	1.65	4.0E-78	AF169148.1	NT	Homo sapiens s-CaBP1 (CABP1) mRNA, complete cds
11883	24764	38350	5.69	4.0E-78	X05844.1	NT	Human transforming growth factor-beta precursor gene exons 4-5 (and joined mature peptide)
12126	24895	38599	2.38	4.0E-78	11024711	NT	Homo sapiens myosin, heavy polypeptide 4, skeletal muscle (MYH4), mRNA
12797	25426	31739	3.89	4.0E-78	AB011399.1	NT	Homo sapiens gene for AF-6, complete cds
162	13265	26189	2.77	3.0E-78	AF095901.1	NT	Homo sapiens eRF1 gene, complete cds
162	13265	26189	2.77	3.0E-78	AF095901.1	NT	Homo sapiens eRF1 gene, complete cds
3778	16818	28190	0.94	3.0E-78	AF095901.1	EST_HUMAN	Homo sapiens eRF1 gene, complete cds
3829	18669	28771	0.69	3.0E-78	4607334	NT	AU140804 PLACES3 Homo sapiens cDNA clone PLACE300373 5' Homo sapiens synaptobrevin 1 (SYNJ1), mRNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4131	18869	29771	0.79	3.0E-78	4507334	NT	Homo sapiens synaptobrevin 1 (SYNJ1), mRNA
10949	23571		5.79	3.0E-78	BE144758.1	EST_HUMAN	CN10-HT0180-041099-065-c07 HT0180 Homo sapiens cDNA
11328	24276	37804	1.8	3.0E-78	BE156318.1	EST_HUMAN	QV0-HT0367-150200-114-909 HT0367 Homo sapiens cDNA
3138	16195		4.1	2.0E-78	U04489.1	NT	Homo sapiens type IV collagen alpha 5 chain (COL4A5) gene, exon 20
4042	17080		1.43	2.0E-78	AA311872.1	EST_HUMAN	EST182583 Jurkat T-cells VI Homo sapiens cDNA 5' end
7705	20662	34027	1.24	2.0E-78	AW402306.1	EST_HUMAN	U1HF-BK0-aal-g-10-Q-J1.1 NIH_MGC_36 Homo sapiens cDNA clone IMAGE:3054139 5'
7705	20662	34028	1.24	2.0E-78	AW402306.1	EST_HUMAN	U1HF-BK0-aal-g-10-Q-J1.1 NIH_MGC_36 Homo sapiens cDNA clone IMAGE:3054139 5'
8003	20942	34335	3.2	2.0E-78	BF689800.1	EST_HUMAN	602186529F1 NIH_MGC_49 Homo sapiens cDNA clone IMAGE:4296599 5'
8375	21344	34756	2.54	2.0E-78	AV714177.1	EST_HUMAN	AV714177 DCB Homo sapiens cDNA clone DCBAWF09 5'
8795	21762	35183	1.51	2.0E-78	AI557509.1	EST_HUMAN	P12_1_16_B07.r tumor2 Homo sapiens cDNA 3'
8795	21762	35184	1.51	2.0E-78	AI557509.1	EST_HUMAN	P12_1_16_B07.r tumor2 Homo sapiens cDNA 3'
11416	24360	37895	2.5	2.0E-78	AI197837.1	EST_HUMAN	q150h05.x1 NC1_CGAP_Bim25 Homo sapiens cDNA clone IMAGE:1859961 3' similar to WP.R90.1
11458	24401	37949	2.03	2.0E-78	N66951.1	EST_HUMAN	CE06325 PROTEIN KINASE :
5378	18482	31357	3.22	1.0E-78	11417304	NT	z44812.s1 Soares fetal liver spleen 1NLS Homo sapiens cDNA clone IMAGE:285823 3'
7144	18376	31264	0.67	1.0E-78	AV648699.1	EST_HUMAN	Homo sapiens GAP-like protein (LOC51306), mRNA
8499	21467		2.95	1.0E-78	U62373.1	NT	AV648699 GLC Homo sapiens cDNA clone GLOBMC01 3'
12323	25125	31847	1.81	1.0E-78	11430460	NT	Human serine/threonine kinase MNB (mnb) mRNA, complete cds
4727	17747	30638	3.81	9.0E-79	11526891	NT	Homo sapiens low density lipoprotein-related protein 2 (LRP2), mRNA
4899	17916	30807	3.55	9.0E-79	BE000837.1	EST_HUMAN	Homo sapiens peptide YY (PYY), mRNA
5507	18807	31537	16.13	9.0E-79	AB028070.1	NT	RC2-BN0074-090300-014-c12 BN0074 Homo sapiens cDNA
6474	19539	32785	2.49	9.0E-79	5454145	NT	Homo sapiens mRNA for activator of S phase Kinase, complete cds
6772	19927	33109	0.87	9.0E-79	11430822	NT	Homo sapiens ubiquitin-conjugating enzyme E2E 3 (homologous to yeast UBC4/5) (UBE2E3) mRNA
7573	25684		1.05	9.0E-79	11424427	NT	Homo sapiens hypothetical protein FLJ11294 (FLJ11294), mRNA
7825	20773	34150	0.84	9.0E-79	11421735	NT	Homo sapiens hypothetical protein FLJ20345 (FLJ20345), mRNA
7825	20773	34151	0.84	9.0E-79	11421735	NT	Homo sapiens cAMP response element-binding protein CRE-BPa (H_GS165L15.1), mRNA
7875	20819	34197	0.55	9.0E-79	D30658.1	NT	Homo sapiens cAMP response element-binding protein CRE-BPa (H_GS165L15.1), mRNA
8689	21657	35079	0.5	9.0E-79	11417260	NT	Human T-cell mRNA for glycyl RNA synthetase, complete cds
8689	21657	35080	0.5	9.0E-79	11417260	NT	Homo sapiens threonyl-tRNA synthetase (TARS), mRNA
9418	22383	35821	5.53	9.0E-79	J02853.1	NT	Homo sapiens threonyl-tRNA synthetase (TARS), mRNA
9418	22383	35822	5.53	9.0E-79	J02853.1	NT	Homo sapiens casein kinase II alpha subunit mRNA, complete cds
9735	22763	36218	0.66	9.0E-79	D87675.1	NT	Homo sapiens casein kinase II alpha subunit mRNA, complete cds
10730	23632	37145	0.65	9.0E-79	11438643	NT	Homo sapiens DNA for amyloid precursor protein, complete cds
							Homo sapiens hypothetical protein FLJ20535 (FLJ20535), mRNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10784	23705	37204	1.53	9.0E-79	AF062348.1	NT	Homo sapiens zinc finger protein 216 splice variant 1 (ZNF216) mRNA, complete cds
10784	23705	37205	1.53	9.0E-79	AF062348.1	NT	Homo sapiens zinc finger protein 216 splice variant 1 (ZNF216) mRNA, complete cds
11406	24350	37892	4.27	9.0E-79	AY008273.1	NT	Homo sapiens TRAF6-regulated I κ B activator 1 beta Uev1A mRNA, complete cds
11841	24724	38310	2.97	9.0E-79	11423827	NT	Homo sapiens suppressor of white apricot homolog 2 (SWAP2), mRNA
11841	24724	38311	2.97	9.0E-79	11423827	NT	Homo sapiens suppressor of white apricot homolog 2 (SWAP2), mRNA
12115	24965	38586	2.71	9.0E-79	7662451	NT	Homo sapiens KIAA1035 protein (KIAA1035), mRNA
13000	25556	31720	1.55	9.0E-79	11417877	NT	Homo sapiens gamma-glutamyltransferase 1 (GGT1), mRNA
3755	16797	29708	1.33	8.0E-79	AL163210.2	NT	Homo sapiens chromosome 21 segment HS21C010
5195	18204	31078	0.66	8.0E-79	8567387	NT	Homo sapiens period (Drosophila) homolog 3 (PER3), mRNA
3286	16320	29242	7.24	7.0E-79	BE919648.1	EST_HUMAN	601472768T1 NIH_MGC 68 Homo sapiens cDNA clone IMAGE:3875657 3'
12170	25020		2.63	6.0E-79	AA699829.1	EST_HUMAN	294604.s1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:462558 3' similar to TR:Q15408 Q15408 NEUTRAL PROTEASE LARGE SUBUNIT ;
11824	24707	38290	4.57	5.0E-79	AL163282.2	NT	Homo sapiens chromosome 21 segment HS21C082
3191	16246		1.35	4.0E-79	8922325	NT	Homo sapiens hypothetical protein FLJ10283 (FLJ10283), mRNA
313	13405	26331	1.46	3.0E-79	AF114488.1	NT	Homo sapiens interectin short isoform (ITSN) mRNA, complete cds
979	14030	26984	2.02	3.0E-79	AF232708.1	NT	Homo sapiens cell-line tsA201a chloride ion current inducer protein (Cin) gene, complete cds
3115	16172	29082	1.82	3.0E-79	U09410.1	NT	Human zinc finger protein ZNF131 mRNA, partial cds
5435	18537	31445	6.05	3.0E-79	AF110322.1	NT	Homo sapiens MSTP016 (MST016) mRNA, complete cds
5812	18902	32085	1.61	3.0E-79	AB020699.1	NT	Homo sapiens mRNA for KIAA0992 protein, partial cds
5841	18931	32115	0.95	3.0E-79	BE789470.1	EST_HUMAN	601482143F1 NIH_MGC 68 Homo sapiens cDNA clone IMAGE:3884554 5'
5841	18931	32116	0.95	3.0E-79	BE789470.1	EST_HUMAN	601482143F1 NIH_MGC 68 Homo sapiens cDNA clone IMAGE:3884554 5'
5863	18952	32138	4.05	3.0E-79	11426770	NT	Homo sapiens netrin 1 (NTN1), mRNA
5863	18952	32139	4.05	3.0E-79	11426770	NT	Homo sapiens netrin 1 (NTN1), mRNA
6909	19961	33257	0.8	3.0E-79	BE256883.1	EST_HUMAN	601112055F1 NIH_MGC 16 Homo sapiens cDNA clone IMAGE:3352885 5'
7262	19997	33294	3.31	3.0E-79	AB014520.1	NT	Homo sapiens mRNA for KIAA0620 protein, partial cds
7262	19997	33295	3.31	3.0E-79	AB014520.1	NT	Homo sapiens mRNA for KIAA0620 protein, partial cds
8504	21472	34986	1.58	3.0E-79	AF249273.1	NT	Homo sapiens Bcl-2-associated transcription factor short form mRNA, complete cds
9758	22899	36156	0.57	3.0E-79	10835038	NT	Homo sapiens tetratricopeptide repeat domain 3 (TTC3), mRNA
10712	23634		0.64	3.0E-79	AV698115.1	EST_HUMAN	AV698115 GKCC Homo sapiens cDNA clone GKCAHE11 5'
287	13382		2.05	2.0E-79	H63129.1	EST_HUMAN	Y44803.s1 Soares_fetal_liver_spleen_1NFLS Homo sapiens cDNA clone IMAGE:208541 3'
635	13701	26622	1.29	2.0E-79	BE379926.1	EST_HUMAN	601159415F2 NIH_MGC 53 Homo sapiens cDNA clone IMAGE:3511107 5'
928	13981	26935	1.35	2.0E-79	4757841	NT	Homo sapiens BCL2-like 2 (BCL2L2) mRNA
985	14036	26990	4.78	2.0E-79	4885234	NT	Homo sapiens Gardner-Rasheed feline sarcoma viral (v-fgr) oncogene homolog (FGR) mRNA
985	14036	26991	4.78	2.0E-79	4885234	NT	Homo sapiens Gardner-Rasheed feline sarcoma viral (v-fgr) oncogene homolog (FGR) mRNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1036	14082		1.02	2.0E-79	AI523747.1	EST_HUMAN	th18h07.x1 NC1 CGAP Pr28 Homo sapiens cDNA clone IMAGE:2118685 3'
1804	14832	27819	0.97	2.0E-79	7657024	NT	Homo sapiens Dickkopf gene 4 (DKK-4), mRNA
1804	14832	27820	0.97	2.0E-79	7657024	NT	Homo sapiens Dickkopf gene 4 (DKK-4), mRNA
1893	14918	27814	0.92	2.0E-79	7662255	NT	Homo sapiens KIAA0703 gene product (KIAA0703), mRNA
2158	15174	28183	4.97	2.0E-79	4585863	NT	Homo sapiens phosphodiesterase 6A, cGMP-specific, rod, alpha (PDE6A), mRNA
2158	15174	28194	4.97	2.0E-79	4585863	NT	Homo sapiens phosphodiesterase 6A, cGMP-specific, rod, alpha (PDE6A), mRNA
2202	15217	28237	0.91	2.0E-79	AJ271408.1	NT	Homo sapiens mRNA for Fas-associated factor, FAF1 (Faf1 gene)
3933	16973	29887	0.83	2.0E-79	AF170482.1	NT	Homo sapiens chloride channel CLC4 (CLC4) mRNA, complete cds
4193	17224	30113	1.15	2.0E-79	AJ271408.1	NT	Homo sapiens mRNA for Fas-associated factor, FAF1 (Faf1 gene)
4716	17736	30628	0.97	2.0E-79	AL183206.2	NT	Homo sapiens chromosome 21 segment HS21C006
5754	18848		1.25	2.0E-79	AA312228.1	EST_HUMAN	EST182928 Jurkat T-cells VI Homo sapiens cDNA 5' end similar to C. elegans hypothetical protein, cosmid B0303.15
5815	18905	32088	0.88	2.0E-79	11181769	NT	Homo sapiens X transporter protein 3 (XT3), mRNA
6371	19439	32682	1.07	2.0E-79	AB020637.1	NT	Homo sapiens mRNA for KIAA0830 protein, partial cds
7153	18385	31273	0.7	2.0E-79	AF263613.1	NT	Homo sapiens membrane-associated calcium-independent phospholipase A2 gamma mRNA, complete cds
7373	20343	33684	1.74	2.0E-79	7382479	NT	Homo sapiens Rho GTPase activating protein 6 (ARHGAP6), transcript variant 4, mRNA
7373	20343	33695	1.74	2.0E-79	7382479	NT	Homo sapiens Rho GTPase activating protein 6 (ARHGAP6), transcript variant 4, mRNA
8437	21408	34818	1.13	2.0E-79	4506442	NT	Homo sapiens retinoblastoma-like 1 (p107) (RBL1) mRNA
8862	21829	35252	2.55	2.0E-79	11427428	NT	Homo sapiens hypothetical protein FLJ11006 (FLJ11006), mRNA
9118	22084	35512	0.46	2.0E-79	8923248	NT	Homo sapiens hypothetical protein FLJ20275 (FLJ20275), mRNA
9118	22084	35513	0.46	2.0E-79	8923248	NT	Homo sapiens hypothetical protein FLJ20275 (FLJ20275), mRNA
9357	22322	35749	1.1	2.0E-79	11432184	NT	Homo sapiens similar to ATPase, H ⁺ transporting, lysosomal (vacuolar proton pump) membrane sector associated protein MB-9 (H. sapiens) (LOC63961), mRNA
10452	23374	36865	3.12	2.0E-79	S72869.1	NT	H4(D10S170)-putative cytoskeletal protein [human, thyroid, mRNA, 3011 nt]
10452	23374	36866	3.12	2.0E-79	S72869.1	NT	H4(D10S170)-putative cytoskeletal protein [human, thyroid, mRNA, 3011 nt]
11368	24315	37840	3.86	2.0E-79	BE064386.1	EST_HUMAN	RC4-BT0310-110300-016-110 BT0310 Homo sapiens cDNA
11368	24315	37841	3.86	2.0E-79	BE064386.1	EST_HUMAN	RC4-BT0310-110300-016-110 BT0310 Homo sapiens cDNA
11666	24602		2.62	2.0E-79	AB036532.1	NT	Homo sapiens p53R2 gene for ribonucleotide reductase, exon 9 and complete cds
12207	18350	31295	3.21	2.0E-79	7662357	NT	Homo sapiens KIAA0879 protein (KIAA0879), mRNA
12293	25107	31837	4.8	2.0E-79	AB020640.1	NT	Homo sapiens mRNA for KIAA0833 protein, partial cds
12524	25254	31804	2.41	2.0E-79	11418322	NT	Homo sapiens cadherin EGF LAG seven-pass G-type receptor 1 (CERSR1), mRNA
6739	25666		3.26	1.0E-79	BF363071.1	EST_HUMAN	MRO-NN0087-260600-017-b10 NN0087 Homo sapiens cDNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6852	19905	33200	0.51	1.0E-79	AI613480.1	EST_HUMAN	U37e08.x1 NCL_CGAP_U12 Homo sapiens cDNA clone IMAGE:2281286 3' similar to TR:Q26623 Q26623
6852	19905	33201	0.51	1.0E-79	AI613480.1	EST_HUMAN	TEKTIN C1.;
8567	21555	34971	0.73	1.0E-79	BE394211.1	EST_HUMAN	U37e08.x1 NCL_CGAP_U12 Homo sapiens cDNA clone IMAGE:2281286 3' similar to TR:Q26623 Q26623
11944	24824	38419	2.64	1.0E-79	BF087405.1	EST_HUMAN	TEKTIN C1.;
3161	16217	29131	6.25	9.0E-80	AA725848.1	EST_HUMAN	QV2-HT0540-120900-358-405 HT0540 Homo sapiens cDNA
3161	16217	29132	6.26	9.0E-80	AA725848.1	EST_HUMAN	ai23e05.s1 Soares_testis_NHT Homo sapiens cDNA clone 1343848 3'
10373	23296	36772	1.02	9.0E-80	BE798603.1	EST_HUMAN	ai23e05.s1 Soares_testis_NHT Homo sapiens cDNA clone 1343848 3'
11608	24544	38104	8.28	9.0E-80	11433924	NT	601581652F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3638061 5'
11608	24544	38105	8.28	9.0E-80	11433924	NT	Homo sapiens solute carrier family 7 (cationic amino acid transporter, y ⁺ system), member 8 (SLC7A8), mRNA
3616	16660		1.22	8.0E-80	U94387.1	NT	Homo sapiens solute carrier family 7 (cationic amino acid transporter, y ⁺ system), member 8 (SLC7A8), mRNA
7862	20806	34183	2.95	8.0E-80	11422647	NT	Homo sapiens Y chromosome spermatogenesis candidate protein (RBM) pseudogene mRNA, partial cds
7862	20806	34184	2.95	8.0E-80	11422647	NT	Homo sapiens KIAA0724 gene product (KIAA0724), mRNA
8757	22698	36154	1.14	8.0E-80	6005921	NT	Homo sapiens KIAA0724 gene product (KIAA0724), mRNA
8757	22698	36155	1.14	8.0E-80	6005921	NT	Homo sapiens triple functional domain (PTPRF Interacting) (TRIO), mRNA
7166	18397	31242	0.58	7.0E-80	AF127882.1	NT	Homo sapiens triple functional domain (PTPRF Interacting) (TRIO), mRNA
							Callithrix jacchus olfactory receptor (CJA80) gene, partial cds
901	13956	28913	0.7	6.0E-80	AI422197.1	EST_HUMAN	tf58d02.x1 NCL_CGAP_Bm23 Homo sapiens cDNA clone IMAGE:2103459 3' similar to SW:NUEM_HUMAN
1650	14682	27655	2.17	6.0E-80	U64896.1	NT	Q16795 NADH-UBIQUINONE OXIDOREDUCTASE 39 KD SUBUNIT PRECURSOR ;
2307	15319	28338	1.17	6.0E-80	6631094	NT	Homo sapiens NRD convertase mRNA, complete cds
2307	15319	28339	1.17	6.0E-80	6631094	NT	Homo sapiens minichromosome maintenance deficient (S. cerevisiae) 3 (MCM3), mRNA
4314	17343	30225	1.1	6.0E-80	AB032981.1	NT	Homo sapiens minichromosome maintenance deficient (S. cerevisiae) 3 (MCM3), mRNA
4314	17343	30226	1.1	6.0E-80	AB032981.1	NT	Homo sapiens tubby like protein 3 (TULP3), mRNA
5899	19886	32177	1.32	6.0E-80	11421462	NT	Homo sapiens tubby like protein 3 (TULP3), mRNA
6194	19268	32503	3.12	6.0E-80	AJ404468.1	NT	Homo sapiens malate dehydrogenase 2, NAD (mitochondrial) (MDH2), mRNA
6355	19424	32666	3.81	6.0E-80	11436736	NT	Homo sapiens mRNA for KIAA1155 protein, partial cds
6403	19471		0.93	6.0E-80	7682393	NT	Homo sapiens mRNA for KIAA1155 protein, partial cds
6455	19520	32770	0.88	6.0E-80	M18533.1	NT	Homo sapiens tubby like protein 3 (TULP3), mRNA
9176	22142	35568	3.06	6.0E-80	11526464	NT	Homo sapiens KIAA0941 protein (KIAA0941), mRNA
							Homo sapiens dystrophin (DMD) mRNA, complete cds
							Homo sapiens G protein-coupled receptor 51 (GPR51), mRNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9176	22142	35569	3.06	6.0E-80	11528484	NT	Homo sapiens G protein-coupled receptor 51 (GPR51), mRNA
9373	22338	35768	1.56	6.0E-80	AL163301.2	NT	Homo sapiens chromosome 21 segment HS21C101
9714	22887	36125	0.94	6.0E-80	AF161495.1	NT	Homo sapiens HSPC146 mRNA, complete cds
9841	22777	36233	0.47	6.0E-80	AJ271735.1	NT	Homo sapiens Xq pseudautosomal region, segment 1/2
10220	23145	36834	1.55	6.0E-80	U20211.1	NT	Human cone photoreceptor cGMP-phosphodiesterase alpha' subunit gene, exon 21
11289	24239	37766	2.43	6.0E-80	11427366	NT	Homo sapiens brefeldin A-inhibited guanine nucleotide-exchange protein 1 (BIG1), mRNA
11558	24498	38054	20.37	6.0E-80	AF228730.1	NT	Homo sapiens Cyf19 mRNA, complete cds
12051	24924	38521	1.64	6.0E-80	AF102265.1	NT	Homo sapiens N-acetylglucosamine-phosphate mutase mRNA, complete cds
12304	25787		2.39	6.0E-80	AF240786.1	NT	Homo sapiens glutathione S-transferase theta 2 (GSTT2), and glutathione S-transferase theta 1 (GSTT1) genes, complete cds
12506	25243		6.41	6.0E-80	AB029900.1	NT	Homo sapiens CST gene for cerebroside sulfoltransferase, exon 1, 2, 3, 4, 5
12994	25914		4.47	6.0E-80	AJ13127.1	NT	Homo sapiens mRNA for sodium-glucose cotransporter (SGLT2 gene)
590	13657	26572	2.89	5.0E-80	4506228	NT	Homo sapiens proteasome (prosome, macropain) 26S subunit, non-A [Pase, 3 (PSMD3)] mRNA
836	13893	26848	1.49	5.0E-80	AF108830.1	NT	Homo sapiens serine-threonine protein kinase (MNBH) mRNA, complete cds
836	13893	26849	1.49	5.0E-80	AF108830.1	NT	Homo sapiens serine-threonine protein kinase (MNBH) mRNA, complete cds
1193	14233		0.96	5.0E-80	X91647.1	NT	H. sapiens ncx1 gene (exon 12)
1450	14483		2.21	5.0E-80	AL163283.2	NT	Homo sapiens chromosome 21 segment HS21C083
2369	15377	28400	1.92	5.0E-80	U83558.1	NT	Human [3]mb protein homolog mRNA, complete cds
2437	15444	28482	6.37	5.0E-80	AB037655.1	NT	Homo sapiens mRNA for KIAA1434 protein, partial cds
2806	15798	28816	5	5.0E-80	4504292	NT	Homo sapiens H3 histone family, member J (H3FJ) mRNA
4069	17105	29938	1.26	5.0E-80	AB019038.1	NT	Homo sapiens HMT-1 mRNA for beta-1,4 mannosyltransferase, complete cds
4069	17105	29999	1.26	5.0E-80	AB019038.1	NT	Homo sapiens HMT-1 mRNA for beta-1,4 mannosyltransferase, complete cds
4991	18006	30894	1.53	5.0E-80	AL163288.2	NT	Homo sapiens chromosome 21 segment HS21C068
8700	21688	35091	1.14	5.0E-80	9910293	NT	Mus musculus keratin complex 2, gene 6g (Krt2-6g), mRNA
9613	22617	36069	15.19	4.0E-80	F25915.1	EST_HUMAN	HSPD13155 HM3 Homo sapiens cDNA clone s4000045F03
218	13318		9.37	3.0E-80	AL163210.2	NT	Homo sapiens chromosome 21 segment HS21C010
4738	17758	30653	1.45	3.0E-80	BF085009.1	EST_HUMAN	PMO-GN0018-04090-002-E03 GN0018 Homo sapiens cDNA
4945	17961		3.11	3.0E-80	BE817465.1	EST_HUMAN	QV4-BN0263-040800-241-g10 BN0263 Homo sapiens cDNA
5919	19005	32197	2.02	3.0E-80	AI091675.1	EST_HUMAN	cc23et12.x1 Soares_NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:1667054 3' similar to TR:O36790 O36790 PIG-L;
1814	14841	27832	4.7	2.0E-80	R35321.1	EST_HUMAN	Y656a08.r1 Soares Infant brain 1N1B Homo sapiens cDNA clone IMAGE:380690 5'
1877	14902	27902	1.49	2.0E-80	AI444821.1	EST_HUMAN	RET4B7 subtracted retina cDNA library Homo sapiens cDNA clone RET4B7
2071	15088	28106	6.1	2.0E-80	AL043116.2	EST_HUMAN	DKFZp434D1323_r1 434 (synonym: htes3) Homo sapiens cDNA clone DKFZp434D1323 5'
6374	19442	32684	0.69	2.0E-80	AI923972.1	EST_HUMAN	vm49c10.x1 NCI_CGAP_Lu19 Homo sapiens cDNA clone IMAGE:2448786 3'

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6374	19442	32885	0.69	2.0E-80	A1923972.1	EST_HUMAN	wn49c10.x1 NCL CGAP_Lu19 Homo sapiens cDNA clone IMAGE:2448786 3'
6977	20200	33530	1.01	2.0E-80	AA582962.1	EST_HUMAN	nm80d01.s1 NCL CGAP_C68 Homo sapiens cDNA clone IMAGE:1090177 3'
7098	20032	33335	1.51	2.0E-80	11421930	NT	Homo sapiens Golgi transport complex protein (90 kDa) (GTC90), mRNA
7463	20429	33786	0.81	2.0E-80	T75215.1	EST_HUMAN	yc88f12.1 Soares infant brain 1N1B Homo sapiens cDNA clone IMAGE:22851 5' similar to
9514	22477	35922	1.22	2.0E-80	AW964270.1	EST_HUMAN	SP:K1CR_XENLA P08902 KERATIN, TYPE I CYTOSKELETAL ENDO B ;
10126	23052	36530	0.97	2.0E-80	AJ007379.1	NT	EST376343 MAGE resequences, MAGH Homo sapiens cDNA
11216	24169	37697	8.05	2.0E-80	AA393362.1	EST_HUMAN	Homo sapiens GGT gene, exon 6
340	13429		2.11	1.0E-80	AL163303.2	NT	z70f12.1 Soares testis_NHT Homo sapiens cDNA clone IMAGE:727727 5' similar to TR:G191315
800	13859	26806	1.95	1.0E-80	AF231820.1	NT	G191315 ANDROGEN-DEPENDENT EXPRESSED PROTEIN. ;
1971	14992		2.82	1.0E-80	A1732656.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C103
4857	17874	30762	0.78	1.0E-80	N96520.1	EST_HUMAN	Homo sapiens chromosome 21 unknown mRNA
5400	18503		3.62	1.0E-80	BE396616.1	EST_HUMAN	nm01f12.x5 NCL CGAP_C68 Homo sapiens cDNA clone IMAGE:1076495 3' similar to contains OFR.11 OFR
6083	19163	32375	6.24	1.0E-80	L10347.1	NT	repetitive element ;
6648	19704	32980	1.3	1.0E-80			z639g07.1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:294972 5' similar to contains
7414	20381	33732	1.09	1.0E-80	AJ224172.1	NT	Alu repetitive element
7824	20772	34148	2.6	1.0E-80	A1948731.1	EST_HUMAN	601274505F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3616433 5'
7824	20772	34149	2.6	1.0E-80	A1948731.1	EST_HUMAN	Human pro-alpha1 type II collagen (COL2A1) gene exons 1-54, complete cds
8573	21541	34961	1.17	1.0E-80	11421211	NT	Homo sapiens malate dehydrogenase 2, NAD (mitochondrial) (MDH2), nuclear gene encoding mitochondrial
9048	22014	35437	0.92	1.0E-80	11421211	NT	protein, mRNA
9048	22014	35438	0.92	1.0E-80	11421211	NT	Homo sapiens mRNA for lipophilin B
9640	22684	36032	1.26	1.0E-80	AF245219.1	NT	wq25c05.x1 NCL CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2472286 3'
9640	22684	36033	1.26	1.0E-80	AF245219.1	NT	wq25c05.x1 NCL CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2472286 3'
10791	23712	37214	1.12	1.0E-80	D63479.2	NT	Homo sapiens protein tyrosine phosphatase, receptor type, A (PTPRA), mRNA
11013	23978	37503	1.72	1.0E-80	11641276	NT	Homo sapiens protein tyrosine phosphatase, receptor type, A (PTPRA), mRNA
11013	23978	37504	1.72	1.0E-80	11641276	NT	Homo sapiens probable mannose binding C-type lectin DC-SIGNR mRNA, complete cds
11443	24386	37926	1.67	1.0E-80	8523939	NT	Homo sapiens mRNA for KIAA0145 protein, partial cds
12578	25287	31779	2.27	1.0E-80	11417901	NT	Homo sapiens similar to rat myomegalin (LOC64182), mRNA
11488	24431	37980	9.7	8.0E-81	BE394625.1	EST_HUMAN	Homo sapiens myosin, heavy polypeptide 2, skeletal muscle, adult (MYH2), mRNA
7464	20430	33787	2.97	7.0E-81	A1822115.1	EST_HUMAN	Homo sapiens merlinoma (disrupted in balanced translocation) 1 (MN1), mRNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4414	17441	30331	4.98	6.0E-81	BE26829.1	EST_HUMAN	601111970F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3352840 5'
4414	17441	30332	4.98	6.0E-81	BE26829.1	EST_HUMAN	601111970F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3352840 5'
5355	18460	31329	1.65	6.0E-81	4501848	NT	Homo sapiens ATP-binding cassette, sub-family A (ABC1), member 3 (ABCA3), mRNA
5355	18460	31330	1.65	6.0E-81	4501848	NT	Homo sapiens ATP-binding cassette, sub-family A (ABC1), member 3 (ABCA3), mRNA
7845	20792	34168	0.98	6.0E-81	AF038660.1	NT	Homo sapiens chromosome 1p33-p34 beta-1,4-galactosyltransferase mRNA, complete cds
9592	22554	36004	1.17	6.0E-81	AA360017.1	EST_HUMAN	EST69129 Fetal lung II Homo sapiens cDNA 5' end
12707	25364	31768	2.68	6.0E-81	BF679022.1	EST_HUMAN	602153966F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4294601 5'
12707	25364	31769	2.68	6.0E-81	BF679022.1	EST_HUMAN	602153966F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4294601 5'
2226	15240	28265	2.27	5.0E-81	BE288042.1	EST_HUMAN	601125505F1 NIH_MGC_8 Homo sapiens cDNA clone IMAGE:3345480 5'
8755	21723	35148	1.57	5.0E-81	AB007923.1	NT	Homo sapiens mRNA for KIAA0454 protein, partial cds
8755	21723	35147	1.57	5.0E-81	AB007923.1	NT	Homo sapiens mRNA for KIAA0454 protein, partial cds
10006	22933	36396	0.81	5.0E-81	M60316.1	NT	Human transforming growth factor-beta (tgf-beta) mRNA, complete cds
10006	22933	36397	0.81	5.0E-81	M60316.1	NT	Human transforming growth factor-beta (tgf-beta) mRNA, complete cds
11908	24789	38378	1.84	5.0E-81	9506834	NT	Homo sapiens hypothetical protein (FLJ11045), mRNA
703	13765	26700	1.21	4.0E-81	AI521435.1	EST_HUMAN	th60e12.x1 NCL_CGAP_Ov23 Homo sapiens cDNA clone IMAGE:2122702 3' similar to TR:Q85560 Q85560
1839	14886	27865	1.36	4.0E-81	AW779612.1	EST_HUMAN	hn98d02.x1 NCL_CGAP_Co14 Homo sapiens cDNA clone IMAGE:3035907 3' similar to SW:GCPG_BOVIN
3186	16241	28159	4.49	4.0E-81	AB037766.1	NT	P53620 COATOMER GAMMA SUBUNIT
3644	18887	29602	0.89	4.0E-81	AW004608.1	EST_HUMAN	Homo sapiens mRNA for KIAA1345 protein, partial cds
4187	17218	30104	1.85	4.0E-81	AF263306.1	NT	ws90h03.x1 NCL_CGAP_Co3 Homo sapiens cDNA clone IMAGE:2505269 3' similar to TR:O43815 O43815
4187	17218	30105	1.85	4.0E-81	AF263306.1	NT	STRATIN ;
4419	17446	30337	1.1	4.0E-81	8928209	NT	Homo sapiens rab3 interacting protein variant 2 mRNA, partial cds
7492	20457	33815	0.93	4.0E-81	4757893	NT	Homo sapiens rab3 interacting protein variant 2 mRNA, partial cds
7629	20589	33952	0.69	4.0E-81	11420544	NT	Homo sapiens hypothetical protein FLJ20220 (FLJ20220), mRNA
8630	21598	35019	2	4.0E-81	X08889.1	NT	Homo sapiens calcium channel, voltage-dependent, L type, alpha 2/delta subunit (CACNA2) mRNA
8890	21856	35276	3.34	4.0E-81	U20197.1	NT	Homo sapiens eis variant gene 1 (ETV1), mRNA
8890	21856	35277	3.34	4.0E-81	U20197.1	NT	Human mRNA for amyloid A4(761) protein
9581	22543	35994	3.82	4.0E-81	AB018001.1	NT	Human cone photoreceptor cGMP-phosphodiesterase alpha' subunit gene, exons 2 and 3
10481	23383	36876	1.82	4.0E-81	11425281	NT	Human cone photoreceptor cGMP-phosphodiesterase alpha' subunit gene, exons 2 and 3
10531	23453	36950	0.67	4.0E-81	11439065	NT	Homo sapiens mRNA for Death-associated protein kinase 2, complete cds
10531	23453	36951	0.67	4.0E-81	11439065	NT	Homo sapiens ligase I, DNA, ATP-dependent (LIG1), mRNA
							Homo sapiens acyl-Coenzyme A dehydrogenase family, member 8 (ACAD8), mRNA
							Homo sapiens acyl-Coenzyme A dehydrogenase family, member 8 (ACAD8), mRNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
11519	24460	38010	3.39	4.0E-81	4759085	NT	Homo sapiens vesicle trafficking protein sec22b (SEC22B) mRNA
11519	24460	38011	3.39	4.0E-81	4759085	NT	Homo sapiens vesicle trafficking protein sec22b (SEC22B) mRNA
12200	25853	31438	3.45	4.0E-81	11417862	NT	Homo sapiens calcineurin binding protein 1 (KIAA0330) mRNA
12200	25853	31439	3.45	4.0E-81	11417862	NT	Homo sapiens calcineurin binding protein 1 (KIAA0330) mRNA
12737	25389	31753	1.71	4.0E-81	11417871	NT	Homo sapiens beta-ureidopropionase (LOC51733) mRNA
12737	25389	31754	1.71	4.0E-81	11417871	NT	Homo sapiens beta-ureidopropionase (LOC51733) mRNA
12878	25472	31729	3.69	4.0E-81	11417974	NT	Homo sapiens transcobalamin II; macrocytic anemia (TCN2) mRNA
1272	14307	27266	10.2	3.0E-81	Y18000.1	NT	Homo sapiens NF2 gene
1272	14307	27267	10.2	3.0E-81	Y18000.1	NT	Homo sapiens NF2 gene
2380	15388	28412	1.65	3.0E-81	AF077188.1	NT	Homo sapiens cullin 4A (CUL4A) mRNA, complete cds
3004	16082	28980	5.19	3.0E-81	4506280	NT	Homo sapiens pleiotrophin (heparin binding growth factor 8, neurite growth-promoting factor 1) (PTN) mRNA
3004	16082	28981	5.19	3.0E-81	4506280	NT	Homo sapiens pleiotrophin (heparin binding growth factor 8, neurite growth-promoting factor 1) (PTN) mRNA
2844	15904	28828	2.48	2.0E-81	BE784636.1	EST_HUMAN	601474072F1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3877121 5'
2844	15904	28829	2.48	2.0E-81	BE784636.1	EST_HUMAN	601474072F1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3877121 5'
3787	18828	29735	0.88	2.0E-81	AW611542.1	EST_HUMAN	hg85601.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2852384 3'
8290	21259	34670	0.53	2.0E-81	8923639	NT	Homo sapiens hypothetical protein (LOC55588) mRNA
13032	18828	29735	2.55	2.0E-81	AW611542.1	EST_HUMAN	hg85601.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2852384 3'
4543	17566	30453	3.12	1.0E-81	AA040370.1	EST_HUMAN	2k45h09.r1 Soares_pregnant_uterus_NHHPU Homo sapiens cDNA clone IMAGE:485825 5' similar to PIR:552437 S82437 CDP-diacylglycerol synthase - fruit fly
4675	17696	30583	9.34	1.0E-81	BE047398.1	EST_HUMAN	tz45c04.y1 NCI_CGAP_Bim52 Homo sapiens cDNA clone IMAGE:2291526 5'
5308	19326	38811	3.31	1.0E-81	U87928.1	NT	Human acortilate hydratase (ACO2) gene, exon 3
5427	18530	31409	3.6	1.0E-81	11432866	NT	Homo sapiens polymerase (DNA directed), gamma (POLG) mRNA
5427	18530	31410	3.6	1.0E-81	11432866	NT	Homo sapiens polymerase (DNA directed), gamma (POLG) mRNA
5580	18676	31639	0.83	1.0E-81	AA255569.1	EST_HUMAN	2r85d08.r1 Soares_NHHPU_S1 Homo sapiens cDNA clone IMAGE:882475 5' similar to SW:PRI2_HUMAN P-49843 DNA PRIMASE 58 KD SUBUNIT
5737	18831	32009	3.37	1.0E-81	U52351.1	NT	Homo sapiens arm-repeat protein NPRAP/neurjungin (CTNND2) mRNA, partial cds
5737	18831	32010	3.37	1.0E-81	U52351.1	NT	Homo sapiens arm-repeat protein NPRAP/neurjungin (CTNND2) mRNA, partial cds
6269	19342	32575	1.55	1.0E-81	BF674841.1	EST_HUMAN	602137864F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4274535 5'
6999	19756	33032	0.56	1.0E-81	11420995	NT	Homo sapiens phosphodiesterase 1C, calmodulin-dependent (70kD) (PDE1C) mRNA
6999	19756	33033	0.56	1.0E-81	11420995	NT	Homo sapiens phosphodiesterase 1C, calmodulin-dependent (70kD) (PDE1C) mRNA
6902	19954	33251	1.26	1.0E-81	AJ133269.1	NT	Homo sapiens caveolin-1/2 locus, Contig1, D7S622, genes CAV2 (exons 1, 2a, and 2b), CAV1 (exons 1 and 2)

Table 4

Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8049	20986	34382	7.53	1.0E-81	11432966	NT	Homo sapiens polymerase (DNA directed), gamma (POLO), mRNA
10134	23060	36537	7.65	1.0E-81	BE56278.1	EST_HUMAN	601645031F1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:3930228 5'
10134	23060	36538	7.65	1.0E-81	BE56278.1	EST_HUMAN	601645031F1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:3930228 5'
10328	23252	36731	4.63	1.0E-81	BE564387.1	EST_HUMAN	601343180F1 NIH_MGC_53 Homo sapiens cDNA clone IMAGE:3685483 5'
							act14d06.s1 StrataGene HeLa cell s3 937216 Homo sapiens cDNA clone IMAGE:868427 3' similar to SW:YB36_YEAST P88126 HYPOTHETICAL 60.5 KD PROTEIN IN RPS101-RPS13 INTERGENIC REGION:
10463	23385	36878	1.09	1.0E-81	AA630784.1	EST_HUMAN	601577339F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3838280 5'
10465	23387	36880	3.01	1.0E-81	BE744545.1	EST_HUMAN	601577339F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3838280 5'
10465	23387	36881	3.01	1.0E-81	BE744545.1	EST_HUMAN	601577339F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3838280 5'
10874	23794	37296	1.7	1.0E-81	AW897560.1	EST_HUMAN	CM3-NN0059-140400-147-at12 NN0059 Homo sapiens cDNA
11425	24369	37905	2.9	1.0E-81	AW844986.1	EST_HUMAN	MRQ-CT0008-250599-019 CT0008 Homo sapiens cDNA
11425	24369	37906	2.9	1.0E-81	AW844986.1	EST_HUMAN	MRQ-CT0008-250599-019 CT0008 Homo sapiens cDNA
11429	24373	37911	6.55	1.0E-81	AW798167.1	EST_HUMAN	RC3-UM0048-290200-011-a06 UM0048 Homo sapiens cDNA
11429	24373	37912	6.55	1.0E-81	AW798167.1	EST_HUMAN	RC3-UM0048-290200-011-a06 UM0048 Homo sapiens cDNA
11851	24734	38321	2.11	1.0E-81	BF204263.1	EST_HUMAN	601867714F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4110459 5'
12414	25185	31822	4.59	1.0E-81	11418138	NT	Homo sapiens phorbol (similar to apolipoprotein B mRNA editing protein) (DU742C19.2), mRNA
13	13133	26031	0.94	8.0E-82	AF161406.1	NT	Homo sapiens HSPC288 mRNA, partial cds
107	13133	26031	2.07	8.0E-82	AF161406.1	NT	Homo sapiens HSPC288 mRNA, partial cds
263	13559	26284	2.7	8.0E-82	U08988.1	NT	Human CRFB4 gene, partial cds
815	13673	26921	14.95	8.0E-82	U08988.1	NT	Human CRFB4 gene, partial cds
888	13943	26901	1.44	8.0E-82	U08988.1	NT	Human CRFB4 gene, partial cds
1487	14520	27493	1.36	8.0E-82	AB037748.1	NT	Homo sapiens mRNA for KIAA1327 protein, partial cds
1666	14698	27674	1.7	8.0E-82	6715601	NT	Homo sapiens glutathione peroxidase 5 (epididymal androgen-related protein) (GPX5), transcript variant 2, mRNA
4114	17148	30040	0.62	8.0E-82	4504116	NT	Homo sapiens glutamate receptor, ionotropic, kainate 1 (GRIK1) mRNA
4272	17301	30181	0.75	8.0E-82	8923432	NT	Homo sapiens hypothetical protein FLJ20461 (FLJ20461), mRNA
1444	14477		2.53	7.0E-82	BF035327.1	EST_HUMAN	601458331F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3862086 5'
2777	15769	28789	1.8	7.0E-82	AU144050.1	EST_HUMAN	AU144050 HEMBA1 Homo sapiens cDNA clone HEMBA1000752 3'
12053	24928	38524	1.75	7.0E-82	AA663747.1	EST_HUMAN	ae63e04.s1 StrataGene schizo brain S11 Homo sapiens cDNA clone IMAGE:968342 3'
1680	14712	27690	26.07	4.0E-82	AF081484.1	NT	Homo sapiens alpha-tubulin isoform 1 mRNA, complete cds
5574	18670	31632	0.89	4.0E-82	BF351691.1	EST_HUMAN	QV2-HT0540-120900-362-08 HT0540 Homo sapiens cDNA
5574	18670	31633	0.89	4.0E-82	BF351691.1	EST_HUMAN	QV2-HT0540-120900-362-08 HT0540 Homo sapiens cDNA
5851	18941	32126	0.99	4.0E-82	M25833.1	NT	Human von Willebrand factor gene, exon 9

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Table 4
Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
12025	24901	38496	7.32	4.0E-82	A1937300.1	EST_HUMAN	wp75e09.x1 NCJ_CGAP_Bm25 Homo sapiens cDNA clone IMAGE:2467624 3' similar to TR:O75276
12657	25337		3.69	4.0E-82	A1937300.1	EST_HUMAN	O75276 PKD1 ;
						NT	Homo sapiens presenilin-1 gene, exons 1 and 2
277	13373	26301	16.34	3.0E-82	4502166	NT	Homo sapiens amyloid beta (A4) precursor protein (protease nexin-II, Alzheimer disease) (APP), mRNA
704	13766	26701	2.76	3.0E-82	BE005706.1	EST_HUMAN	RC2-BN0120-010400-013-02 BN0120 Homo sapiens cDNA
788	13847	26794	10.4	3.0E-82	5174702	NT	Homo sapiens transforming growth factor beta-activated kinase-binding protein 1 (TAB1), mRNA
871	13927	26885	6.11	3.0E-82	4502166	NT	Homo sapiens amyloid beta (A4) precursor protein (protease nexin-II, Alzheimer disease) (APP), mRNA
1062	14108		53.62	3.0E-82	AA725848.1	EST_HUMAN	ai23e05.x1 Soares testis NHT Homo sapiens cDNA clone 1343648 3'
1357	14382	27363	1.01	3.0E-82	AW875073.1	EST_HUMAN	RC6-PT0001-190100-021-B02 PT0001 Homo sapiens cDNA
1462	14495	27499	2.51	3.0E-82	AL163285.2	NT	Homo sapiens chromosome 21 segment HS21C085
1917	14941	27937	1.95	3.0E-82	BE813232.1	EST_HUMAN	RC1-BN0005-260700-018-g04 BN0005 Homo sapiens cDNA
2023	15043	28056	1.2	3.0E-82	4501922	NT	Homo sapiens adenylate cyclase activating polypeptide 1 (pituitary) receptor type 1 (ADCYAP1R1), mRNA
3285	16339		2.31	3.0E-82	5453811	NT	Homo sapiens neurotrophic tyrosine kinase, receptor, type 2 (NTRK2), mRNA
8492	21460	34877	2.7	3.0E-82	11425206	NT	Homo sapiens ankyrin-like with transmembrane domains 1 (ANKTM1), mRNA
8902	21868	35292	0.77	3.0E-82	11432889	NT	Homo sapiens contactin 6 (CNTN6), mRNA
8902	21868	35293	0.77	3.0E-82	11432889	NT	Homo sapiens contactin 6 (CNTN6), mRNA
10183	23108	36590	3.98	3.0E-82	AB029000.1	NT	Homo sapiens mRNA for KIAA1077 protein, partial cds
10183	23108	36591	3.98	3.0E-82	AB029000.1	NT	Homo sapiens mRNA for KIAA1077 protein, partial cds
12108	24978	38577	1.6	3.0E-82	11432889	NT	Homo sapiens contactin 6 (CNTN6), mRNA
12108	24978	38578	1.6	3.0E-82	11432889	NT	Homo sapiens contactin 6 (CNTN6), mRNA
599	13666	26579	1.96	2.0E-82	AB023216.1	NT	Homo sapiens mRNA for KIAA0999 protein, partial cds
599	13666	26580	1.96	2.0E-82	AB023216.1	NT	Homo sapiens mRNA for KIAA0999 protein, partial cds
1694	14724	27707	2.13	2.0E-82	AL048390.1	EST_HUMAN	DKFZp434M17.1 434 (synonym: hsa3) Homo sapiens cDNA clone DKFZp434M17.5
2891	16049	28970	0.76	2.0E-82	AL163201.2	NT	Homo sapiens chromosome 21 segment HS21C001
3860	18899	29802	1.07	2.0E-82	DB7875.1	NT	Homo sapiens DNA for amyloid precursor protein, complete cds
4052	17089	29884	0.85	2.0E-82	U76833.1	NT	Human integral membrane serine protease Seprease mRNA, complete cds
4261	17290	30171	1.07	2.0E-82	4504116	NT	Homo sapiens glutamate receptor, ionotropic, kainate 1 (GRIK1), mRNA
4588	17610	30505	1.09	2.0E-82	AB029019.1	NT	Homo sapiens mRNA for KIAA1096 protein, partial cds
4588	17610	30506	1.09	2.0E-82	AB029019.1	NT	Homo sapiens mRNA for KIAA1096 protein, partial cds
4904	17921	30813	3.21	2.0E-82	AF045555.1	NT	Homo sapiens wbscr1 (WBSCR1) and wbscr5 (WBSCR5) genes, complete cds, alternatively spliced and replication factor C subunit 2 (RFC2) gene, complete cds

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Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5117	18127	31002	1.53	2.0E-82	4507580	NT	Homo sapiens tumor necrosis factor receptor superfamily, member 5 (TNFRSF5) mRNA
5117	18127	31003	1.53	2.0E-82	4507580	NT	Homo sapiens tumor necrosis factor receptor superfamily, member 5 (TNFRSF5) mRNA
5546	18643	31593	3.46	2.0E-82	AB018270.1	NT	Homo sapiens mRNA for KIAA0727 protein, partial cds
6299	19371	32610	4.99	2.0E-82	AF234892.1	NT	Homo sapiens FAM4A1 splice variant a (FAM4A1) mRNA, complete cds
7945	26004		0.86	2.0E-82	A1476428.1	EST_HUMAN	fm21g05.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2157272 3'
8104	21041	34440	0.89	2.0E-82	8923130	NT	Homo sapiens hypothetical protein FLJ20128 (FLJ20128), mRNA
8689	21557	34973	0.48	2.0E-82	11431845	NT	Homo sapiens nucleotide binding protein 1 (E.coli MinD like) (NUBP1), mRNA
8648	21618	35038	1.94	2.0E-82	11321570	NT	Homo sapiens slit (Drosophila) homolog 3 (SLIT3), mRNA
9017	21983	35402	0.47	2.0E-82	7657340	NT	Homo sapiens microchidia (mouse) homolog (MORC), mRNA
9017	21983	35403	0.47	2.0E-82	7657340	NT	Homo sapiens microchidia (mouse) homolog (MORC), mRNA
10468	23390	36884	1.66	2.0E-82	Y08032.1	NT	Human endogenous retrovirus-K, LTR U5 and gag gene
10468	23390	36885	1.66	2.0E-82	Y08032.1	NT	Human endogenous retrovirus-K, LTR U5 and gag gene
11600	24538	38095	3.95	2.0E-82	11417191	NT	Homo sapiens leucylcystinyl aminopeptidase (LNPEP), mRNA
11600	24538	38096	3.95	2.0E-82	11417191	NT	Homo sapiens leucylcystinyl aminopeptidase (LNPEP), mRNA
11638	24575	38140	2.31	2.0E-82	U80736.1	NT	Homo sapiens CAGF9 mRNA, partial cds
11638	24575	38141	2.31	2.0E-82	U80736.1	NT	Homo sapiens CAGF9 mRNA, partial cds
12227	25062		1.94	2.0E-82	N94950.1	EST_HUMAN	zb31d10.s1 Soares_parathyroid_tumor_NbHPA Homo sapiens cDNA clone IMAGE:305203 3'
12760	25403		4.39	2.0E-82	AA011278.1	EST_HUMAN	z01g09.r1 Soares_fetal_liver_spleen_1NPLS_S1 Homo sapiens cDNA clone IMAGE:429568 5'
13064	25598		1.53	2.0E-82	11418097	NT	Homo sapiens SRY (sex determining region Y-box 10) (SOX10), mRNA
594	13661	26574	1.27	1.0E-82	11545921	NT	Homo sapiens SRY (sex determining region Y-box 10) (SOX10), mRNA
1213	14251		1.09	1.0E-82	BE885106.1	EST_HUMAN	601510859F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3912207 5'
1290	14325	27286	2.11	1.0E-82	BE084386.1	EST_HUMAN	RC4-BT0310-110300-015-f10 BT0310 Homo sapiens cDNA
1291	14326	27287	1.07	1.0E-82	AB011110.2	NT	Homo sapiens mRNA for KIAA0538 protein, partial cds
9294	22260	35689	1.09	1.0E-82	AB037898.1	NT	Homo sapiens mRNA for KIAA1417 protein, partial cds
10011	22938	36403	0.56	1.0E-82	AB014562.1	NT	Homo sapiens mRNA for KIAA0662 protein, partial cds
10606	23528		1.24	1.0E-82	BF515938.1	EST_HUMAN	UIH-BW1-ecaf-03-0-UJ.s1 NCI_CGAP_Sub7 Homo sapiens cDNA clone IMAGE:3084053 3'
11097	24057	37581	1.87	1.0E-82	AL163209.2	NT	Homo sapiens chromosome 21 segment HS21C009
9065	22031	35454	4.87	9.0E-83	BF672220.1	EST_HUMAN	602150403F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4281561 5'
10637	23559	37058	0.62	9.0E-83	BE253347.1	EST_HUMAN	601117160F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3357734 5'
1412	14445	27417	1.55	8.0E-83	BE383973.1	EST_HUMAN	601273346F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3614362 5'
1691	15820	27702	4.08	8.0E-83	N66951.1	EST_HUMAN	za48f12.s1 Soares_fetal_liver_spleen_1NPLS Homo sapiens cDNA clone IMAGE:295823 3'
1359	14394	27364	0.99	7.0E-83	AW385629.1	EST_HUMAN	QV4-LT0016-271299-068-h11 L10016 Homo sapiens cDNA
							no12h01.s1 NCI_CGAP_Phe1 Homo sapiens cDNA clone IMAGE:1100497 3' similar to contains Alu repetitive element
2876	15935		1.92	7.0E-83	AA584655.1	EST_HUMAN	

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4853	17870		7.64	7.0E-83	BF221813.1	EST_HUMAN	7a37a07.x1 NCI_CGAP_P28 Homo sapiens cDNA clone IMAGE:3647893 3' similar to TR:Q9Y316 Q9Y316
6169	19244	32476	0.73	7.0E-83	11428657	NT	Homo sapiens KIAA0100 gene product (KIAA0100), mRNA
403	13476	28410	3.07	6.0E-83	M33320.1	NT	Human platelet Glycoprotein IIb (GPIIb) gene, exons 2-29
1802	14830	27817	1.08	6.0E-83	AW573088.1	EST_HUMAN	h31103.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2933525 3' similar to
3030	16083	29008	0.64	6.0E-83	AW816405.1	EST_HUMAN	SW:YBEB_HAEN P44471 HYPOTHETICAL PROTEIN H10034. ;
3064	16121		0.97	6.0E-83	AF231919.1	NT	QV4-S10234-181198-037-05 ST0234 Homo sapiens cDNA
3083	16140	29051	1.03	6.0E-83	AA701457.1	EST_HUMAN	Homo sapiens chromosome 21 unknown mRNA
3575	16620	29541	2.54	6.0E-83	11430241	NT	259c05.s1 Soares_fetal_liver_spleen_INFLS_S1 Homo sapiens cDNA clone IMAGE:435080 3'
5167	18176	31054	1.2	6.0E-83	4827033	NT	Homo sapiens hypothetical protein FLJ10379 (FLJ10379), mRNA
5366	18471	31342	1.53	6.0E-83	4507866	NT	Homo sapiens tumor necrosis factor (ligand) superfamily, member 18 (TNFSF18) mRNA
6139	19215	32444	1.32	6.0E-83	AJ010770.1	NT	Homo sapiens VAMP (vesicle-associated membrane protein)-associated protein A (33kD) (VAPA) mRNA, and translated products
7745	20699	34065	2.1	6.0E-83	11422024	NT	Homo sapiens hyperion gene, exons 1-50
10035	22962	36430	2.5	6.0E-83	4505314	NT	Homo sapiens met proto-oncogene (hepatocyte growth factor receptor) (MET), mRNA
10127	23053	36531	0.76	6.0E-83	11430847	NT	Homo sapiens myomesin (M-protein) 2 (165kD) (MYO2), mRNA
10127	23053	36532	0.76	6.0E-83	11430647	NT	Homo sapiens pre-mRNA splicing factor similar to S. cerevisiae Prp18 (PRP18), mRNA
11859	24741		2.01	6.0E-83	AA486105.1	EST_HUMAN	Homo sapiens pre-mRNA splicing factor similar to S. cerevisiae Prp18 (PRP18), mRNA
12179	25027		5.85	6.0E-83	AF240786.1	NT	ab14e10.s1 Stragene lung (#937210) Homo sapiens cDNA clone IMAGE:840810 3' similar to contains
945	13998		1.42	5.0E-83	U17883.1	NT	THR12 THR repetitive element;
2066	15823		1	5.0E-83	AF006905.1	NT	Homo sapiens glutathione S-transferase theta 2 (GSTT2) and glutathione S-transferase theta 1 (GSTT1) genes, complete cds
3652	16695	29610	0.97	6.0E-83	AL133207.2	NT	Human succinate dehydrogenase iron-protein subunit (sdhB) gene, exon 5
3826	16966	29879	1.02	5.0E-83	4885190	NT	Homo sapiens 26S proteasome regulatory subunit (SUG2) mRNA, complete cds
5115	18125	31000	14.32	5.0E-83	4557013	NT	Novel human gene mapping to chromosome X
5115	18125	31001	14.32	5.0E-83	4557013	NT	Homo sapiens deoxyribonuclease 1 (DNASE1), mRNA
5245	18253	31124	0.93	5.0E-83	4505802	NT	Homo sapiens catalase (CAT) mRNA
641	13707	26628	2.28	4.0E-83	AF224669.1	NT	Homo sapiens catalase (CAT) mRNA
3525	16571	29494	1	4.0E-83	BE88078.1	EST_HUMAN	Homo sapiens phosphatidylinositol 3-kinase, catalytic, gamma polypeptide (PIK3CG) mRNA
989	14050		6.39	3.0E-83	AA368311.1	EST_HUMAN	Homo sapiens phosphatidylinositol 3-kinase, catalytic, gamma polypeptide (PIK3CG) mRNA
							Homo sapiens mannosidase, beta A, lysosomal (MANBA) gene, and ubiquitin-conjugating enzyme E2D 3 (UBE2D3) genes, complete cds
							601511580F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3913195 5'
							EST179542 Placenta1 Homo sapiens cDNA similar to endogenous retrovirus ERV9

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2788	15780		1.82	3.0E-83	AA632654.1	EST_HUMAN	np87c07.s1 NCI_CGAP_Thy1 Homo sapiens cDNA clone IMAGE:1133292 similar to contains THR:12 THR
6730	19786		0.72	3.0E-83	A121723.1	EST_HUMAN	replicative element ; q173s06.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1755682 3'
1816	14843	27834	1.88	2.0E-83	AA993492.1	EST_HUMAN	o164g05.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1621592 3' similar to TR:Q92614 Q92614 MYELOBLAST KIAA0216 ;
1816	14843	27835	1.88	2.0E-83	AA993492.1	EST_HUMAN	o164g05.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1621592 3' similar to TR:Q92614 Q92614 MYELOBLAST KIAA0216 ;
1942	14966	27963	3.01	2.0E-83	N66951.1	EST_HUMAN	Q92614 MYELOBLAST KIAA0216 ;
2864	15924	28843	1.36	2.0E-83	BE828694.1	EST_HUMAN	Q92614 MYELOBLAST KIAA0216 ;
3282	16336		2.14	2.0E-83	11430834	NT	Q92614 MYELOBLAST KIAA0216 ;
3788	16829		0.87	2.0E-83	AL163202.2	NT	Q92614 MYELOBLAST KIAA0216 ;
4363	17390	30272	9.76	2.0E-83	AF202879.1	NT	Q92614 MYELOBLAST KIAA0216 ;
4681	17702	30590	6.03	2.0E-83	7706398	NT	Q92614 MYELOBLAST KIAA0216 ;
4681	17702	30591	6.03	2.0E-83	7706398	NT	Q92614 MYELOBLAST KIAA0216 ;
5343	18448	31319	0.94	2.0E-83	U06679.1	NT	Q92614 MYELOBLAST KIAA0216 ;
5547	18644	31584	1.09	2.0E-83	11024711	NT	Q92614 MYELOBLAST KIAA0216 ;
5547	18644	31585	1.09	2.0E-83	11024711	NT	Q92614 MYELOBLAST KIAA0216 ;
5945	19031	32224	0.54	2.0E-83	11428081	NT	Q92614 MYELOBLAST KIAA0216 ;
6076	19157	32369	1.21	2.0E-83	BE985401.1	EST_HUMAN	Q92614 MYELOBLAST KIAA0216 ;
7669	20628	33992	5.47	2.0E-83	AF129533.1	NT	Q92614 MYELOBLAST KIAA0216 ;
8103	21039	34438	0.52	2.0E-83	BF105097.1	EST_HUMAN	Q92614 MYELOBLAST KIAA0216 ;
8175	21145	34551	0.55	2.0E-83	AB001025.1	NT	Q92614 MYELOBLAST KIAA0216 ;
8175	21145	34552	0.55	2.0E-83	AB001025.1	NT	Q92614 MYELOBLAST KIAA0216 ;
8319	21288	34702	1.46	2.0E-83	U66707.1	NT	Q92614 MYELOBLAST KIAA0216 ;
8657	21625	35045	2.5	2.0E-83	AF011920.1	NT	Q92614 MYELOBLAST KIAA0216 ;
8657	21625	35046	2.5	2.0E-83	AF011920.1	NT	Q92614 MYELOBLAST KIAA0216 ;
9952	22879	36342	0.48	2.0E-83	5453381	NT	Q92614 MYELOBLAST KIAA0216 ;
9952	22879	36343	0.46	2.0E-83	5453381	NT	Q92614 MYELOBLAST KIAA0216 ;
10242	23167	36654	0.43	2.0E-83	BF128748.1	EST_HUMAN	Q92614 MYELOBLAST KIAA0216 ;
10394	23316	36795	2.53	2.0E-83	M22094.1	NT	Q92614 MYELOBLAST KIAA0216 ;
10394	23316	36796	2.53	2.0E-83	M22094.1	NT	Q92614 MYELOBLAST KIAA0216 ;
10475	23397	36895	1.2	2.0E-83	AU117659.1	EST_HUMAN	Q92614 MYELOBLAST KIAA0216 ;
10549	23471	36966	0.74	2.0E-83	AW506000.1	EST_HUMAN	Q92614 MYELOBLAST KIAA0216 ;
11195	24150	37681	3.48	2.0E-83	11436448	NT	Q92614 MYELOBLAST KIAA0216 ;

Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
11272	24224	37749	1.84	2.0E-83	AL134452.1	EST_HUMAN	DKFZp547J135_r1 547 (synonym: hibr1) Homo sapiens cDNA clone DKFZp547J135 5'
11272	24224	37750	1.84	2.0E-83	AL134452.1	EST_HUMAN	DKFZp547J135_r1 547 (synonym: hibr1) Homo sapiens cDNA clone DKFZp547J135 5'
12802	25429		4.91	2.0E-83	AB011399.1	NT	Homo sapiens gene for AF-6, complete cds
1410	14443	27414	1.56	1.0E-83	4504326	NT	Homo sapiens hydroxycyl-Coenzyme A dehydrogenase/3-ketocyl-Coenzyme A thiolase/enoyl-Coenzyme A hydratase (trifunctional protein), beta subunit (HADHB) mRNA
1410	14443	27415	1.56	1.0E-83	4504326	NT	Homo sapiens hydroxycyl-Coenzyme A dehydrogenase/3-ketocyl-Coenzyme A thiolase/enoyl-Coenzyme A hydratase (trifunctional protein), beta subunit (HADHB) mRNA
1453	14486	27461	0.93	1.0E-83	AF105087.1	NT	Homo sapiens lipopolysaccharide-binding protein (LBP) mRNA, complete cds
1453	14486	27462	0.93	1.0E-83	AF105087.1	NT	Homo sapiens lipopolysaccharide-binding protein (LBP) mRNA, complete cds
2665	15662	28681	1.16	1.0E-83	BE863690.1	EST_HUMAN	601507376F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3908754 5'
3198	16253	29173	0.65	1.0E-83	7682349	NT	Homo sapiens cell recognition molecule Caspr2 (KIAA0868), mRNA
3882	16822	28830	3.33	1.0E-83	AF053768.1	NT	Rattus norvegicus brain specific cortactin-binding protein CBF90 mRNA, partial cds
4273	17302	30182	2.31	1.0E-83	Z28822.1	NT	H. sapiens gene for mitochondrial dodecenoyl-CoA delta-isoemerase, exon 3
6854	19907	33203	1.53	1.0E-83	AI027614.1	EST_HUMAN	9198508.X1 Soares, testis_NHT Homo sapiens cDNA clone IMAGE:3958853 5'
3810	18650	29758	3.98	7.0E-84	BE901209.1	EST_HUMAN	601676023F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3958853 5'
1298	14333	27294	4.11	8.0E-84	BE838864.1	EST_HUMAN	RC2-FN0118-200600-011-g05 FN0119 Homo sapiens cDNA
1298	14333	27295	4.11	8.0E-84	BE838864.1	EST_HUMAN	RC2-FN0118-200600-011-g05 FN0119 Homo sapiens cDNA
2407	15414	28438	5.78	8.0E-84	AA776574.1	EST_HUMAN	aa86a03.s1 Stralagene schizo brain S11 Homo sapiens cDNA clone IMAGE:971020 3'
5311	18328		1.9	6.0E-84	AL042863.2	EST_HUMAN	DKFZp434H0322_r1 434 (synonym: htes3) Homo sapiens cDNA clone DKFZp434H0322 5'
5596	18692	31662	1.69	6.0E-84	AA897339.1	EST_HUMAN	aa47g03.s1 Soares, NFL_T, GBC S1 Homo sapiens cDNA clone IMAGE:1460500 3' similar to gb:M14338
5743	18837	32018	1.09	6.0E-84	11426718	NT	VITAMIN K-DEPENDENT PROTEIN S PRECURSOR (HUMAN); Homo sapiens acyl LDL receptor; SREC= scavenger receptor expressed by endothelial cells (SREC), mRNA
5743	18837	32019	1.09	6.0E-84	11426718	NT	Homo sapiens acyl LDL receptor; SREC= scavenger receptor expressed by endothelial cells (SREC), mRNA
7714	20871	34038	3.35	6.0E-84	BE910371.1	EST_HUMAN	PMO-L1T0019-190600-004-F02 LT0019 Homo sapiens cDNA
7855	20866	34289	0.89	6.0E-84	AF033391.1	NT	Homo sapiens pre-mRNA splicing factor (PRP16) mRNA, complete cds
8408	21377	34783	2.05	6.0E-84	BE770189.1	EST_HUMAN	PM4-FT0054-160600-004-e10 FT0054 Homo sapiens cDNA
715	13777	26712	0.81	5.0E-84	AA382811.1	EST_HUMAN	EST66094 Testis 1 Homo sapiens cDNA 5' end
3027	15084		1.54	5.0E-84	AF109718.1	NT	Homo sapiens chromosome 3 subtelomeric region
6227	19301	32534	0.49	5.0E-84	AA167678.1	EST_HUMAN	zc39s07_r1 Stralagene hNT neuron (#637233) Homo sapiens cDNA clone IMAGE:632100 5' similar to TR:G483915 G483915 RETROTRANSPOSABLE L1 ELEMENT LRE2 FROM CHROMOSOME 1Q.;

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Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
11871	24753	38334	2.06	5.0E-84	11428740	NT	Homo sapiens regulatory factor X, 3 (influences HLA class II expression) (RFX3), mRNA
11964	24843	38437	2.29	5.0E-84	AB032957.1	NT	Homo sapiens mRNA for KIAA1131 protein, partial cds
11964	24843	38438	2.29	5.0E-84	AB032957.1	NT	Homo sapiens mRNA for KIAA1131 protein, partial cds
1409	14442	27413	1.68	4.0E-84	AI685321.1	EST_HUMAN	wa76c04.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2302086 3' similar to SW:NRDC_HUMAN O43847 NARDILYSIN PRECURSOR;
4987	18002	30891	0.99	4.0E-84	4505928	NT	Homo sapiens polymerase (DNA-directed), alpha (70KD) (POLA2), mRNA
4988	18003	30892	2.19	4.0E-84	AF069601.2	NT	Homo sapiens myosin light chain kinase isoform 2 (MLCK) mRNA, complete cds
5335	18440	31193	0.53	4.0E-84	AF022835.1	NT	Homo sapiens multidrug resistance protein (MRP), exon 13
5642	18738	31902	1.28	4.0E-84	11386168	NT	Homo sapiens protein tyrosine phosphatase, receptor type, G (PTPRG), mRNA
5642	18738	31903	1.28	4.0E-84	11386168	NT	Homo sapiens histone deacetylase 3 (HDAC3) gene, complete cds
6399	19467	32714	1.89	4.0E-84	AF059650.1	NT	Homo sapiens KIAA0783 gene product (KIAA0783), mRNA
7909	20852	34239	12.53	4.0E-84	11421326	NT	Homo sapiens discs, large (Drosophila) homolog 2 (chapsyn-110) (DLG2) mRNA
9262	22228	35658	0.9	4.0E-84	4557526	NT	Homo sapiens discs, large (Drosophila) homolog 2 (chapsyn-110) (DLG2) mRNA
9262	22228	35659	0.9	4.0E-84	4557526	NT	Homo sapiens discs, large (Drosophila) homolog 2 (chapsyn-110) (DLG2) mRNA
11263	24215	37739	5.34	4.0E-84	AB032956.1	NT	Homo sapiens mRNA for KIAA1130 protein, partial cds
316	13408	26334	1.92	3.0E-84	AF026200.1	NT	Homo sapiens Bach1 protein homolog mRNA, partial cds
1157	14199	27149	5.95	3.0E-84	4758081	NT	Homo sapiens chondroitin sulfate proteoglycan 2 (versican) (GSPG2) mRNA
1977	14998	28000	1.24	3.0E-84	5453855	NT	Homo sapiens pericentriolar material 1 (PCM1) mRNA
2024	15044	28057	3.11	3.0E-84	AL068860.1	NT	Novel human mRNA containing Zinc finger C2H2 type domains
3604	16849	29565	1.15	3.0E-84	AB026898.1	NT	Homo sapiens DNA, DLEC1 to ORCTL4 gene region, section 1/2 (DLEC1, ORCTL3, ORCTL4 genes, complete cds)
3762	16803	29715	6.28	3.0E-84	AF014459.1	NT	Homo sapiens X-linked juvenile retinoschisis precursor protein (XLR51) mRNA, complete cds
11226	24179		17.2	3.0E-84	AI983801.1	EST_HUMAN	wu20d05.x1 Soares Dieckgraebe_colon_NHCD Homo sapiens cDNA clone IMAGE:2520585 3' similar to gb:L05093.60S RIBOSOMAL PROTEIN L18A (HUMAN);
2116	15132	28153	5.68	2.0E-84	BE065397.1	EST_HUMAN	GM1-BT0795-190600-272-b08 BT0795 Homo sapiens cDNA
2115	15132	28154	5.68	2.0E-84	BE065397.1	EST_HUMAN	GM1-BT0795-190600-272-b08 BT0795 Homo sapiens cDNA
2954	16012	28939	7.98	2.0E-84	AF036043.1	NT	Homo sapiens myelin transcription factor 1-like (MYT1L) mRNA, complete cds
2973	16031	28954	1.35	2.0E-84	X89211.1	NT	H. sapiens DNA for endogenous retroviral like element
5604	18700	31671	0.88	2.0E-84	BF511575.1	EST_HUMAN	UI-H-B14-ad-a-02-Q-UI.s1 NCI CGAP Sub8 Homo sapiens cDNA clone IMAGE:3084963 3'
5604	18700	31672	0.88	2.0E-84	BF511575.1	EST_HUMAN	UI-H-B14-ad-a-02-Q-UI.s1 NCI CGAP Sub8 Homo sapiens cDNA clone IMAGE:3084963 3'
6793	19847	33132	0.88	2.0E-84	H63370.1	EST_HUMAN	Yf56e11.s1 Soares fetal liver spleen 1NFS Homo sapiens cDNA clone IMAGE:209324 3'
8392	21361		1.62	2.0E-84	AL163204.2	NT	qm87c09.x1 NCI CGAP Lu5 Homo sapiens cDNA clone IMAGE:1895728 3'
8728	21896	35121	0.56	2.0E-84	AL163204.2	NT	Homo sapiens chromosome 21 segment HS21C004
8728	21896	35122	0.56	2.0E-84	AL163204.2	NT	Homo sapiens chromosome 21 segment HS21C004

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9701	22854	36108	0.99	2.0E-84	AU120280.1	EST_HUMAN	AU120280 HEMBB1 Homo sapiens cDNA clone HEMBB1000339 5'
10089	23015	36491	0.55	2.0E-84	H22841.1	EST_HUMAN	ym49e1.1 Soares infant brain 1N1B Homo sapiens cDNA clone IMAGE:51383 5' similar to SP:APOH_RAT P26644 BETA-2-GLYCOPROTEIN I;
12445	25206	31829	3.26	2.0E-84	BF448000.1	EST_HUMAN	nae30a02.X1 Lupski_sympathetic_trunk Homo sapiens cDNA clone IMAGE:4080251 3' similar to TR:Q9UGS3 Q9UGS3 DJ756G23.1;
12445	25206	31830	3.26	2.0E-84	BF448000.1	EST_HUMAN	nae30a02.X1 Lupski_sympathetic_trunk Homo sapiens cDNA clone IMAGE:4080251 3' similar to TR:Q9UGS3 Q9UGS3 DJ756G23.1;
312	13404	28330	1.44	1.0E-84	AF114488.1	NT	Homo sapiens Intersectin short isoform (ITSN) mRNA, complete cds Homo sapiens tyrosine 3-monooxygenase/tyrosine 5-monooxygenase activation protein, zeta polypeptide (VWHAZ) mRNA
551	13621	28541	15.79	1.0E-84	4507952	NT	Homo sapiens complement component 5 (C5), mRNA
721	13783		1.16	1.0E-84	11427631	NT	am85b11.s1 Stratagene schizo brain S11 Homo sapiens cDNA clone IMAGE:1628885 3'
1286	14331	27292	3.1	1.0E-84	AA984379.1	EST_HUMAN	60130800F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3628257 5'
2070	15087	28105	2.34	1.0E-84	BE382137.1	EST_HUMAN	Homo sapiens pericentriolar material 1 (PCM1), mRNA
2232	15246	28269	1.27	1.0E-84	11427197	NT	nm1206.s1 NCL_CGAP_S51 Homo sapiens cDNA clone IMAGE:1239108 3'
3764	16806	29717	2.47	1.0E-84	AA720851.1	EST_HUMAN	Homo sapiens 959 kb contig between AML1 and CBR1 on chromosome 21q22; segment 1/3
4446	17472	30360	3.92	1.0E-84	AJ229041.1	NT	DKFZp434N0323_r1 434 (synonym: htes3) Homo sapiens cDNA clone DKFZp434N0323 5'
4728	17748	30639	2.66	1.0E-84	AL043314.2	EST_HUMAN	DKFZp434N0323_r1 434 (synonym: htes3) Homo sapiens cDNA clone DKFZp434N0323 5'
4728	17748	30640	2.66	1.0E-84	AL043314.2	EST_HUMAN	Homo sapiens 959 kb contig between AML1 and CBR1 on chromosome 21q22; segment 1/3
4949	17472	30360	2.12	1.0E-84	AJ229041.1	NT	Homo sapiens speckle-type POZ protein (SPOP), mRNA
6029	19112	32314	0.86	1.0E-84	11434422	NT	utethe water channel=28 kDa erythrocyte integral membrane protein homolog [human, uterus, mRNA, 1340 nt]
6314	19385	32627	1.38	1.0E-84	S73482.1	NT	Novel human gene mapping to chromosome 13
7064	20086	33394	1.44	1.0E-84	AL049784.1	NT	Novel human gene mapping to chromosome 13
7064	20086	33395	1.44	1.0E-84	AL049784.1	NT	Novel human gene mapping to chromosome 13
7314	20285	33626	2.66	1.0E-84	AL049784.1	NT	Novel human gene mapping to chromosome 13
7708	20665	34032	4.72	1.0E-84	8989994	NT	Homo sapiens polymerase (DNA directed), alpha (POLA), mRNA
7814	20763	34139	0.63	1.0E-84	11430846	NT	Homo sapiens NGF-A binding protein 1 (ERG1 binding protein 1) (NAB1), mRNA
7859	20763	34139	2.13	1.0E-84	11430846	NT	Homo sapiens NGF-A binding protein 1 (ERG1 binding protein 1) (NAB1), mRNA
9893	22846		2.91	1.0E-84	5031684	NT	Homo sapiens nuclear transport factor 2 (placental protein 15) (PP15), mRNA
10128	23054	36533	0.62	1.0E-84	AF224511.1	NT	Homo sapiens Ca2+-binding protein CABP3 (CABP3) gene, exon 6 and partial cds
10150	18337	31285	2.65	1.0E-84	4507848	NT	Homo sapiens ubiquitin specific protease 13 (isopeptidase T-3) (USP13), mRNA
10150	18337	31286	2.65	1.0E-84	4507848	NT	Homo sapiens ubiquitin specific protease 13 (isopeptidase T-3) (USP13), mRNA
12121	20285	33626	2.67	1.0E-84	AL049784.1	NT	Novel human gene mapping to chromosome 13
12324	26126		2.03	1.0E-84	11417812	NT	Homo sapiens putrefactive receptor P2X-like 1, orphan receptor (P2RXL1), mRNA

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
12436	25201	31825	2.32	1.0E-84	11418185	NT	Homo sapiens aconitase 2, mitochondrial (ACO2), mRNA
968	14020		1.9	9.0E-85	AL163209.2	NT	Homo sapiens chromosome 21 segment HS21C009
1074	14119	27069	2.21	9.0E-85	U51432.1	NT	Homo sapiens nuclear protein Skip mRNA, complete cds
1074	14119	27070	2.21	9.0E-85	U51432.1	NT	Homo sapiens nuclear protein Skip mRNA, complete cds
1581	14614	27586	1.31	9.0E-85	M33282.1	NT	Human plasminogen gene, exon 7
1581	14614	27587	1.31	9.0E-85	M33282.1	NT	Human plasminogen gene, exon 7
1684	14715	27695	2.95	9.0E-85	7657020	NT	Homo sapiens DKFZp434P211 protein (DKFZP434P211), mRNA
4280	17309	30188	1.11	9.0E-85	AL163280.2	NT	Homo sapiens chromosome 21 segment HS21C080
4913	17930	30821	1.05	9.0E-85	5901879	NT	Homo sapiens heat shock transcription factor 2 binding protein (HSF2BP), mRNA
4950	17965	30855	1	9.0E-85	AL163268.2	NT	Homo sapiens chromosome 21 segment HS21C088
1138	14181	27132	13.33	7.0E-85	L05094.1	NT	Homo sapiens ribosomal protein L27 mRNA, complete cds
11958	24837		9.76	7.0E-85	AF113210.1	NT	Homo sapiens MSTP030 mRNA, complete cds
11745	24630	38209	2.51	6.0E-85	11438573	NT	Homo sapiens DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 10 (RNA helicase) (DDX10), mRNA
11745	24630	38210	2.51	6.0E-85	11438573	NT	Homo sapiens DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 10 (RNA helicase) (DDX10), mRNA
2340	15350	28371	1.67	5.0E-85	AL163284.2	NT	Homo sapiens chromosome 21 segment HS21C084
5526	18625	31560	1.37	5.0E-85	BF035674.1	EST_HUMAN	601458646F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3862402 5'
5528	18625	31561	1.37	5.0E-85	BF035674.1	EST_HUMAN	601458646F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3862402 5'
13030	18344		6.19	5.0E-85	AF211189.1	NT	Homo sapiens T-type calcium channel alpha1 subunit Alpha1I-a isoform (CACNA1I) mRNA, complete cds
6271	19344	32576	1.42	4.0E-85	BF677910.1	EST_HUMAN	602084730F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4249087 5'
6271	19344	32577	1.42	4.0E-85	BF677910.1	EST_HUMAN	602084730F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4249087 5'
7013	20139	33456	0.58	4.0E-85	AI628119.1	EST_HUMAN	ly84g01.x1 NCL_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2285808 3'
10937	23857		1.35	4.0E-85	BE079263.1	EST_HUMAN	RC1-BT0623-120200-011-c07 BT0623 Homo sapiens cDNA
12375	25772		1.31	4.0E-85	Z18867.1	EST_HUMAN	HSDHEG003 Stratagene cDNA library Human heart, cat#936208 Homo sapiens cDNA clone HEG003
1302	14338	27301	1.02	3.0E-85	AF096197.1	NT	Homo sapiens protein phosphatase 2A BR gamma subunit gene, exon 6
1795	14924	27808	3.9	3.0E-85	T97495.1	EST_HUMAN	ye53g09.1 Soares fetal liver spleen 1NF1S Homo sapiens cDNA clone IMAGE:121504 5'
4935	17951	30842	1.37	3.0E-85	11024695	NT	Homo sapiens F-box only protein 24 (FBXO24), mRNA
4935	17951	30843	1.37	3.0E-85	11024695	NT	Homo sapiens F-box only protein 24 (FBXO24), mRNA
5475	18576	31485	0.65	3.0E-85	11436001	NT	Homo sapiens lacrimal proline rich protein (LPRP), mRNA
6204	19278	32511	0.66	3.0E-85	11422024	NT	Homo sapiens met proto-oncogene (hepatocyte growth factor receptor) (MET), mRNA
6257	19330	32560	5.69	3.0E-85	7662309	NT	Homo sapiens KIAA0783 gene product (KIAA0783), mRNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6257	19330	32561	5.69	3.0E-85	7662309	NT	Homo sapiens KIA07933 gene product (KIA07933), mRNA
7140	20116		7.73	3.0E-85	AJ404468.1	NT	Homo sapiens mRNA for dynein heavy chain (DNAH9 gene)
7626	20586	33949	0.88	3.0E-85	11416870	NT	Homo sapiens GTPase regulator associated with the focal adhesion kinase pp125(FAK); KIAA0621 protein (KIAA0621), mRNA
8204	21174	34584	1.64	3.0E-85	U44953.1	NT	Homo sapiens DENN mRNA, complete cds
8853	21820	35240	1.06	3.0E-85	11525829	NT	Homo sapiens CGI-81 protein (LOC51108), mRNA
9329	22284	35723	3.37	3.0E-85	11430889	NT	Homo sapiens phospholipase C, epsilon (PLCE), mRNA
9661	22818	36272	1.03	3.0E-85	11421422	NT	Homo sapiens small nuclear ribonucleoprotein polypeptide B' (SNRNPB2), mRNA
9661	22818	36273	1.03	3.0E-85	11421422	NT	Homo sapiens small nuclear ribonucleoprotein polypeptide B'' (SNRNPB2), mRNA
10849	23769	37268	1.16	3.0E-85	AF08942.1	NT	Homo sapiens phospholipid scramblase mRNA, complete cds
11834	24717	38303	1.72	3.0E-85	5031660	NT	Homo sapiens EGF-like repeats and discoidin-like domains 3 (EDIL3), mRNA
12919	25495		2.14	3.0E-85	11418177	NT	Homo sapiens Ran GTPase activating protein 1 (RANGAP1), mRNA
964	14016	26970	0.87	2.0E-85	7657269	NT	Homo sapiens KIA0929 protein Mx2 interacting nuclear target (MINT) homolog (KIA0929), mRNA
1041	14087	27039	2.52	2.0E-85	AF248540.1	NT	Homo sapiens intersecin 2 (SH3D1B) mRNA, complete cds
1418	14451	27424	8.49	2.0E-85	5174775	NT	Homo sapiens apolipoprotein C-II (APOC2) mRNA
1418	14451	27425	8.49	2.0E-85	5174775	NT	Homo sapiens apolipoprotein C-II (APOC2) mRNA
2239	15253	28277	1.8	2.0E-85	U10525.1	NT	Human DNA polymerase beta gene, exons 12 and 13
2834	14375		14.69	2.0E-85	7657468	NT	Homo sapiens similar to rat integral membrane glycoprotein POM121 (POM121L1), mRNA
3035	16093	29011	1.16	2.0E-85	M30938.1	NT	Human Ku (p70/p80) subunit mRNA, complete cds
4361	17388	30270	4.83	2.0E-85	4503880	NT	Homo sapiens plasminogen (PLG) mRNA
4848	17964	30854	0.93	2.0E-85	AL163284.2	NT	Homo sapiens chromosome 21 segment HS21C084
5178	18187	31064	1.37	2.0E-85	4502212	NT	Homo sapiens arginase, liver (ARG1) mRNA
9628	22572	36022	2.67	2.0E-85	A1760820.1	EST_HUMAN	w87h08.x1 NCJ_CGAP_Kid12 Homo sapiens cDNA clone IMAGE:2398431 3' similar to contains element
10007	22834	36398	0.94	2.0E-85	A1914456.1	EST_HUMAN	MSR1 repetitive element
10825	23547	37048	1.31	2.0E-85	A1886384.1	EST_HUMAN	w449d03.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2331461 3'
2295	15307		2.51	1.0E-85	BE794306.1	EST_HUMAN	wm94d12.x1 NCJ_CGAP_U12 Homo sapiens cDNA clone IMAGE:2443607 3'
2403	15410	28434	6.6	1.0E-85	BE618392.1	EST_HUMAN	601591416F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3945818 5'
2403	15410	28435	6.6	1.0E-85	BE618392.1	EST_HUMAN	601462817F1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:3868021 5'
8091	21027	34428	0.52	1.0E-85	BE062951.1	EST_HUMAN	601462817F1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:3868021 5'
10140	23066	36542	2.41	1.0E-85	BE257917.1	EST_HUMAN	MRO-BT0284-221199-002-003 BT0284 Homo sapiens cDNA
10571	23493	36985	0.53	1.0E-85	AW813525.1	EST_HUMAN	601109739F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3350563 5'
11269	24221	37745	2.01	1.0E-85	AA778785.1	EST_HUMAN	RC1-S10196-081095-011-405 ST0196 Homo sapiens cDNA
							z44503.s1 Soares_fetal_liver_spleen_INFLS_S1 Homo sapiens cDNA clone IMAGE:463245 3'